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GenCore version 5 Copyright (c) 1993 - 2005 C protein search, using sw model April 18, 2005, 19:58:50; Sea	US-10-627-685A-1 120 1 CXIXNQXCXQXLDDCCSXXCX BLOSUM62DX Gapop 10.0 , Gapext 0.5 2105692 seqs, 386760381	of hits satisfying chosen parameters q length: 0 eq length: 20000000000. eq ingth: 20000000000. eq ingth: Annimum Match 0% insting first 100 summaries	A_Geneseq_16Dec04:* 1. geneseqp1980s:* 2. geneseqp2000s:* 4. geneseqp2000s:* 5. geneseqp2001s:* 6. geneseqp2003s:* 7. geneseqp2003s:* 8. geneseqp2003s:*	is the number of eater than or equal erived by analysis Query Match Length DB	120 100.0 27 4 AAU10208 120 100.0 27 4 AAU10195 120 100.0 27 4 AAU10195 120 100.0 27 4 AAU10195 120 100.0 27 4 AAU10196 120 100.0 27 4 AAU10196 120 100.0 27 4 AAU10196 120 100.0 27 4 AAU10202 120 100.0 27 4 AAU10202 120 100.0 27 4 AAU10204 120 100.0 27 6 AAE38345 120 100.0 27 6 AAE38345 120 100.0 27 6 AAE38345 120 100.0 27 6 AAE38335 120 100.0 27 6 AAE38336 120 100.0 27 6 AAE38336
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AAU10200 standard; peptide; 27 AA.

RESULT 2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     potassium channels and can be e.g. autoimmune diseases.
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Abb07821 Constitut
Adi16933 Human NOV
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used to augment neurotransmitter release in
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                                                         ALIGNMENTS
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'note= "disulphide bond"
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/note= "disulphide bond"
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Matches 17; Conserv
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Disulfide-bond
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                                                                                               Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; R2A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappa-
                                                                                                                                                                                                                                                         /note= "The C-terminus is either a carboxyl group or an
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                                                                      Snail Kappa-conotoxin PVIIA analogue R2A
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20-JUL-2000; 2000US-0219438P.
                                                                                                                                                                                                                                                                          amide group"
                                         (first entry)
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                                                                                                                                                          Conus purpurascens.
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Les 18; Conserv
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             AAU10200;
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(COGN-) COGNETIX INC
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Synthetic.
                             Cornell-Bell AH,
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                                       Jones RR;
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/note= "Other= Phe, Tyr, meta-Tyr, ortho-Tyr, nor-Tyr,
mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr,
nitro-Tyr, (D,L)-Trp, neo-Trp or (D,L)-halo-Trp"
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                                                                Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac i cerebral ischaemia; ocular ischaemia; asthma.
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                                               Snail Kappa-conotoxin PVIIA analogue #1.
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                            (first entry)
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                                                                                                       Conus purpurascens.
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                            16-JAN-2002
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         AAU10195
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The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention
                                                                                                                                           Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappaconotoxin PVIIA peptide.
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Mccabe RT;
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   Temple DL,
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   Pemberton KB,
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20-JUL-2000; 2000US-0219438P.
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ses 27; Conservative
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The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with channel, especially cardiac schaemed by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia, and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; K19A.
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activating a KATP channel by administering to an individual a kappa-
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Pred. No. 0.00084;
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66.7%; E
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20-JUL-2000; 2000US-0219438P.
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                                                                              Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappa-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; F9M.
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amide group"
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Pred. No. 0.00084;
9; Mismatches 0;
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20-JUL-2000; 2000US-0219438P.
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Best Local Similarity 66.7
Matches 18; Conservative
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                         WPI; 2001-648090/74.
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The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappa-
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                                                                                                              ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention
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20-JUL-2000; 2000US-0219438P
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amide group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Treating disorders associated with radical depolarization of excitable
radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention
                                                                                                                                          Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RT;
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                                                                                                            27;
                                                                                                                                      Indels
                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Layer RT,
                                                                                                            Score 120; DB 4;
Pred. No. 0.00084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Temple DL,
                                                                                                                                      9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                    Snail Kappa-conotoxin PVIIA analogue K25A.
                                                                                                                                                                    27
                                                                                                                                                                                    'note= "Hyroxyproline"
                                                                                                                                                                    1 CXIXNOXCXQXLDDCCSXXCNXXNXCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 27; 46pp; English
                                                                                                                                                                                                                                                                          AAU10202 standard; peptide; 27
                                                                                                         100.0%;
ilarity 66.7%; Conservative 9
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20-JUL-2000; 2000US-0219438P.
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                                                                                                          Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                purpurascens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cornell-Bell AH,
                                                                              Sequence 27 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                          AAU10202;
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                                                                                                                                                                                                                                                                                                                Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; R22A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappa-conotoxin PVIIA peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treating disorders associated with radical depolarization of excitable
                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mccabe RT;
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0
                         100.0%; Score 120; DB 4; Length 27; 66.7%; Pred. No. 0.00084; ive 9; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 27;
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Pred. No. 0.00084;
9; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                    Snail Kappa-conotoxin PVIIA analogue R22A.
                                                                                     1 CXIXNOXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                        |:|||||:||:||:|||||||:|||:|||:|||CRIXNQKCFQHLDDCCSRKCNRFNACV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "Hyroxyproline"
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                                                                                                                                                                                           AAU10197 standard; peptide; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-SEP-2000; 2000WO-US025827.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amide group"
                                                                                                                                                                                                                                                       (first entry)
                                         Local Similarity 66.7
nes 18; Conservative
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Synthetic.
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Sequence 27
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                                                                                                                                                                                                                         AAU10197;
                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                            Best Loc
Matches
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The invention relates to treating disorders associated with radical compensation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, conlar ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
                                                                                                                                                                                                                                                                                                                                                                    Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; coular ischaemia; asthma; F9Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappaconotoxin PVIIA peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Temple DL,
                                                                                                                                                                                                                                                                                                                        Snail Kappa-conotoxin PVIIA analogue F9Y
                       1 CXIXNOXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
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                                                                                                                                                                     AAU10206 standard; peptide; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-SEP-1999; 99US-0155135P.
20-JUL-2000; 2000US-0219438P.
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Best Local Similarity
Matches 18; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             purpurascens.
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Gaps

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66.7%;

18; Conservative

Local Similarity

Best Loca Matches

us-10-627-685a-1.rag

(first entry)

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Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; F9A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappaconotoxin PVIIA peptide.
                                                 Snail Kappa, conotoxin PVIIA analogue F9A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 27; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                            Cornell-Bell AH, Pemberton KB,
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20-JUL-2000; 2000US-0219438P.
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                                                                                                                           Conus purpurascens.
Synthetic.
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                           16-JAN-2002
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AAU10201;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conctoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conctoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular analogue of the invention
                                                                                                                                                  cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      asthma comprises
                                                                                                                                                                                                                                                                                or an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   membrane e.g. cardiac, cerebral and ocular ischemia and asthma compr
activating a KATP channel by administering to an individual a kappa-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mccabe RT;
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                                                                                                                                      Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 120; DB 4; Length 27; 66.7%; Pred. No. 0.00084; ive 9; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Layer RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Temple DL,
                                                                                                             Snail Kappa-conotoxin PVIIA analogue R2Q.
                                                                                                                                                                                                                                                    'note= "Hyroxyproline"
                                                                                                                                                                                                                           Location/Qualifiers
                                    AAU10207 standard; peptide; 27 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pemberton KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 28; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                           22-SEP-1999; 99US-0155135P.
20-JUL-2000; 2000US-0219438P.
                                                                                                                                                                                                                                                                                          amide group"
                                                                                                                                                                                                                                                                                                                                                                    21-SEP-2000; 2000WO-US025827
                                                                                     (first entry)
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Best Local Similarity 66.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            conotoxin PVIIA peptide.
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                                                                                   16-JAN-2002
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                                                                                                                                                                                                     Synthetic
                                                            AAU10207;
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             RESULT 11
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Mccabe RT;

Layer RT,

Temple DL,

/note= "The C-terminus is either a carboxyl group or an

amide group"

'note= "Hyroxyproline"

Location/Qualifiers

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The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-contoxan PVIIA (Kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention
                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                Score 120; DB 4; Length 27
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                                                                                                                                                                                                                                                                                                                            9; Mismatches
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Matches 18; Conservative
                                                                                                                                                                                                                                   Sequence 27 AA;
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Gaps

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CXIXNOXCXQXLDDCCSXXCNXXNXCV 27

8 셤

COIXNOKCFOHLDDCCSRKCNRFNKCV

AAU10201 standard; peptide; 27 AA.

RESULT 12 AAU10201 ID AAU1 XX /note= "The C-terminus is either a carboxyl group or an

amide group"

WO200121648-A1

29-MAR-2001

'note= "Hyroxyproline" Location/Qualifiers

Key Modified-site Modified-site

Conus purpurascens.

Synthetic

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conctoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and astebma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention
                Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; K7A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappaconotoxin PVIIA peptide.
                                                                                                                                                                                   'note= "The C-terminus is either a carboxyl group or an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       Mccabe RT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 27;
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                                                                                                                                                                                                                                                                                                                                                                                                      Temple DL, Layer RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 120; DB 4;
Pred. No. 0.00084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Mismatches
              Purple cone snail; kappa-conotoxin PVIIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CXIXNOXCXQXLDDCCSXXCNXXNXCV 27
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                                                                                                                                                      note= "Hyroxyproline"
                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                    Pemberton KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 28; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
66.7%; F
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                                                                                                                                                                                                                                                                                                                          99US-0155135P
                                                                                                                                                                                                                                                                                                                                        20-JUL-2000; 2000US-0219438P
                                                                                                                                                                                                   amide group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 66.7"
                                                                                                                                                                                                                                                                                                                                                                     (COGN-) COGNETIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-648090/74.
                                                                            Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                 Cornell-Bell AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 27 AA;
                                                                                                                                                                                                                               WO200121648-A1
                                                                                                                                      Modified-site
                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                        22-SEP-1999;
                                                                                                                                                                                                                                                              29-MAR-2001
                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                   Jones RR
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Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappa-conotoxin PVIIA peptide.

Claim 1; Page 28; 46pp; English.

Mccabe RT;

Layer RT,

Temple DL,

Cornell-Bell AH, Pemberton KE,

Jones RR;

WPI; 2001-648090/74.

(COGN-) COGNETIX INC

21-SEP-2000; 2000WO-US025827 22-SEP-1999; 99US-0155135P 20-JUL-2000; 2000US-0219438P

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                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-contoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; R2K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 120; DB 4; 63.0%; Pred. No. 0.00084;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Snail Kappa-conotoxin PVIIA analogue R2K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |:|:|:|:||:||:|CRIANQKCFQHLDDCCSRKCNRFNKCV 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU10203 standard; peptide; 27 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 63.0°
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conus purpurascens
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU10203;
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Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; O4A.

Snail Kappa-conotoxin PVIIA analogue 04A

(first entry)

16-JAN-2002

AAU10218;

AAU10218 standard; peptide; 27

RESULT 14 AAU1021 Mcintosh JM;

Temple DL,

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Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
                                                                                                                                                                                                                                                                                                                                                        invention relates to kappa-PVIIA-related conotoxins and their use as
                                                                                                                                                                                                                                                                                                                                                                       organ protectants. The invertion also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, acute heart failure, peripheral circulation disturbances, hypertension, angins, cerebral vasospasm accompanying subarachnoid haemorrhage, anxiety disorder, escrebral ischaemic, coronary artery bypass graft (CARG) surgery, ischaemic heart disease, aethma and congestive heart failure. The presensequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conus purpurascens kappa-PVIIA analogue peptide, K7A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 120; DB 6; 63.0%; Pred. No. 0.00084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CXIXNOXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                     Disclosure; Page 7; 32pp; English
                                                                                                                                                                      Jones RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE38344 standard; peptide; 27
                                        28-JAN-2003; 2003WO-US002384
                                                                           29-JAN-2002; 2002US-0352219P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 63.0
Matches 17; Conservative
                                                                                                                COGNETIX INC.
UNIV UTAH RES
                                                                                                                                                                      Pemberton-Goodman KB,
                                                                                                                                                                                                                            WPI; 2003-679464/64.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 27 AA;
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Modified-site
     07-AUG-2003
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                                                                                                                                                                                         Olivera BM;
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                                                                                                                (COGN-)
                                                                                                                                 (UTAH )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Purple cone snail; kappa-PVIIA-related conotoxin, urinary incontinence; ischaemic heart disease; cerebral ischaemia, anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
                                    'note= "The C-terminus is either a carboxyl group or an
                                                                                                                                                                                                                                                                                                                                                                                              excitable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PVIIA) peptide or its analogue, derivative or physiologically active salt. The conctoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                            depolarization of excital ischemia and asthma computo an individual a kappa
                                                                                                                                                                                                                                                                                                   Mccabe RT;
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                                                                                                                                                                                                                                                                                                   Layer RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conus purpurascens kappa-PVIIA analogue peptide, K25A.
                                                                                                                                                                                                                                                                                                 Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                          Treating disorders associated with radical membrane e.g. cardiac, cerebral and ocular activating a KATP channel by administering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |:||||:|:||:||:||CKIXNQKCFOHLDDCCSRKCNRFNKCV 27
/note= "Hyroxyproline"
27
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                                                                                                                                                                                                                                                                                                 Cornell-Bell AH, Pemberton KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 27; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE38342 standard; peptide; 27
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                                                                                                                                                                                                       22-SEP-1999; 99US-0155135P
20-JUL-2000; 2000US-0219438P
                                                                                                                                                                  21-SEP-2000; 2000WO-US025827
                                                         amide group'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.7%;
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Best Local Similarity 66.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    conotoxin PVIIA peptide.
                                                                                                                                                                                                                                                             (COGN-) COGNETIX INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 27 AA;
                                                                                            WO200121648-A1
                   Modified-site
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Modified-site
                                                                                                                                                                                                                                                                                                                   Jones RR;
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27

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6; Length 27;

Olivera BM;

us-10-627-685a-1.rag

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Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
                                                                                                                                                                                                      organ protectants. The invertion also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, nephropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral vasospasm accompanying subarachnoid haemorrhage, anxiety disorder, ischaemia, coronary artery bypass graft (CARG) surgery, ischaemic heart disease, asthma and congestive heart failure. The present sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
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                                                                                                                                                                                        invention relates to kappa-PVIIA-related conotoxins and
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                                                                                                                                                 Disclosure, Page 6; 32pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                         WPI; 2003-679464/64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 27 AA;
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Modified-site
  Olivera BM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide
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                                                                                                                                                                                                                                                                            The invention relates to kappa-PVIIA-related conotoxins and their use as organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, peripheral circulation disturbances, hypertension, angina, carebral existence accompanying subarachnoid haemorrhage, arxiety disorder, cerebral ischaemia, coronary artery bypass graft (CABG) surgery, ischaemic heart disease, asthma and congestive heart failure. The present sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
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                                                                                                                                                                             Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
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                                                                               Mcintosh JM;
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                                                                               Temple DL,
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                                                                                                                                                                                                                                             Disclosure; Page 7; 32pp; English.
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                                                                             Јопев КМ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pemberton-Goodman KE, Jones RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE38336 standard; peptide; 27
                                   FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-JAN-2003; 2003WO-US002384
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           (COGN-) COGNETIX INC. (UTAH ) UNIV UTAH RES
                                                                        Pemberton-Goodman KE,
                                                                                                                                        WPI; 2003-679464/64.
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Best Local Similarity
Matches 17; Conserv
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Disclosure, Page 6; 32pp; English.
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63.0%; P
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UNIV UTAH RES
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Best Local Similarity
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                                                                                                                                                        Sequence 27 AA;
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                                                                                                                                 peptide
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                                                 use as
                                            The invention relates to kappa-PVIIA-related conotoxins and their use as organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, nephropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral vasospasm accompanying subarachnoid haemorrhage, anxiety disorder, cerebral ischaemia, connary arrety bypass graff (CABG) surgery, ischaemic heart disease, asthma and congestive heart failure. The presen sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
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                                                                                                                                                                                                                                          100.0%; Score 120; DB 6; Length 27; 63.0%; Pred. No. 0.00084;
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use of a compound binding to kappa-PVIIA-binding site.
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                                                                                                                                                                                                                                                                   10; Mismatches
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                       Disclosure; Page 7; 32pp; English
                                                                                                                                                                                                                                                                                                                                                                              AAE38345 standard; peptide; 27 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JAN-2002; 2002US-0352219P.
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                                                                                                                                                                                                                    Sequence 27 AA;
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Modified-site
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The invention relates to kappa-PVIIA-related conotoxins and their use as organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury,
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organ protectants. The invention also relates to a method of arresting, related concroting an organ of a mammal using kappa-PVIIA-related conoctoxins. The conoctoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, uninary incontinence, reperfusion injury, diabetes, retinogathy, neuropathy, neptropathy, acute heart failure, peripheral circulation disturbances, hypertension, angine, cerebral vasospasm accompanying subarachnoid haemorrhage, anxiety disorder, eschebral ischaemia, coronary artery bypass graft (CABG) surgery, ischaemic heart disease, asthma and congestive heart failure. The present sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
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/label= Arg, Orn, Lys, His, OTHER
hone="OTHER = Homo-Arg, N-methyl-Lys, N-N-dimethyl-Lys,
N-N-Ltrimethyl-Lys, any synthetic basic amino acid, halo-
His; preferably Arg"
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Anote= "OTHER = Homo-Arg, N-methyl-Lys, N-N-trimethyl-Lys, N-N-N-trimethyl-Lys, any synthetic basic amino acid, halo-His; preferably Lys"
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//note= "OTHER = Meta-Tyr, ortho-Tyr, nor-Tyr, mono- halo-Tyr, di-halo-Tyr, O-Bulpho-Tyr, O-phospho-Tyr, nitro-Tyr, D or L-Trp, neo-Trp, D or L-halo-Trp or any synthetic aromatic amino acid; preferably Phe"
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//note= "OTHER = Homo-Arg, N-methyl-Lys, N-N-trimethyl-Lys, any synthetic basic amino acid, halo-His; preferably Lys"
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/note= "OTHER = Meta-Tyr, ortho-Tyr, nor-Tyr, mono- halo-
Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Purple cone snail, kappa-PVIIA-related conotoxin, urinary incontinence, ischaemic heart disease, cerebral ischaemia, anxiety disorder, diabetes, organ protectant, arrhythmia, reperfusion injury, hypertension, angina, retinopathy; coronary artery bypass graft surgery, acute heart failure,
      sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
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/note= "OTHER = Halo-His; preferably His"
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                                                                                                                     Length
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                                                                                                                Score 120; DB 6;
Pred. No. 0.00084;
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diabetes, retinopathy, neuropathy, nephropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral vasospasa accompanying subarachnoid haemorrhage, anxiety disorder, cerebral ischaemia, coronary artery bypass graft (CABG) surgery, ischaemic heart disease, astham and congestive heart failure. The present sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
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; Pred. No. 0.00084;
10; Mismatches 0;
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                                                                                                                                                                                                                                                                                                   1 CXIXNOXCXQXLDDCCSXXCNXXNXCV 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE38340 standard; peptide; 27
                                                                                                                                                                                                               ch 100.0%;
1 Similarity 63.0%; 117; Conservative 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JAN-2002; 2002US-0352219P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-679464/64.
                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conus purpurascens
                                                                                                                                                                         Sequence 27 AA;
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Modified-site
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07-AUG-2003

Olivera BM;

20-NOV-2003

AAE38340

Best Loca Matches

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/label= Hyp

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                                                 /label= Arg, Orn, Lyg, His, OTHER //label= Arg, Orn Lyg, N-methyl-Lyg, N-N-trimethyl-Lyg, N-N-N-trimethyl-Lyg, any synthetic basic amino acid, halo-His; preferably Lyg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present
                                                                                                                                                                                                                                                                                                                                                                                                                             Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertenation; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to kappa-PVIIA-related conotoxins and their use an organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence is Conus purpurascens (purple cone snail) kappa PVIIA peptide
D or L-Trp, neo-Trp, D or L-halo-Trp or any synthetic aromatic amino acid; preferably Phe"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    related contoxing. The contoxing can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, nephropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral vasospsem accompanying subarachnoid hemorrhinge, anxiety disorder, cerebral ischaemia, coronary artery bypass graft (CABG) surgery, ischaemic heart disease, asthma and congestive heart failure. The pre
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                                                                                                                                                                                                                                                                                                                                        Temple DL, Mcintosh JM;
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                                                                                                                                                                                                                                                                                                                                        Jones RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE38346 standard; peptide; 27
                                                                                                                                                                                                              28-JAN-2003; 2003WO-US002384.
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(UTAH ) UNIV UTAH RES FOUND.
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Best Local Similarity
                                   Misc-difference
                                                                                                                                            WO2003063782-A2
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                         Olivera BM;
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The invention relates to kappa-PVIIA-related conotoxins and their use as organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrivthmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, nephropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral vasospasm accompanying subarachnoid haemorrhage, anxiety disorder, cerebral schaemic heart disease, asthma and congestive heart failure. The present sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
                                                                                                                                                                                                                                                                                a mammal comprises
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                                                                                                                                                                                                      Mcintosh JM;
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                                                                                                                                                                                                                                                                                  Protection and preservation of an organ e.g. heart of
use of a compound binding to kappa-PVIIA-binding site.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; DB 6;
0.00084;
                                                                                                                                                                                                      Pemberton-Goodman KE, Jones RM, Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cch 120; B Score 120; D Similarity 63.0%; Pred. No. 0.00 17; Conservative 10; Mismatches
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                                                                                            28-JAN-2003; 2003WO-US002384.
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Best Local Similarity
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                               WO2003063782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 27 AA;
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                                                                                                                                                                                                                       Olivera BM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, nephropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral exerbral schaemia, coronary artery bypass graft (CABG) surgery, ischaemic heart disease, and congestive heart failure. The present sequence is Conus purpurascens (purple cone smail) kappa PVIIA analogue
                                                                                                                                                                                                                                                                                                                                                                                                                               Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to kappa-PVIIA-related conotoxins and their use
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63.0%; Pred. No. 0.00084;
iive 10; Mismatches 0;
                                                                                                                                                                                                                                                                     Temple DL,
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                                                                                                                                                                                                                                                                     Jones RM,
                                  28-JAN-2003; 2003WO-US002384.
                                                                                                 29-JAN-2002; 2002US-0352219P.
                                                                                                                                                                (COGN-) COGNETIX INC.
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nes 17; Conservative
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AAE38358
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Mcintosh JM;

Temple DL,

Pemberton-Goodman KE, Jones RM,

9-JAN-2002; 2002US-0352219P (COGN-), COGNETIX INC. (UTAH) UNIV UTAH RES FOUND.

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organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, carebral earbaral ischaemia, coronary artery bypass graft (CABG) surgery, ischaemic heart disease, asthma and congestive heart failure. The present sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
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                                    Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
                                                                                                                                     invention relates to kappa-PVIIA-related conotoxins and their use as
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0.00084;
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                                                                                              Disclosure; Page 8; 32pp; English
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Best Local Similarity 63.0
Matches 17; Conservative
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WPI; 2003-679464/64.
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                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 27 AA;
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Modified-site
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WPI; 2003-679464/64.
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Best Local Similarity
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                                                                                                                                             Sequence 27 AA;
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                                                                                                                                                                                                                                                                                                                   AAE38348;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to kappa-PVIIA-related conotoxins and their use as
                                                                                                                                                                                                                                                                                                                                                                                                                                         Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrivthmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
                                         The invention relates to kappa-PVIIA-related conotoxins and their use as organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrivthmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, nephropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral ecrebral ischaemia, coronary artery bypass graft (CABG) surgery, ischaemia, heart disease, asthma and congestive heart failure.
                                                                                                                                                                    sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
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                                                                                                                                                                                                                          100.0%; Score 120; DB 6; Length 27; 63.0%; Pred. No. 0.00084; ive 10; Mismatches 0; Indel8
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 of a compound binding to kappa-PVIIA-binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                       purpurascens kappa-PVIIA analogue peptide, R2Q.
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                                                                                                                                                                                                                                                                       1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
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                                                                                                                                                                                                                                                                                                                                                     AAE38347 standard; peptide; 27 AA
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(UTAH ) UNIV UTAH RES FOUND.
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                                                                                                                                                                                                                                     Best Local Similarity
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                                                                                                                                                                                                      Sequence 27 AA;
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-AUG-2003.
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                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    heart of a mammal comprises
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organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conctoxins. The conctoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, repertusion injury, diabetes, retinopathy, neuropathy, nephropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral vasospassm accompanying subarachnoid haemorrhage, anxiety disorder, cerebral ischaemia, coronary arrery bypass graft (CABG) surgery, ischaemic heart disease, asthma and congestive heart failure. The prese
                                                                                                                                                                                                                                                                                                                                                                                            sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 120; DB 6; Length 27; Pred. No. 0.00084;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conus purpurascens kappa-PVIIA analogue peptide, H11A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.08;
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UNIV UTAH RES
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ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; S17A.
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diabetes, retinopathy, neuropathy, nephropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral vasospasm accompanying subarachnoid haemorrhage, anxiety disorder, cerebral ischaemia, coronary artery bypass graft (CABG) surgery, ischaemic heart disease, asthma and congestive heart failure. The presensequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
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                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CXIXNQXCXQXLDDCCSXXCNXXNXCV
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20-JUL-2000; 2000US-0219438P.
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Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                         Sequence 27 AA;
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                                                                                                                                                                                                  peptide
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AAU 10
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                                                                                                                                                                                                                                                                                                                                                                           Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischemic heart disease; cerebral ischemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; andina; retinopathy; coronary artery bypass graft surgery; acute heart failure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a mammal comprises
                                                                                               Gaps
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                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              congestive heart failure; neuropathy; nephropathy; CABG
                                                               Length
                                                                                                                                                                                                                                                                                                                                              Conus purpurascens kappa-PVIIA analogue peptide, S17A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protection and preservation of an organ e.g. heart of use of a compound binding to kappa-PVIIA-binding site.
                                                             Score 117; DB 4;
Pred. No. 0.0015;
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                                                                                               10; Mismatches
                                                                                                                                1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                   27
                                                                                                                                                 CRIXNQKCFQHLDDCCARKCNRFNKCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                              AAE38352 standard; peptide; 27
                                                           97.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-JAN-2003; 2003WO-US002384.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= Hyp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FOUND
                                                                                                                                                                                                                                                                                                             (first entry)
analogue of the invention
                                                                                               17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (COGN-) COGNETIX INC. (UTAH ) UNIV UTAH RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pemberton-Goodman KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-679464/64.
                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conus purpurascens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2003063782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 27 AA;
                              Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
Modified-site
                                                                                                                                                                                                                                                                                                             20-NOV-2003
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AAE3835'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conctoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                  Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; V27A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       comprises
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprise activating a KATP channel by administering to an individual a kappa-conotoxin PVIIA peptide.
                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "The C-terminus is either a carboxyl group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mccabe RT;
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                              Length 27;
                                                                        0; Indels
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                            97.5%; Score 117; DB 6; 59.3%; Pred. No. 0.0015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Temple DL,
                                                                      11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                          Snail Kappa-conotoxin PVIIA analogue V27A.
                                                                                                                                      1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "Hyroxyproline"
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                                                                                                                                                                                                                                                          AAU10217 standard; peptide; 27
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20-JUL-2000; 2000US-0219438P.
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                                                                        Conservative
Query Match
Best Local Similarity
16; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conus purpurascens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 27 AA;
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The invention relates to kappa-PVIIA-related conotoxins and their use as organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, nephropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral vasospasm accompanying subarachnoid haemorrhage, anxiety disorder, ecrebral ischaemia, coronary artery bypass graft (GABG) surgery, ischaemic heart disease, asthma and congestive heart failure. The present sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                heart of a mammal comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
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larity 61.5%; Pred. No. 0.0019;
Conservative 10; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mcintosh JM;
                                                                                                                                                                                                                                                                                                                                                                                                           Conus purpurascens kappa-PVIIA analogue peptide, V27A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protection and preservation of an organ e.g. heart of a use of a compound binding to kappa-PVIIA-binding site.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CXIXNOXCXQXLDDCCSXXCNXXNXC 26
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CRIXNOKCFQHLDDCCSRKCNRFNKC
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Best Local Timilitity 63.0%; Pit 1. No. 0.0023;
Matches 17; Conservative 9; Aismatches 1; Indels
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                                                                                                                  n PVIIA cir.; channel cr.j., c
ue 13A.
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ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
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Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
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The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                      Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and coular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappa-conctoxin PVIIA peptide.
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Pred. No. 0.0028;
                                                                                                                                                                                                                                                                                         Temple DL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 28; 46pp; English.
                                                                      21-SEP-2000; 2000WO-US025827
                                                                                                                                   22-SEP-1999; 99US-0155135P
20-JUL-2000; 2000US-0219438P
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Best Local Similarity 63.0°
Matches 17, Conservative
                                                                                                                                                                                                                         (COGN-) COGNETIX INC
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            29-MAR-2001
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                                                                                                                                                                                                                                                                                                                  Jones RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE38356;
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            NAME OF COLOR OF COLO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-contoxin PVIIA (Kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular sischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappaconotoxin PVIIA peptide.
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/note= "The C-terminus is either a carboxyl group or
amide group"
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Pred. No. 0.0028;
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                                                                                                                                                                                                         21-SEP-2000; 2000WO-US025827.
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20-JUL-2000; 2000US-0219438P.
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nes 17; Conservative
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Synthetic.
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                                                                                      WO200121648-A1
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RESULT 39 AAU1021 ID AA

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Length 27; 1; Indels

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Treating disorders associated with radical depolarization of excitable
  WPI; 2003-679464/64.
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                                                                        Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
                                                                                                                                      organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving sometic calls. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, neptropathy, acute heart failure, peripheral circulation disturbance, hypertension, angina, cerebral escipantial schemmia, cornary artery bypass graft (ARG) surgery, ischaemic heart disease, askima and congestive heart failure. The presensequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
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                                                                                                                               kappa-PVIIA-related conotoxins and their use
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                                                                                                                                                                                                                                                                                                           DB 6; Length 27;
                      Mcintosh JM;
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                                                                                                                                                                                                                                                                                                        95.0%; Score 114; DB 6; 59.3%; Pred. No. 0.0028; ive 10; Mismatches
                      Temple DL,
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                                                                                                         Disclosure; Page 8; 32pp; English.
                      Jones RM,
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(UTAH ) UNIV UTAH RES FOUND.
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(UTAH ) UNIV UTAH RES FOUND.
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                                                                                                                              The invention relates to
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                     Pemberton-Goodman KE,
                                                     WPI; 2003-679464/64
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tes 16; Conserv
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                                 Olivera BM;
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Matches
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Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
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                                                                                                                                                                                                                                                                   related concoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, nephropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral vasospasm accompanying subarachnoid haemorrhage, anxiety disorder, cerebral ischaemia, coronary artery bypass graft (CABG) surgery, ischaemic heart disease, asthma and congestive heart failure. The presen sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
                                                                                                                                                                  The invention relates to kappa-PVIIA-related conotoxins and their use a organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting.
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                                                                                                       Disclosure; Page 7; 32pp; English
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20-JUL-2000; 2000US-0219438P.
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The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conctoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention
membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappa-
                                                                                                 Claim 1; Page 28; 46pp; English.
                                                   conotoxin PVIIA peptide
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Gaps
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         Length 27;
      Score 112; DB 4; Length 27
Pred. No. 0.0041;
9; Mismatches 1; Indels
                                                              1 CXIXNOXCXQXLDDCCSXXCNXXNXCV 27
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CRIXNQKCFQHLDDCCSRKCNRFAKCV 27
    93.3%;
Query Match
Best Local Similarity 63.0
Matches 17, Conservative
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AAU10209 standard; peptide; 27 (first entry) 16-JAN-2002 AAU10209;

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Snail Kappa-conotoxin PVIIA analogue D14A.

Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP charnel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; D14A.

Conus purpurascens. Synthetic.

/note= "The C-terminus is either a carboxyl group or an amide group" note= "Hyroxyproline" Location/Qualifiers Modified-site Modified-site

WO200121648-A1

29-MAR-2001

21-SEP-2000; 2000WO-US025827. 22-SEP-1999; 99US-0155135P. 20-JUL-2000; 2000US-0219438P. 22-SEP-1999;

(COGN-) COGNETIX INC.

Mccabe RT; Layer RT, Temple DL, Pemberton KE, Cornell-Bell AH, Jones RR;

WPI; 2001-648090/74.

Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappaconotoxin PVIIA, peptide

Claim 1; Page 28; 46pp; English.

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                 The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention
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63.0%; Pred. No. 0.0041;
live 9; Mismatches 1.
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Best Local Similarity 63.0
Matches 17; Conservative
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RESULT 44

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AAU10219 standard; peptide; 27 AA.

AAU10219;

(first entry) 16-JAN-2002

Snail Kappa-conotoxin PVIIA analogue N5A

Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; N5A.

Conus purpurascens.

Synthetic.

/note= "The C-terminus is either a carboxyl group 'note= "Hyroxyproline" Location/Qualifiers amide group" Modified-site Modified-site

or an

WO200121648-A1

29-MAR-2001

21-SEP-2000; 2000WO-US025827.

22-SEP-1999; 99US-0155135P. 20-JUL-2000; 2000US-0219438P.

(COGN-) COGNETIX INC.

Mccabe RT; Layer RT, Temple DL, Pemberton KE, Cornell-Bell AH, RR;

WPI; 2001-648090/74.

Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappaconotoxin PVIIA peptide

Claim 1; Page 28; 46pp; English.

The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active

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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; D13A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappa-
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salt. The conotoxing are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
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                                                                                                                                                                                                                                                1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                      'note= "Hyroxyproline"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-SEP-1999; 99US-0155135P.
20-JUL-2000; 2000US-0219438P.
                                                                                                                                                                  93.3%;
63.0%;
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                                                                                     analogue of the invention
                                                                                                                                                                                                        17; Conservative
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                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conus purpurascens.
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                                                                                                                         Sequence 27 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; N21A.
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   Length 27;
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                                                           Indels
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Score 112; DB 4; L
Pred. No. 0.0041;
9; Mismatches 1;
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                                                                                                                      1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                        |:||||:|:||:|| || ||||::||:||:|| CRIXNQKCFQHLADCCSRKCNRFNKCV 27
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63:0%;
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Query Match 93.3%;
Best Local Similarity 63.0%;
Matches 17; Conservative
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conotoxin PVIIA peptide
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Synthetic.
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Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.

Conus purpurascens kappa-PVIIA analogue peptide, N21A.

(first entry)

20-NOV-2003

AAE38351;

AAE38351 standard; peptide; 27 AA.

RESULT 48

AAE38351

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                                                                                                                                                                                                                                                             Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
      Gaps
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      Indels
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   Mismatches
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                                                Location/Qualifiers
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                                                                                                                                     AAE38353 standard; peptide; 27
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UNIV UTAH RES FOUND.
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                                                                                                                                                                                                   (first entry)
 17; Conservative
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Matches 16; Conservative
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Modified-site
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Matches
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AAE38355
ID AAE38355 standard; peptide; 27 AA.
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Best Local Similarity 59.3%,
Best Local Similarity 59.3%,
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Modified-site
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Conus purpurascens kappa-PVIIA analogue peptide, D14A.
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                                                                              Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
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                                                         Conus purpurascens kappa-PVIIA analogue peptide, D13A.
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CRIPNQKCFQHLADCCSRKCNRFNKCV 27
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(UTAH ) UNIV UTAH RES FOUND.
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                                                                                                                                                                                                                                                                                                                                                         Pemberton-Goodman KE,
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                                                                                                                                                        Conus purpurascens.
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                                  20-NOV-2003
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            AAE38355;
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AAE38349
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Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
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 retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
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Pred. No. 0.0041;
9; Mismatches 1; Indels
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(UTAH ) UNIV UTAH RES FOUND.
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retinopathy; coronary
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                                               Conus purpurascens.
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Use of omega-cono-peptide(s) which selectively inhibit voltage-gated calcium channels - to induce analgesia, enhance opiate analgesics, treat

Claim 1; Fig 2; 90pp; English.

pain etc.

Miljanich GP,

Valentino KL,

Gohil K,

Singh T,

Justice A,

WPI; 1993-227270/28

(NEUR-) NEUREX CORP

30-DEC-1991;

92WO-US011349. 91US-00814759

30-DEC-1992;

/note= "Amidated C-terminal"

Location/Qualifiers

Disulfide-bond Disulfide-bond Disulfide-bond

Modified-site

WO9313128-A1

08-JUL-1993

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ischaemia; neuronal; omega-conotoxin; OCT; MVIIA; MVIIC; MVIIB; GVIA; GVIIA; GVIIA; VVIA; SVIIA; TVIA; SVIB; SNX-207; stroke; delayed treatment; antihistamine; blood pressure; N-type voltage-gated Ca currents; N-channel mediated neurotransmitter release.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67.5%; Score 81; DB 2; Length 26; 34.6%; Pred. No. 2; ive 13; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CXIXNQXCXQXLDDCCSXXCNXXNXC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR37774 standard; peptide; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 34.00,
Than 9; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disulfide-bond
Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ischaemia; ne
GVIA; GVIIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAR-2003
08-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                              field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR37774;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNX-202.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 53
AAR37774
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Omega conopeptide; OCT; analgesia; inhibition; voltage-gated; calcium channel; neurone; contraction; guinea pig; ileum; MVIIA; binding site; toxin; marine; snail; Conus; opiod; chronic pain;

Synthetic

AAR39628 standard; peptide; 26 AA

AAR39628

(first entry)

(revised)

25-MAR-2003 20-DEC-1993

SNX-202.

AAR39628;

Kristipati R;

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peptides from Conus sp. (cone snails). The peptides and their analogues are used as analgesics acting by blocking N-type voltage-sensitive calcium channels. The OGs can be used to treat neuropathic pain as a result of e.g. insult to the spinal cord or peripheral nerves, cancer, bone degenerative diseases, AIDS, reflex sympathetic dystrophy, herpes caster neuropathy, diabetic neuropathy, hyperesthesia, allodynia or hyperalgesia. The OGs are preferably administered in a medicament via an epidural route in a continuous infusion or sustained release formulation. The OGs can provide pain relief when administered epidurally in the cansence of a permeation enhancer, at doses that are comparable to effective analgesic doses using intrathecal administration. OC formulations comprising an OC and a carboxylic acid buffer anti-oxidant. They also confer stability to solutions containing them for prolonged
                                                                                                                                                                                                                                                                                  Stable omega conopeptide compositions - for producing analgesia and for inhibiting progression of neuropathic pain disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Omega conopeptide, analgesic, treatment, neuropathic pain; inhibition, neuronal damage; schizophrenia; tardive dyskinesia; analgesia; acute dystonic reactions; inflammation; epilepsy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 26;
                                                                                                                                                                        3, Gohil K, Adriaenssens PI,
Luther RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 67.5%; Score 81; DB Local Similarity 34.6%; Pred. No. 2; es 9; Conservative 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         treatment methods and long-term storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW12985 standard; peptide; 26 AA
                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 4; 47pp; English.
                                                               95US-00496847
96US-00613400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93US-00049794.
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92WO-US011349.
                                                                                                                                                                          Bowersox SS,
Pettus MR, Lu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Omega conopeptide SNX-202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (revised)
                                                                                                                                 (NEUR-) NEUREX CORP.
                                                                                                                                                                                                                                       WPI; 1997-100012/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (NEUR-) NEUREX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 26 AA;
                                                                 27-JUN-1995;
                                                                                        08-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-APR-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-MAR-2003
22-APR-1997
                                                                                                                                                                          Amstutz GA,
Gadbois T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JS5587454-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW12985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                 The C-terminal is amidated. Ischaemia-related neuronal damage in mammals is reduced by admin., 4-24 hr after onset of ischaemia, of a cpd. (I) which binds selectively to an omega-conotoxin (OCT) WNIIA site in neuronal tissue. (I) has selectivity at least 100 expressed as ratio of binding affinity for the MVIIA site to that for the MVIIC site. (I) is come of the OCTS MVIIA, MVIIB, GVIA, GVIA or RVIA or It is the cpd. SIX-CC 207. (I) is esp. used to reduce neuronal damage caused by stroke. By delaying admin. for some time (compare USSOS1403 where cpds. are given within 1 hr of the onset of ischaemia) a greater redn. in neuronal damage is achieved. (I) is admin. e.g. by intracerebroventricular (ICV) considered to 1.-20 microg/Kg, but can also be given iv. (opt. after injection at 0.1-20 microg/Kg, but can also be given iv. (opt. after creatment with antihistamines to minimise redn. in blood pressure caused by (I)). (I) is also at least as effective as the specified conotoxins for (1) selective inhibition of N-type vollage-gated ca currents in neuronal tissue and (2) selective inhibition of N-channel mediated neuronal tissue and (2) selective inhibition of Primary sequences of omega-conopeptides are given in AAR37752-62. Several analog omega-conopeptides

care given in AAR37753-76. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                  Redn. of neuronal damage caused by ischaemia - by admin. of cpds. that
bind specifically to omega-conotoxin MVIIA binding sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conopeptide, cone snail; pain; analgesic; neuropathy; epidural; N-type voltage-sensitive calcium channel; block; Conus.
                                                                                                                                                                                                                                       Valentino KL, Bitner RS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNX-202, omega conopeptide derivative used for pain relief.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67.5%; Score 81; DB 2; Length 26; 34.6%; Pred. No. 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | ::: | :| ::: | | | | | :: | :: : | CKLKGQSCSRLMYDCCSGSCGRSGKC 26
                                                                                                                                                                                                                                       Fox JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 2; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW19570 standard; peptide; 26 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "amidated"
                                                                                    92WO-US009766
                                                                                                                            91US-00789913
92US-00916478
                                                                                                                                                                                                                                       Bowersox SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                            (NEUR-) NEUREX CORP.
                                                                                                                                                                                                                                                                                                         WPI; 1993-182487/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
les 9; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ä
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Modified-Bite
                                                                                                                                                                                                                                     Miljanich GP,
Yamashiro DH;
WO9310145-A1
                                                                                      12-NOV-1992;
                                                                                                                            12-NOV-1991;
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                                             27-MAY-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW19570;
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Best Loc Matches

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RESULT 54

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Gaps

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4; Indels

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Justice A,

Valentino KL,

Miljanich GP,

Gohil KC,

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RESULT 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conus genus; marine snail; cone snail; omega-conopeptide; analgesia; nociceptive pain; neuropathic pain; neuropal tissue; conocoxin; inflammation; schizophrenia; tardive dyskinesia; acute dystonic reaction; rheumatoid arthritis; epilepsy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A method has been developed for the treatment of inflammation in a subject. The method comprises administration of an omega-conopeptide effective to: (i) block voltage-gated calcium channels; (ii) bind with high affinity to an omega-conopeptide binding site; and (iii) inhibit neurotransmitter release from nervous tissue. The method is used to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Treatment of inflammation, comprises administration of omega-conopeptide - effective to block voltage-gated calcium channels, bind with high affinity to omega-conopeptide binding site, and inhibit neuro-transmitter
                                                                                                                                                                                  especially for treating neuropathic pain. The peptide, which can be prepared by solid phase synthesis, can also be used to inhibit neuronal damage and treat schizophrenia, tardive dyskinesia, acute dystonic reactions, inflammation and epilepsy. (Updated on 25-MAR-2003 to correct PP field.)
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                          peptide is an omega conopeptide, useful as an analgesic,
                                                                          - useful as analgesics, esp. for treating
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                                                                                                                                                                                                                                                                                                                                                                        Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Justice A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conus genus analogue omega-conopeptide SNX-202.
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                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                   67.5%; Score 81;
34.6%; Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gohil KC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26
                                                                                                                                     Col 51-52; 58pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CKLKGQSCSRLMYDCCSGSCGRSGKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CXIXNOXCXOXLDDCCSXXCNXXNXC
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                                                                                                                                                                                                                                                                                                                                                                                                             13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW72625 standard; peptide; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91US-00814759.
93US-00049794.
96US-00675354.
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                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 34.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (revised)
(first entry)
                                                                          Omega cono:peptide(s)
                              WPI; 1997-064830/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (NEUR-) NEUREX CORP.
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                                                                                             neuropathic pain.
                                                                                                                                                                                                                                                                                                                          Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Miljanich GP,
                                                                                                                                  Disclosure;
                                                                                                                                                                            The present
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03-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-AUG-2003
06-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US5824645-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW72625;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW72625
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inflammation and associated pain. The treatment can also be used to produce analgesia (especially in subjects experiencing neuropathic pain); and to treat schizophrenia, tardive dyskinesia and acute dystonic reactions, rheumatoid arthritis, and epilepsy. The present sequence represents an analogue omega-conopeptide. Omega-conopeptides are components of peptide toxins produced by marine snails of the genus conus, and which act as calcium channel blockers. (Updated on 27-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Omega-conopeptides are components of peptide toxins produced by marine snails of the genus Conus, and which act as calcium channel blockers. The invention relates to a method of producing analgesia in a mammal that comprises administering an omega conopeptide having activities in all libibiting electrically stimulated contraction of guinea pig ileum and blo salectively binding to omega conopeptide MVIA binding sites in neuronal tissue, where these activities are within the ranges of those of omega-conotoxins MVIIA and TVIA. The method is used for treating chronic pain, especially neuropathic pain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequences AAW95574-589 represent sequences of analog omega-conopeptides.
                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     toxin; snail; calcium channel blocker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Omega-conopeptide; peptide toxin; snail; calcium channel blocker analgesia; guinea pig ileum; omega-conotoxin; pain; neuropathic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Production of analgesia in mammal - by administration of omega
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Singh T;
                                                                                                                                                                                             Length 26;
                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Justice A,
                                                                                                                                                                                                                               4.
                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                             13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "C-terminal amide"
                                                                                                                                                                                             67.5%; Score 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Valentino KL,
                                                                                                                                                                                                                                                            1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                 |::: |:|::: | | | | | | :: | CKLKGQSCSRLMYDCCSGSCGRSGKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 2A-B; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                    Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Analog omega-conopeptide SNX-202.
                                                                                                                                                                                                                                                                                                                                                                                AAW95584 standard; protein; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96US-00675354.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91US-00814759.
                                                                                                                                                                                                            34.68;
                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KC,
                                                                                                                       to correct OS field.)
                                                                                                                                                                      Query Match
Best Local Similarity
9; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gohil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NEUR-) NEUREX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-120002/10.
                                                                                                                                                           Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Miljanich GP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US5859186-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                 AAW95584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conus sp.
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34.6%;

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                                                                                                                                                                                                                                                                                                              Omega conopeptide; analgesic; nociceptive; neuropathic; pain; conotoxin; marine snail; peptide toxin; inflammation; binding; voltage-gated calcium channel; inhibition; norepinephrine; noradrenaline;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pain. Analgesia caused by selected compounds may reduce the reliance on opioid analgesic agents of the prior art which cause dependency and tolerance, requiring potentially dangerous increases in opioid doses to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              achieve the analgesic effect. The present sequence represents an omega conopeptide given in the present invention
                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Measuring the activity of test compounds in blocking voltage-gated calcium channels, binding to the omega conopeptide binding site and inhibiting norepinephrine (noradrenaline) release for treating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gohil KC;
                                Length 26;
                                                              Indels
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3
                              67.5%; Score 81; DB 34.6%; Pred. No. 2; ive 13; Mismatches
                                                                                        1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                         1 CKLKGQSCSRLMYDCCSGSCGRSGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Valentino KL,
                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                   Analogue omega conopeptide SNX-202,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "amidated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 2; 47pp; English.
                                                                                                                                                                                               AAY56496 standard; peptide; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91US-00814759.
93US-00049794.
96US-00675354.
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                                                              Conservative
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Query Match
Rest Local Similarity
9; Conserve
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                                                                                                                                                                                                                                                                                                                                                            anti-inflammatory.
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Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
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01-NOV-1996;
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                                                                                                                                                                                                                                                                                                                                                                                        Conus sp
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67.5%; Score 81; DB 3; Length 26;

Query Match

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                                                                                                                                                                                                                                            Marine snail; omega-conopeptide; calcium channel blocker; SNX-202; toxin; analgesic; antiinflammatory; anticonvulsant; neuroleptic; norepinephrine release inhibitor; schizophrenia; tardive dyskinesia; acute dystonic reaction; inflammation; epilepsy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is an omega-conopeptide analogue. Omega-conopeptides are components of peptide toxins produced marine snails of the genus conous. Omega-conopeptides and their derivatives act as calcium channel blockers and may be useful for producing analogus in nociceptive and neuropathic pain. The peptides bind to omega-conopeptide binding sites, which are present mainly in neuronal tissue, and inhibit norepinephrine release from nervous tissue. Conopeptides such as MVIIA and TVIA are effective as therapeutic agents for treating neurogenic conditions such as schizophrenia, tardive dyskinesia and acute dystonic reactions,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Selecting a compound for producing analgesia involves measuring activity of test compound in blocking voltage-gated calcium channels, binding to omega conopeptide binding site and inhibiting norepinephrine release.
              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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              Indela
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               4.
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13; Mismatches
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                                       26
                                                        CKLKGQSCSRLMYDCCSGSCGRSGKC
                                         CXIXNOXCXOXIDDCCSXXCNXXNXC
                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gohil KC, Valentino KL,
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                                                                                                                                      AAB14370 standard; peptide; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91US-00814759.
93US-00049794.
96US-00675354.
96US-00742774.
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                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                    Omega-conopeptide SNX-202
               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              as schizophrenia, tardive inflammation and epilepsy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Conservative
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8. .20
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Local Similarity
les 9; Conserv
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Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                    Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
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03-JUL-1996;
01-NOV-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-JUL-2000
                                                                                                                                                                                                                                                                                                                 Conus sp.
Synthetic.
                                                                                                                                                               AAB14370;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Loc
Matches
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                                                                                                                        AAB14370
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56

1 CXIXNQXCXQXLDDCCSXXCNXXNXC

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The present sequence represents an omega-conopeptide analogue. Omegaconopeptides are components of peptide toxins which act as voltage-gated calcium channel inhibitors. The peptides are used to enhance the analogues of effect produced by an opiate in a mammalian subject. The method comprises administering to the subject an omega-conopeptide which is able on inhibit electrically stimulated contraction of the guinea pig ileum and bind to omega-conopeptide MVIIA binding sites present in neuronal tissue. Omega-conopeptides are useful for enhancing the analogusic effect broduced by an opiate. Omega-conopeptides may also be used in the treatment of pain, in reducing neuronal damage related to an ischemic condition in mammals, and in treating schizophrenia, tardive dyskinesia and acute dystonic reactions, inflammation and epilepsy
                                                                                                                                                                                                                     Omega-conopeptide; voltage-gated calcium channel inhibitor; analgesic; peptide toxin; opiate; pain; neuronal damage; ischemic condition; schizophrenia; tardive dyskinesia; acute dystonic reaction; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enhancing analgesia produced by opiates by administering an omega-
conopeptide that inhibits electrically stimulated contraction of guinea
pig ilium and binds to omega-conopeptide MVIIA binding sites in neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Justice A;
                                                                                                                                                                                         Sequence of an omega-conopeptide analogue designated SNX-202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Miljanich GP,
                                                                                                                                                                                                                                                                                                                                                                       /note= "amidated residue"
   26
                              26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Col 51-52; 58pp; English.
                    1 CXIXNQXCXQXLDDCCSXXCNXXNXC
                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                       Ą.
                                                                                                    AAB19462 standard; peptide; 26
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93US-00081863.
96US-00675354.
96US-00138439.
99US-00138439.
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                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHARM INC.
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                                                                                                                                                                                                                                                                                                                                        Key
Modified-site
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23-APR-1999;
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                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                AAB19462;
                                                                                                                                                                                                                                                                    epilepsy.
                                                                                                                                                                                                                                                                                                              Conus sp.
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                                                                                      AAB19462
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The invention relates to isolated omega-conopeptides, nucleic acid
sequences encoding them, and propeptide sequences. The activity of the
sequences encoding them, and propeptide sequences. The activity of the
peptides of the invention may be described as, analgesic, anticonvulsant,
vasotropic, cardiant, neuroprotective, cerebroprotective, cardiovascular,
antinflammatory, antimigrathe, antidiabetic, tranquiliser, vulnerary,
antipsychotic, anxiolytic and neuroleptic. Peptides of the invention act
by modulating the activity of voltage gated ion channels. They may be
used for treating or preventing disorders associated with voltage gated
to channels such as neurological disorders, e.g. seizure (associated
with epilepsy), neurocroxic injury associated with conditions of hypoxia,
anoxia, ischaemia, stroke, cerebrovascular accident, brain or spinal
chord trauma, drowning, suffocation, perinatal asphyxia or hypoglycaemic
conditions of migraine; inflammation or cardiovascular disorders.
They may also be used for treating psychiatric disorders e.g. psychosis,
anxiety or schizophrenia. The analgesic agents of the invention show
diminished side effects and toxicity, and are non-addictive. The
sequences given in records ABB96807-ABB96905 represent omega-conopeptide
                                                                                                                                                                                                                                                                                                          neuroprotective; cerebroprote, cardiovascular; antiinflammatory; antimigraine; antidiabetic; tranquiliser; vulnerary; antipsychotic; antiolytic; neuroleptic; voltage gated ion channel; seizure; epilepsy; neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia; stroke; cerebrovascular accident; brain trauma; spinal chord trauma; drowning; suffocation; perinatal asphyxia; hypoglycaemic event; pain; migraine; inflammation; cardiovascular disorder; psychiatric disorder; psychosis; anxiety; schizophrenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New omega-conopeptides useful for treating disorders associated with voltage gated ion channels e.g. pain, inflammation, neurologic or cardiovascular disorders.
                                                                                                                                                                                                                                                                                        Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shon K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mcintosh JM, Watkins M, Garrett JE, Jones RM, Cartier GE;
               26
                                                                                                                                                                                                                                                  Omega-conopeptide S6.2 toxin sequence.
| ::: |:|:: ::: | | | | | :: | :: : : | | | | CKLKGQSCSRLMYDCCSGSCGRSGKC
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                                                                                                                  ABB96887 standard; peptide; 26
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05-FEB-2001; 2001US-0265888P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jacobsen R,
                                                                                                                                                             ABB96887;
                                                                            RESULT 61
                                                                                                ABB96887
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Length

67.5%; Score 81; DB 5;

Sequence 26 AA;

Query Match

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Gaps ;

67.5%; Score 81; DB 4; Length 26; 34.6%; Pred. No. 2; ive 13; Mismatches 4; Indels

Best Local Similarity 34.6 Matches 9; Conservative

Query Match

Sequence 26 AA;

31

Sequence 30 AA;

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The invention relates to isolated omega-conopeptides, nucleic acid sequences encoding them, and propeptide sequences. The activity of the sequences encoding them, and propeptide sequences. The activity of the peptides of the invention may be described as, analgesic, anticonvalsant, vasotropic, cardiant, neuroprotective, cerebroprotective, cardiovascular, antinflammatory, antimigraine, antidiabetic, tranquiliser, vulnerary, antinflammatory, antimigraine, antidiabetic, tranquiliser, vulnerary, antinflammatory of voltage gated ion channels. They may be used for treating or preventing disorders associated with voltage gated ion channels such as neurological disorders, e.g. seizure (associated with epilepsy), neurotoxic injury associated with conditions of hypoxia, anoxia, ischaemia, stroke, cerebrovascular accident, brain or spinal chort trauma, drowning, suffocation, perinatal asphyxia or hypoglycaemic coverts; pain e.g. migraine; inflammation or cardiovascular disorders. They may also be used for treating psychiatric disorders e.g. psychosis, anxiety or schizophrenia. The analgesic agents of the invention show analgesic squences given in records ABB95695-ABB96697 represent omega-conopeptide propertide sequences
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                                                                                                                                                                                                                                                                                                                                                         Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiant; neuroprotective; cerebroprotective; cardiovascular; antiinflammatory; antimigraine; antidiabetic; tranquiliser; vulnerary; antipsychotic; anxiolytic; neuroleptic; voltage gated ion channel; seizure; epilepsy; neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia; stroke; cerebrovascular accident; brain trauma; spinal chord trauma; drowning; sulfocation; perinatal asphyxia; hypoglycaemic event; pain; migraine; inflammation; cardiovascular disorder; psychiatric disorder; psychosis; anxiety; schizophrenia.
                        Gaps
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cardiovascular disorders.
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                        4; Indels
  Pred. No. 2; 3; Mismatches
                                                           1 CXIXNOXCXQXLDDCCSXXCNXXNXC 26
                                                                                | ::: |:|::: |||||::| ::: | | CKLKGQSCRRTMYDCCSGSCGRRGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1(c); Page 62; 195pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cartier GE;
                                                                                                                                                                                                                                                                                                                      Omega-conopeptide S6.2 propeptide.
                                                                                                                                                                                                  ABB96679 standard; peptide; 30 AA
  llarity 34.6%; Pro
Conservative 13;
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05-FEB-2001; 2001US-0265888P.
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(COGN-) COGNETIX INC.
                                                                                                                                                                                                                                                                              (first entry)
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Jacobsen R, Jones RM, Ca
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Similarity
9; Conserv
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  Best Local
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequences given in AAR39608-30 are omega conopeptides (OCTs) and derivatives of these, which may be used to produce analgesia in a mammal. These OCTs inhibit voltage-gated calcium channels selectively in neuronal tissue. This is shown by the peptides ability to stimulate contraction in guinea pig ileum and to bind to OCT MVIIA binding sites present in neuronal tissue. OCTs are components of peptide toxins derived from marine snalls of the genus Conus, and act as calcium channel blockers. These OCTs may be used to replace opiods in the treatment of chronic pain or to reduce the opiod dosage required. This helps to reduce dependence on and tolerance to opiod narcotics. (Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Use of omega-cono-peptide(s) which selectively inhibit voltage-gated calcium channels - to induce analgesia, enhance opiate analgesics, treat
                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                      Omega conopeptide; OCT; analgesia; inhibition; voltage-gated; calcium channel; neurone; contraction; guinea pig; ileum; MVIIA; binding site; toxin; marine; snail; Conus; opiod; chronic pain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Miljanich GP
 Length 30;
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                          Indels
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  DB 5;
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            ; Pred. No. 2.2, 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12; Mismatches
  67.5%; Score 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64.2%; Score 77; 34.6%; Pred. No.
                                                     1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                      Location/Qualifiers
1. .16
8. .20
                                                                                                                                                 AAR39615 standard; peptide; 26 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gohil K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Fig 1; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92WO-US011349.
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                                                                                                                                                                                                                    (first entry)
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Query Match
Best Local Similarity 34.6
Matches 9; Conservative
                                                                                                                                                                                                        (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Singh T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NEUR-) NEUREX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1993-227270/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                 Disulfide-bond
Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                        W09313128-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-DEC-1992;
                                                                                                                                                                                                     25-MAR-2003
20-DEC-1993
                                                                                                                                                                                                                                              SVIB/SNX183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Justice A,
                                                                                                                                                                                                                                                                                                                   narcotics.
                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                           AAR39615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pain etc.
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Matches
                                                                                                                                 AAR39615
                                                                                                                      RESULT
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1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26

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AAR37760 standard; peptide; 26
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Best Local Similarity 34.0.
                                                                          1. .16
8. .20
15. .26
                                                                                                                           (NEUR-) NEUREX CORP.
                                                                                                                                               WPI; 1993-182487/22.
                                                                         Disulfide-bond
Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                   Sequence 26 AA;
                                                                                                                                  Miljanich GP,
Yamashiro DH;
                                   SVIB/SNX-183
                                                                                        WO9310145-A1
                                                                                                        12-NOV-1992;
                                                                                                               12-NOV-1991;
17-JUL-1992;
                       25-MAR-2003
08-SEP-1993
                                                                                                27-MAY-1993
                                                              Synthetic
               AAR37760;
RESULT 64
    AAR37760
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Stable omega conopeptide compositions - for producing analgesia and inhibiting progression of neuropathic pain disorders.
                                                                                                                                                                                                                                                                                                           Conopeptide, cone snail; pain; analgesic; neuropathy; epidural; N-type voltage-sensitive calcium channel; block; Conus.
                                                                                                                                                                                                                                                                        Natural omega-conopeptide SVIB/SNX-183 used for pain relief.
                                 | ::: |::: | | | | | | :: | :: : | CKLKGQSCRKTSYDCCSGSCGRSGKC 26
           1 CXIXNOXCXQXLDDCCSXXCNXXNXC
                                                                                                                                          AAW19551 standard; peptide; 26 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amstutz GA, Bowersox Si
Gadbois T, Pettus MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (NEUR-) NEUREX CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                  27-AUG-2003
13-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9701351-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27~JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-JAN-1997.
                                                                                                                                                                               AAW19551;
                                                                                                                                                                                                                                                                                                                                                                    Conus.
                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ischaemia-related neuronal damage in mammals is reduced by admin., 4-24

In after onset of ischaemia, of a cpd. (1) which binds selectively to an omega-conotoxin (OCT) MVIDA site in neuronal fissue. (1) has selectivity at least 100 expressed as ratio of binding affinity for the MVIDA site to that for the MVID site. (1) is of the OCTS MVIDA, MVIDB, GVIDA, GVIDA, OR NVIDA or It is the cpd. SNX-207. (I) is esp. used to reduce neuronal amage caused by stroke. By delaying admin. for some time (compare US5051403 where opds. are given within 1 hr of the onset of ischaemia) a circacebroventricular (ICV) injection at 0.1-20 microg/kg, but can also be given i.v. (opt. after treatment with antihistamines to minimise redn. in blood pressure caused by (I)). (I) is also at least as effective as in blood pressure caused by (I)). (I) is also at least as effective as the specified conotoxins for (1) selective inhibition of N-channel mediated neurotransmitter release in neuronal tissue. Primary omega-conopeptides are given in AAR37752-62. Several analog correct PN field.)
                                                                                                                                                                                                                                                                              Ischaemia, neuronal, omega-conotoxin, OCT; MVIIA, MVIIC, MVIID, MVIIB, GVIA, GVIIA, RVIA, SVIA, TVIA, SVIB, SNX-207; stroke, delayed treatment, antihistamine; blood pressure; N-type voltage-gated Ca currents, N-channel mediated neurotransmitter release.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Redn. of neuronal damage caused by ischaemia - by admin. of cpds. that bind specifically to omega-conotoxin MVIIA binding sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Valentino KL, Bitner RS;
Fox JA,
                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 1; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92WO-US009766.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bowersox SS,
                                                                                                                                                                                        (revised)
(first entry)
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SS, Gohil K, Adriaenssens PI, Kristipati Luther RR;

/note= "optionally amidated"

96WO-US011041. 95US-00496847. 96US-00613400.

Location/Qualifiers 26

(first entry)

(revised)

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AAW19544-W19553 are naturally occurring omega conopeptides (OCs) isolated from Conus sp. (cone snails). The peptides and their analogues are used as analogasics acting by blocking N-type voltage-sensitive calcium channels. The OCs can be used to treat neuropathic pain as a result of e.g. insult to the spinal cord or peripheral nerves, cancer, bone of degenerative diseases. AIDS, reflex sympathetic dystrophy, herpes zoster neuropathy, diabetic neuropathy, hyperesthesia, allodynia or hyperalgesia. The OCs are preferably administered in a medicament via an phyperalgesia. The OCs are preferably administered epidurally in the copidural route in a continuous infusion or sustained release formulation. The OCs can provide pain relief when administered epidurally in the absence of a permeation enhancer, at doses that are comparable to coffective analgesic doses using intrathecal administration. Occ formulations comprising an OC and a carboxylic acid buffer anti-oxidant. They also confer stability to solutions containing them for prolonged concerned and long-term storage. (Updated on 27-AUG-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Disclosure; Fig 2, Fig 3; 47pp; English:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CXIXNOXCXOXLDDCCSXXCNXXNXC 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
9, Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 26 AA;
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Gaps

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64.2%; Score 77; DB 2; Length 26; 34.6%; Pred. No. 4.4; ive 12; Mismatches 5; Indels

us-10-627-685a-1.rag

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WPI; 1998-582596/49.
                                                                                                    (NEUR-) NEUREX CORP.
                                                                                                                                                                                                                                                                                                                                                              Sequence 26 AA;
                                                                                                                     Miljanich GP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
Modified-site
                                            01-NOV-1996;
                                                                        15-APR-1993;
03-JUL-1996;
                                                              30-DEC-1991;
       US5824645-A.
                          20-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US5859186-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW95571;
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                                                                                                                                                                                       release
                                                                                                                                                                                                                                                                                                                                           field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 68
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%XCCCCCCCCCCX%X44444X4X4X4X4X4X4X4X4XAX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conus genus; marine snail; cone snail; omega-conopeptide; analgesia;
nociceptive pain; neuropathic pain; neuronal tissue; conotoxin;
inflammation; schizophrenia; tardive dyskinesia; acute dystonic reaction;
                                                                                                                                                                                                                                                                                                                                                            The present peptide is an omega conopeptide, useful as an analgesic, especially for treating neuropathic pain. The peptide, which can be prepared by solid phase synthesis, can also be used to inhibit neuronal damage and treat schizophrenia, tardive dyskinesia, acute dystonic reactions, inflammation and epilepsy. (Updated on 25-MAR-2003 to correct
                                                                                                            Omega conopeptide, analgesic, treatment, neuropathic pain, inhibition, neuronal damage; schizophrenia, tardive dyskinesia, analgesia, acute dystonic reactions, inflammation; epilepsy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                Omega cono:peptide(s) - useful as analgesics, esp. for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                           Singh
                                                                                                                                                                                                                                                                                                                                                                                                                                                 64.2%; Score 77; DB 2; Length 26; 34.6%; Pred. No. 4.4; ive 12; Mismatches 5; Indels
                                                                                                                                                                                                                                                                            Justice A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conus genus natural omega-conopeptide SVIB/SNX-183.
                                                                                                                                                                                                                                                                           Valentino KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CXIXNOXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |::: |:|::: | | | | | |:: | :: : | CKLKGOSCRKTSYDCCSGSCGRSGKC 26
                                                                                                                                                                                                                                                                                                                                           Disclosure; Col 45-46; 58pp; English.
                         AAW12974 standard; peptide; 26 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW72612 standard; peptide; 26 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rheumatoid arthritis; epilepsy.
                                                                                                                                                                                                           93US-00049794
                                                                                                                                                                                                                           91US-00814759.
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Ouery Match
Best Local Similarity 34.00.
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(first entry)
                                                                         (first entry)
                                                                                          Omega conopeptide SNX-183.
                                                                                                                                                                                                                                                                           Miljanich GP,
                                                                (revised)
                                                                                                                                                                                                                                                        (NEUR-) NEUREX CORP.
                                                                                                                                                                                                                                                                                              WPI; 1997-064830/06
                                                                                                                                                                                                                                                                                                                           neuropathic pain.
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 26 AA;
                                                                                                                                                                                                           LS-APR-1993;
                                                                                                                                                                                                                            30-DEC-1991;
                                                              25-MAR-2003
22-APR-1997
                                                                                                                                                                                                                                      30-DEC-1992;
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06-JAN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                             PF field.)
                                                                                                                                                                                                                                                                          Gohil KC,
                                                                                                                                                  Synthetic
                                            AAW12974;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW72612
                AAW129'
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A method has been developed for the treatment of inflammation in a subject. The method comprises administration of an omega-conopeptide effective to: (i) bind with high affective to: (i) bind with high affinity to an omega-conopeptide binding site; and (ii) inhibit neurotransmitter release from nervous tissue. The method is used to treat inflammation and associated pain. The treatment can also be used to produce analgesia (especially in subjects experiencing neuropathic pain); and to treat schizophrenia, tardive dyskinesia and acute dystonic reactions, rheumatoid arthritis, and epilepsy. The present sequence represents a natural omega-conopeptide. Omega-conopeptides are components of peptide toxins produced by marine snalls of the genus Conus, and which act as calcium channel blockers. (Updated on 27-AUG-2001 to correct OS
                                                                                                                                                                                                                                                                                                                                                                                   Treatment of inflammation, comprises administration of omega-conopeptide - effective to block voltage-gated calcium channels, bind with high affinity to omega-conopeptide binding site, and inhibit neuro-transmitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Omega-conopeptide; peptide toxin; snail; calcium channel blocker; analgesia; guinea pig ileum; omega-conotoxin; pain; neuropathic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                        Justice A, Singh T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Pred. No. 4.4;
12; Mismatches
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/note≃ "C-terminal amide"
                                                                                                                                                                                                                                                           Gohil KC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW95571 standard; protein; 26
                                                           91US-00814759.
93US-00049794.
96US-00675354.
96US-00742774.
                                                                                                                                                                                                                                                        Valentino KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 34.v...
Best Local 9; Conservative
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inflammation. The method comprises measuring the activity of the test compound in blocking voltage-gated calcium channels, binding to the omega rengebuide binding site and inhibiting norepinephrine (noradrenaline) release from nervous tissue. The method is useful for selecting compounds for treating inflammation. The selected compounds are capable of producing analgesia in a mammalian subject with chronic or intractable pain. Analgesia caused by selected compounds may reduce the reliance on opioid analgesic agents of the prior art which cause dependency and achieve the analgesic effect. The present sequence represents an omega conopeptide given in the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Marine snail; omega-conopeptide; calcium channel blocker; SVIB; SNX-183; toxin, analgesic; antilnilammatory; anticonvulsant; neuroleptic; norepinephrine release inhibitor; schizophrenia; tardive dyskinesia; acute dystonic reaction; inflammation; epilepsy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Selecting a compound for producing analgesia involves measuring activity
       calcium channels, binding to the omega conopeptide binding site and inhibiting norepinephrine (noradrenaline) release for treating inflammation.
                                                                                                                  A method has been developed of selecting a test compound for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Justice A;
                                                                                                                                                                                                                                                                                                                                                                                                  3; Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Miljanich GP,
                                                                                                                                                                                                                                                                                                                                                                                                  DB
                                                                                                                                                                                                                                                                                                                                                                                                                                   12; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                64.2%; Score 77; 34.6%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CKLKGQSCRKTSYDCCSGSCGRSGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CXIXNOXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Valentino KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB14359 standard; peptide; 26 AA.
                                                                               Disclosure, Fig 1; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Omega-conopeptide SVIB/SNX-183.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93US-00049794.
96US-00675354.
96US-00742774.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gohil KC,
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-490177/43.
                                                                                                                                                                                                                                                                                                                                                             Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US6087091-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-APR-1993,
03-JUL-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB14359;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB14359
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                                                                                                                                                                                                                                                                                       Sequences AAW95564-573 represent primary sequences of natural omegaconopeptides. Omega-conopeptides are components of peptide toxins produced by marine snails of the genus Conus, and which act as calcium channel blockers. The invention relates to a method of producing analgesia in a mammal that comprises administering an omega conopeptide having activities in (a) inhibiting electrically stimulated contraction of guinea pig ileum and (b) selectively binding to omega conopeptide of guinea pig ileum and (b) selectively binding to omega conopeptide WIIA binding sites in neuronal tissue, where these activities are within used for treating chronic pain, especially neuropathic pain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neuropathic; pain; conotoxin;
binding;
norepinephrine; noradrenaline;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                              Production of analgesia in mammal - by administration of omega cono-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Measuring the activity of test compounds in blocking voltage-gated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
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                                                                                                                                  Singh T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64.2%; Score 77; DB 2; Length 26; 34.6%; Pred. No. 4.4; ive 12; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gohil
                                                                                                                                Justice A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Miljanich GP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Omega conopeptide; analgesic; nociceptive; marine snall; peptide toxin; inflammation; voltage-gated calcium channel; inhibition; anti-inflammatory.
                                                                                                                              Valentino KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | CKLKGQSCRKTSYDCCSGSCGRSGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Natural omega conopeptide SVIB/SNX-183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Valentino KL,
                                                                                                                                                                                                                                                          Disclosure, Fig 1B; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY56480 standard; peptide; 26 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91US-00814759.
93US-00049794.
96US-00675354.
96US-00742774.
96US-00675354
                                  91US-00814759
93US-00049794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9; Conservative
                                                                                                                            Gohil KC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ELAN-) ELAN PHARM INC
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                                                                                       (NEUR-) NEUREX CORP.
                                                                                                                                                               WPI; 1999-120002/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 26 AA;
                                                                                                                          Miljanich GP,
03-JUL-1996;
                                                    15-APR-1993;
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03-JUL-1996;
01-NOV-1996;
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                                                                                                                                                                                                                   peptide(s)
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AAY56480;

Best Loc Matches

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Conus sp.

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Gaps

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                                                                                       The present sequence is an omega-conopeptide from marine snails of the genus Conus. Omega-conopeptides are components of peptide toxins produced by the cone snails, and which act as calcium channel blockers. Natural omega-conopeptides and their derivatives may be useful for producing analgesia in nociceptive and neuropathic pain. The peptides bind to omega-conopeptide binding sites, which are present mainly in neuronal tissue, and inhibit norepinephrine release from nervous tissue. Conopeptides such as MVITA and TVIA are effective as therapeutic agents for treating neurogenic conditions such as schizophrenia, tardive dyskinesia and acute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (III) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity.
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of test compound in blocking voltage-gated calcium channels, binding omega conopeptide binding site and inhibiting norepinephrine release.
                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.
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                                                                                                                                                                                                                                                                                                                                     Length 26;
                                                                                                                                                                                                                                                                                                                                                                         5; Indels
                                                                                                                                                                                                                                                                                                                                       77; DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Holmes DL,
                                                                                                                                                                                                                                                               dystonic reactions, inflammation and epilepsy
                                                                                                                                                                                                                                                                                                                                   64.2%; Score 77; DB 34.6%; Pred. No. 4.4; ive 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 653-654; 733pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                    | ::: |::: |:|::: | | | | | :: | :: :| CKLKGOSCRKTSYDCCSGSCGRSGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Milner PG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB92221 standard; peptide; 26 AA
                                                        Example 4; Fig 1; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0134406P.
99US-0153406P.
99US-0159783P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Toxin peptide SEQ ID NO:1397.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-MAY-2000; 2000WO-US013576
                                                                                                                                                                                                                                                                                                                 Query Match
Query Match
Best Local Similarity 34.0.,
Best Local 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CONJ-) CONJUCHEM INC
                                                                                                                                                                                                                                                                                                  Sequence 26 AA;
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10-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB92221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ношо
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB9222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enhancing analgesia produced by opiates by administering an omega-
conopeptide that inhibits electrically stimulated contraction of guinea
pig ilium and binds to omega-conopeptide MVIIA binding sites in neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents an omega-conopeptide. Omega-conopeptides
vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular uptake and interference with physiological processes. AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention
                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                 Primary sequence of a natural omega-conopeptide SVIB/SNX-183.
                                                                                                                                                                         Length 26
                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Miljanich GP,
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                                                                                                                                                                                                     12; Mismatches
                                                                                                                                                                         64.2%; Score 77;
                                                                                                                                                                                                                               1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                AAB19449 standard; peptide; 26
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93US-00081863.
96US-00675354.
96US-00742774.
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                                                                                                                                                                                       34.6%;
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                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                      Best Local Similarity
Matches 9; Conserv
                                                                                                                                             Sequence 26 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                            AAB19449;
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                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        epilepsy
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us-10-627-685a-1.rag

Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiant;

Omega-conopeptide S6.2 generic toxin sequence.

(first entry)

12-JUL-2002

ABB96786;

ABB96786 standard; peptide; 26 AA.

ABB96786

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are components of peptide toxins which act as voltage-gated calcium channel inhibitors. The peptides are used to enhance the analgesic effect produced by an optate in a mammalian subject. The method comprises administering to the subject an omega-conopeptide which is able to inhibit electrically stimulated contraction of the guinea pig ileum and bind to omega-conopeptide MVIIA binding sites present in neuronal tissue. Omega-conopeptides are useful for enhancing the analgesic effect produced by an opiate. Omega-conopeptides are useful for enhancing the analgesic effect produced by an opiate. Omega-conopeptides may also be used in the treatment of pain, in reducing neuronal damage related to an ischemic condition in ammals, and in treating schizophrenia, tardive dyskinesia and acute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cone snail; venomous saliva; calcium channel blocking activity; stenocardia; hypertension; myocarditis; arrhythmia; cerebral ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A new peptide derived from venomous saliva of assassin bug, has calcium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64.2%; Score 77; DB 4; Length 26; 34.6%; Pred. No. 4.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Indels
                                                                                                                                                                                                                                                                                                                                                                             dystonic reactions, inflammation and epilepsy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.6%; Preq. nc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |::: |:|:: ||||:: | CKLKGQSCRKTSYDCCSGSCGRSGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cone snail w-conotoxin peptide SVIB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 4; 26pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAO15126 standard; peptide; 26 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-SEP-2000; 2000JP-00266187.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-SEP-2000; 2000JP-00266187.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; Conservative
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SUNR ) SUNTORY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JP2002080499-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA015126;
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Jabel= OTHER / 1251-Tyr, mono-iodo-Tyr or di-iodo-Tyr or O-iodo-Tyr or O-sulpho-Tyr or O-Phospho-Tyr"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to isolated omega-conopeptides, nucleic acid sequences encoding them, and propeptide sequences. The activity of the peptides of the invention may be described as, analgesic, anticonvulsant,
                                                                                                                                                       neuroprotective; cerebroprotective; cardiovascular; antiinflammatory; antimigraine; antidiabetic; tranquiliser; vulnerary; antipsychotic; anxidiytic; neuroleptic; voltage gated ion channel; seizure; epilepsy; neurological disorder; neurovic injury; hypoxia; anoxia; ischaemia; stroke; cerebrovascular accident; brain trauma; spinal chord trauma; drowning; suffocation; perinatal asphyxia; hypoglycaemic event; pain; migraine; inflammation; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New omega-conopeptides useful for treating disorders associated voltage gated ion channels e.g. pain, inflammation, neurologic o cardiovascular disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shon K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Garrett JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M, Watkins M,
Cartier GE;
                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Page 62; 195pp; English.
                                                                                                                                                                                                                                                                                           psychosis; anxiety; schizophrenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-JUL-2001; 2001WO-US023041.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-2000; 2000US-0219616P.
05-FEB-2001; 2001US-0265888P.
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Jones RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         toxin sequences
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(COGN-) COGNETIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-257318/30.
                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference 13
                                                                                                                                                                                                                                                                                                                                 Conus striatus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jacobsen R,
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Gaps

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Indels

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64.2%; Score 77; DB 5; Length 26;

34.6%; Pred. No. 4.4; ive 12; Mismatches

Query Match
Best Local Similarity 34.6 Matches 9; Conservative

CXIXNOXCXQXLDDCCSXXCNXXNXC 26

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Query Match
Best Local Similarity
Matches 9; Conserv
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Jacobsen R,
                                                                                                                                                                      ABB96790;
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                                                                                                                        RESULT 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method for detecting or measuring the form of Motch that mediates Norch signal transduction in a sample of cells. The method involves detecting or measuring the expression of a Norch heterodimer containing reducing agent-sensitive linkage in the cells and comparing detected or measured expression to the detected or measured expression of full-length Notch in the cells. The present sequence is Xenopus Notch/Xotch (XenN) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or
                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detecting or measuring forms of Notch mediating Notch signal transduction, by comparing detected or measured expression of Notch meterodimer containing reducing agent-sensitive linkage to detected measured expression of full-length Notch.
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/note= "Nuclear localisation signal (NLS)"
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  Length 26;
                        4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "Nuclear localisation signal,
                                                                                                                                                                                                                                                                                                                                                     /note="EGF repeat"
1447. 1561
/note="Lin-12/Notch repeat (LN)"
1728. 1749
/note = Transmembrane (TN) domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2451. .2509
/note= "PEST-containing region"
 DB 5;
            Pred. No. 8; ; Mismatches
                                                                                                                                                                                                                                                                                                                      20. .2523
/note= "Mature N2 protein"
20. .1425
61.7%; Score 74;
34.6%; Pred. No. 8
                                                                                                                                                                                                           Xenopus sp. Notch/Xotch (XenN) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "Ankyrin repeat"
                                                56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 3; 63pp; English.
                                                             | ::: |:|::: | | | | | | :: | :: : | CKLKGQSCRRTMXDCCSGSCGRRGKC 26
                                                                                                                                                                                                                                                                                              1. .19
/label= Signal_peptide
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                                                                                                                                                                                                                                   Notch; signal transduction; detection
                                                1 CXIXNQXCXQXLDDCCSXXCNXXNXC
                                                                                                                                   ADL26915 standard; protein; 2523 AA
                                                                                                                                                                                                                                                                                   Location/Qualifiers
                        13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qi H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-00121457
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                                                                                                                                                                                   (first entry)
                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-178437/17.
           Local Similarity
les 9; Conserv
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                                                                                                                                                                                   20-MAY-2004
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                                                                                                                                                                                                                                                            Xenopus sp
                                                                                                                                                           ADL26915;
Query Match
                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                      Protein
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                                                                                                                                                                                                                                                                                                                                                                                               Domain
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                        Matches
                                                                                                          RESULT 75
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Sequence 2523 AA;

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/note= "OTHER is Tyr, 1251-Tyr, mono-iodo-Tyr or di-iodo-
Tyr or O-sulpho-Tyr or O-Phospho-Tyr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to isolated omega-conopeptides, nucleic acid sequences encoding them, and propeptide sequences. The activity of the peptides of the invention may be described as, analgesic, anticonvulsant, vasotropic, cardiant, neuroprotective, cerebroprotective, cardiovascular, antiinflammatory, antimigraine, antidiabetic, tranquiliser, vulnerary, antipsychotic, anxiolytic and neuroleptic. Peptides of the invention act by modulating the activity of voltage gated ion channels. They may be used for treating or preventing disorders especiated with voltage gated ion channels such as neurological disorders, e.g. seizure (associated with epilepsy), neurotoxic injury associated with conditions of hypoxia, anoxia, ischaemia, stroke, cerebrovascular accident, brain or spinal chord trauma, drowning, suffocation, perinatal asphyxia or hypoglycaemic
                                                                                                                                                                                                                                                                                                                                                                          neuroprotective; cerebroprotective; cardiovascular; antiinflammatory; antimigraine; antidiabetic; tranquiliser; vulnerary; antipsychotic; antidiabetic; voltage gated ion channel; seizure; epilepsy; neurological disorder; neurotoxic injury; hypoxia; anoxia; sehamia; stroke; cerebrovascular accident; brain trauma; spinal chord trauma; drowning; suffocation; perinatal asphyxia; hypoglycaemic event; pain; migraine; inflammation; cardiovascular disorder; psychosis; anxiety; schizophrenia.
                                        Gaps
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   Length 2523;
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                                                                                                                                                                                                                                                                                                                                                              Omega-conopeptide; analgesic; anticonvulsant; vasotropic;
                                      Indels
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                                                                                                                                                                                                                                                                                                                         Omega-conopeptide w-SVIB generic toxin sequence.
60.0%; Score 72; DB 8; ilarity 34.6%; Pred. No. 7e+02; Conservative 12; Mismatches
                                                                                               247 GFSGQNCEENIDDCPSNNCRNGGTCV 272
                                                                          2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
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Cartier GE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                        ABB96790 standard; peptide; 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-2000; 2000US-0219616P.
05-FEB-2001; 2001US-0265888P.
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COGNETIX INC.
                                                                                                                                                                                                                                                                                    (first entry)
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Jones RM,
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38

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Gaps

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Length 26; Indels

; 7

57.5%; Score 69; DB 30.8%; Pred. No. 22; ive 12; Mismatches

Similarity 30.8% 8; Conservative

Query Match Best Local S

Matches

Sequence 26 AA;

56 26

> Ä 56

AAR39617 standard; peptide;

AAR39617

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(revised)
(first entry)

25-MAR-2003 20-DEC-1993

SNX231.

AAR39617;

1 CXIXNQXCXQXLDDCCSXXCNXXNXC |: : :|::: | | | | | :: | CKGKGAPCRKTMYDCCSGSCGRRGKC

us-10-627-685a-1.rag

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events; pain e.g. migraine; inflammation or cardiovascular disorders. They may also be used for treating psychiatric disorders e.g. psychosis, anxiety or schizophrenia. The analgesic agents of the invention show diminished side effects and toxicity, and are non-addictive. The sequences given in records ABB96698-A3B96806 represent omega-conopeptide generic toxin sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Use of omega-cono-peptide(s) which selectively inhibit voltage-gated calcium channels - to induce analgesia, enhance opiate analgesics, treat
                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                Omega conopeptide, OCT, analgesia, inhibition, voltage-gated, calcium channel, neurone, contraction, guinea pig, ileum, MVIIA, binding site, toxin, marine, snail, Conus, opiod, chronic pain,
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                                                                                                  5; Length 26
                                                                                                                      Indels
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                                                                                                                      5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Valentino KL,
                                                                                               58.3%; Score 70; DB 34.6%; Pred. No. 18; ive 12; Mismatches
                                                                                                                                        1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                     |::: |:|::: |||||::| CKLKGQSCRKTSXDCCSGSCGRSGKC 26
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                                                                                                                                                                                                                 AAR39616 standard; peptide; 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92WO-US011349
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                                                                                                                                                                                                                                                             (revised)
(first entry)
                                                                                                                     Conservative
                                                                                  Query Match
Best Local Similarity
9; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NEUR-) NEUREX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1993-227270/28
                                                                           AA;
                                                                                                                                                                                                                                                                                                                                                                                                   Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                           Disulfide-bond
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                                                                           Seguence 26
                                                                                                                                                                                                                                                                                           MVIIC/SNX230
                                                                                                                                                                                                                                                           25-MAR-2003
20-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-JUL-1993.
                                                                                                                                                                                                                                                                                                                                                  narcotics.
                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                        AAR39616;
                                                                                                                                                                                             RESULT 77
                                                                                                                                                                                                        AAR39616
                                                                                                                                                                                                                 8.5666666
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Omega conopeptide; OCT; analgesia; inhibition; voltage-gated; calcium channel; neurone; contraction; guinea pig; ileum; MVIIA; binding site; toxin; marine; snail; Conus; opiod; chronic pain;

Location/Qualifiers

1. .16

Key Disulfide-bond

narcotics. Synthetic. Modified-site

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The sequences given in AAR39608-30 are omega conopeptides (OCTS) and derivatives of these, which may be used to produce analgesia in a mammal. These OCTs inhibit voltage-gated calcium channels selectively in neuronal tissue. This is shown by the peptides ability to stimulate contraction in guinea pig ileum and to bind to OCT MVIIA binding sites present in neuronal tissue. OCTs are components of peptide toxins derived from marine snails of the genus Conus, and act as calcium channel blockers. These OCTs may be used to replace opiods in the treatment of chronic pain or to reduce the opiod dosage required. This helps to reduce dependence on and tolerance to opiod narcotics. (Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Use of omega-cono-peptide(s) which selectively inhibit voltage-gated calcium channels - to induce analgesia, enhance opiate analgesics, treat
                                                                                                                                                                                                                                                                                                                                                                                                                                    Miljanich GP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.5%; Score 69; DB 2;
30.8%; Pred. No. 22;
iive 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                 Valentino KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gohil K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 1; 90pp; English.
                                                                                                                                                                                                                                                "4Hyp"
                                                                                                                                                                                                                                                                                                                                                      92WO-US011349.
                                                                                                                                                                                                                                                                                                                                                                                91US-00814759.
                                                                                                                                                                                                                                               /note= "
8. .20
15. .26
                                                                                                                                                                                                                                                                                                                                                                                                                                Singh T,
                                                                                                                                                                                                                                                                                                                                                                                                       (NEUR-) NEUREX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1993-227270/28.
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 26 AA;
                                                                                                                                                                                                                                                            Disulfide-bond
                                                                                                                                                                                                                                                                          Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                             10-DEC-1991;
                                                                                                                                                                                                                                                                                                 409313128-A1
                                                                                                                                                                                                                                                                                                                                                      30-DEC-1992;
                                                                                                                                                                                                                                                                                                                           08-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                 Justice A,
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Gaps

; 0

Conservative

The sequences given in AAR39608-30 are omega conopeptides (OCTS) and derivatives of these, which may be used to produce analgesia in a mammal. These OCTS inhibit voltage-gated calcium channels selectively in neuronal tissue. This is shown by the peptides ability to stimulate contraction in guinea pig ileum and to bind to OCT MVIIA binding sites present in marrons itssue. OCTS are components of peptide toxins derived from marine snails of the genus Conus, and act as calcium channel blockers. These OCTS may be used to replace opiods in the treatment of chronic pain or to reduce the opiod dosage required. This helps to reduce dependence on and tolerance to opiod narcotics. (Updated on 25-MAR-2003 to correct PN field.)

Claim 1; Fig 1; 90pp; English.

pain etc.

Length 26; 6; Indels

Gaps

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Length 26; Indels

7

57.5%; Score 69; DB llarity 30.8%; Pred. No. 22; Conservative 12; Mismatches

Local Similarity les 8; Conserv

1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26

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AAR37761 standard; peptide; 26

(first entry) (revised)

25-MAR-2003 08-SEP-1993

AAR37761;

WVIIC/SNX-230.

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Query Match
                Best Loc
Matches
                                                                                                                                        RESULT 80
                                                                                                                                                          AAR37761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inchaemia-related neuronal damage in mammals is reduced by admin., 4-24

The after onset of ischaemia, of a cpd. (I) which binds selectively to an onega-conotoxin (OCT) MVITA site in neuronal Lissue. (I) has selectivity

at least 100 expressed as ratio of binding affinity for the MVITA site to that for the MVITG site. (I) is one of the OCTS MVITA, MVITB, GVIA, GVIIA

CC that for it is the cpd. SNX-207. (I) is esp. used to reduce neuronal camage caused by stroke. By delaying admin. for some time (compare USSO51403 where cpds. are given within 1 hr of the onset of ischaemia) a cylorater redn. in neuronal damage is achieved. (I) is admin. e.g. by compare co
                                                                                                                                                                                                                                                                  Ischaemia; neuronal; omega-conotoxin; OCT; MVIIA; MVIIC; MVIID; MVIIB; GVIA; GVIIA; RVIA; SVIA; TVIA; SVIB; SNX-207; stroke; delayed treatment; antihistamine; blood pressure; N-type voltage-gated Ca currents; N-channel mediated neurotransmitter release.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Redn. of neuronal damage caused by ischaemia - by admin. of cpds. that bind specifically to omega-conotoxin MVIIA binding sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fox JA, Valentino KL, Bitner RS;
                                                                                                                                                                                                                                                                                                                                                                                                                               note= "hydroxyproline"
                                CXIXNOXCXOXIDDCCSXXCNXXNXC
                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 1; 103pp; English.
                                                                                                                        AAR37762 standard; peptide; 26 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92WO-US009766.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91US-00789913
92US-00916478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bowersox SS,
                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                 1. .16
                                                                                                                                                                                      (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1993-182487/22.
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                                                                                                                                                                                                                                                                                                                                                                                                Disulfide-bond
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Disulfide-bond
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Yamashiro DH;
                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
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17-JUL-1992;
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                                                                                                                                                                                                       08-SEP-1993
                                                                                                                                                                                      25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                       AAR37762;
                                                                                                            AAR37763
                                                                                            RESULT
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Ischaemia, neuronal, omega-conotoxin, OCT, MVIIA, MVIIC; MVIID; MVIIB; QVIA, GVIIA, RVIA, VIA, SVIA, TVIA, SVIB, SMX-207; stroke, delayed treatment; antihistamine, blood pressure, N-type voltage-gated Ca currents; N-channel mediated neurotransmitter release.

Location/Qualifiers

Disulfide-bond Disulfide-bond Disulfide-bond

Synthetic

WO9310145-A1.

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rechaemia-related neuronal damage in mammals is reduced by admin., 4-24

hr after onset of ischaemia, of a cpd. (I) which binds selectively to an omega-conoctomia (OCT) WVITA site in neuronal tissue. (I) has selectivity

that for the MVIIC site. (I) is one of the OCTS MVIIA, MVIIB, GVIIA, GVIIA, at least 100 expressed as ratio of binding affinity for the MVIIA site to that for the MVIIC site. (I) is esp. used to reduce neuronal damage caused by stroke. By delaying admin. For some time (compare USSOS1403 where cpds. are given within 1 hr of the onset of ischaemia) a greater redn. in neuronal damage is achieved. (I) is admin. e.g. by intracerbroventricilar (ICV) injection at 0.1-20 microg/Kg, but can also be given i.v. (opt. after treatment with antihistamines to minimise redn. in blood pressure caused by (I)). (I) is also at least as effective as the specified conotoxins for (I) selective inhibition of N-the specified conotoxins for (I) selective inhibition of N-channel mediated neurotransmitter release in neuronal tissue. Primary sequences of omega-conopeptides are given in AAR37752-62. Several analog or of the specified sare given in AAR37752-62. Several analog or omega-conopeptides are given in AAR37752-62. Several analog
Disclosure; Fig 1; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          correct PN field.
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correct PN field.) Sequence 26 AA;

Redn. of neuronal damage caused by ischaemia - by admin. of cpds. that bind specifically to omega-conotoxin MVIIA binding sites.

WPI; 1993-182487/22.

Miljanich GP, Yamashiro DH;

Bitner RS;

Bowersox SS, Fox JA, Valentino KL,

(NEUR-) NEUREX CORP.

92WO-US009766. 91US-00789913.

12-NOV-1992; 12-NOV-1991; 17-JUL-1992;

27-MAY-1993

Query Match

ð 셤 27-AUG-2003 13-OCT-1997

AAW19552;

RESULT 81 AAW19552

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The present peptide is an omega conopeptide, useful as an analgesic, especially for treating neuropathic pain. The peptide, which can be prepared by solid phases synthesis, can also be used to inhibit neuronal damage and treat schizophrenia, tardive dyskinesia, acute dystonic reactions, inflammation and epilepsy. In a rat paw formalin test, the peptide had an EDSO of greater than 1.0 microg in phase 1, and greater than 1.0 microg in phase 1, and greater than 1.0 microg in phase 2 (by intrathecal administration). (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                              Omega conopeptide; analgesic; treatment; neuropathic pain; inhibition; neuronal damage; schizophrenia; tardive dyskinesia; analgesia; acute dystonic reactions; inflammation; epilepsy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Omega cono:peptide(s) - useful as analgesics, esp. for treating neuropathic pain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.5%; Score 69; DB 2; Length 26; 34.6%; Pred. No. 22; ive 11; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conus genus natural omega-conopeptide MVIIC/SNX-230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Justice A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Valentino KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | : : | | : : : | | | : : : | CKGKGAXCRKTMYDCCSGSCGRRGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Col 53-54; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                    AAW12987 standard; peptide; 26 AA.
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92WO-US011349.
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                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                       Omega conopeptide SNX-231
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-APR-1993;
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30-DEC-1992;
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22-APR-1997
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06-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
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                                                                                                                                AAW12987;
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ID AAW7

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAM19544-W19553 are naturally occurring omega conopeptides (OCS) isolated from Conus sp. (cone snails). The peptides and their analogues are used as analgesics acting by blocking N-rype voltage-sensitive calcium channels. The OCS can be used to treat neuropathic pain as a result of e.g. insult to the spinal cord or peripheral nerves, cancer, bone degenerative diseases, AIDS, reflex sympathetic dystrophy, herpes zoster neuropathy, diabetic neuropathy, hyperesthesia, allodynia or hyperalgesia. The OCs are preferably administered in a medicament via an chyperalgesia. The OCs are preferably administered in a medicament via an epidence of a permeation endancer, at doses that are comparable to absence of a permeation enhancer, at doses that are comparable to effective analgesic doses using intrathecal administration. OC effective analgesic doses using intrathecal administration. OC commulations comprising an OC and a carboxylic acid buffer anti-oxidant. They also confer stability to solutions containing them for prolonged contains the containing th
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                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conopeptide; cone snail; pain; analgesic; neuropathy; epidural; N-type voltage-sensitive calcium channel; block; Conus.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Natural omega-conopeptide MVIIC/SNX-230 used for pain relief.
            Length 26;
                                                        6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 26;
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; Pred. No. 22;
12; Mismatches
DB '
  57.5%; Score 69; DB
30.8%; Pred. No. 22;
iive 12; Mismatches
                                                                                                1 CXIXNQXCXQXLDDCCSXXCNXXNXC 25
                                                                                                                           1 CXIXNQNCXQXLDDCCSXXCNXXNXC 26
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CKGKGAPCRKTMYDCCSGSCGRRGKC 26
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Luther RR;
                                                                                                                                                                                                                                                              AAW19552 standard; peptide; 26 AA.
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                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                   8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bowersox SS,
Pettus MR, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stable omega conopeptide
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                      Best Local Similarity
Matches 8: Conserv
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Best Local Similarity
Matches 8; Conserv
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08-MAR-1996;
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Amstutz GA, Gadbois T,

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16-JAN-1997

Singh

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Gaps

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                                                                                                                                                                                                                                                                                                                                   A method has been developed for the treatment of inflammation in a subject. The method comprises administration of an omega-conopeptide effective to: (i) block voltage-gated calcium channels; (ii) bind with high affainty to an omega-conopeptide binding site; and (iii) inhibit neurotransmitter release from nervous tissue. The method is used to treatmention and associated pain. The treatment can also be used to produce analgesia (especially in subjects experiencing neuropathic pain); and to treat schizophrenia, tardive dyskinesia and acute dystonic represents a natural omega-conopeptide. Omega-conopeptides are components of peptide toxins produced by marine snails of the genus components act as calcium channel blockers. (Updated on 27-AUG-2003 to correct OS
         Conus genus; marine snail; cone snail; omega-conopeptide; analgesia; nociceptive pain; neuropathic pain; neuronal tissue; conotoxin; inflammation; schizophrenia; tardive dyskinesia; acute dystonic reaction; rheumatoid arthritis; epilepsy;
                                                                                                                                                                                                                                                           Treatment of inflammation, comprises administration of omega-conopeptide - effective to block voltage-gated calcium channels, bind with high affinity to omega-conopeptide binding site, and inhibit neuro-transmitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conus genus; marine snail; cone snail; omega-conopeptide; analgesia; nociceptive pain; neuropathic pain; neuronal tissue; conotoxin; inflammation; schizophrenia; tardive dyskinesia; acute dystonic reaction; rheumatoid arthritis; epilepsy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                  Singh T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Indels
                                                                                                                                                                                                                    Justice A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genus natural omega-conopeptide SVX-231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12; Mismatches
                                                                                                                                                                                                                  Gohil KC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57.5%; Score 69;
30.8%; Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |: : : |:::: || || || |:: | :: : | CKGKGAPCRKTMYDCCSGSCGRRGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW72613 standard; peptide; 26 AA
                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 1; 58pp; English.
                                                                                                                                                  91US-00814759.
93US-00049794.
96US-00675354.
                                                                                                                                                                                                                  Valentino KL,
                                                                                                                               96US-00742774.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

Query Match

Best Local Similarity 30.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (revised)
(first entry)
                                                                                                                                                                                              (NEUR-) NEUREX CORP.
                                                                                                                                                                                                                                         WPI; 1998-582596/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 26 AA;
                                                                                                                                                                                                                 Miljanich GP,
                                                                                                                                                  30-DEC-1991;
15-APR-1993;
03-JUL-1996;
                                                                                                                               01-NOV-1996;
                                                                                    US5824645-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-AUG-2003
06-JAN-1999
                                                                                                          20-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW72613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Н
                                                                                                                                                                                                                                                                                             release
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       field.)
                                                               Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 84
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A method has been developed for the treatment of inflammation in a subject. The method comprises administration of an omega-conopeptide effective to: (i) block voltage-gated calcium channels; (ii) bind with high affanity to an omega-conopeptide binding site; and (iii) inhibit neurotransmitter release from nervous tissue. The method is used to treat inflammation and associated pain. The treatment can also be used to produce analgesia (especially in subjects experiencing neuropathic pain); and to treat schizophrenia, tardive dyskinesia and acute dystonic reactions, rheumatoid arthritis, and epilepsy. The present sequence represents a natural omega-conopeptide. Omega-conopeptides are components of peptide toxins produced by marine snails of the genus Conus, and which act as calcium channel blockers. (Updated on 27-AUG-2003 to correct OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treatment of inflammation, comprises administration of omega-conopeptide - effective to block voltage-gated calcium channels, bind with high affinity to omega-conopeptide binding site, and inhibit neuro-transmitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Omega-conopeptide; peptide toxin; snail; calcium channel blocker; analgesia; guinea pig ileum; omega-conotoxin; pain; neuropathic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Singh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Justice A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gohil KC,
                                               /label= Hyp
/note= "hydroxyproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CXIXNOXCXQXLDDCCSXXCNXXNXC 26
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | : : : | | | | | : : : : | CKGKGAPCRTMYDCCSGSCGRRGKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                        91US-00814759.
93US-00049794.
96US-00675354.
                                                                                                                                                                                                                                         96US-00742774.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Valentino KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= 4Hyp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Omega-conopeptide SNX-231.
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                                                                                                                                                                                                                                                                                                                                                                                                       (NEUR-) NEUREX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-582596/49.
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Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 26 AA;
Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Miljanich GP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
Modified-site
                                                                                                                                                                                                                                         01-NOV-1996;
                                                                                                                                                                                                                                                                                             30-DEC-1991;
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03-JUL-1996;
                                                                                                                               US5824645-A
                                                                                                                                                                                    20-OCT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW95572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     release
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 85
AAW95572
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15-APR-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US5994305-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5-APR-1993
                                                                               peptide(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                 Conus sp
                                                                                                                                                                                                                                                                                                    RESULT 87
AAY56482
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                                                                                                                                                                                                     Sequences AAW95564-573 represent primary sequences of natural omegaconopeptides. Omega-conopeptides are components of peptide toxins produced by marine snails of the genus Conus, and which act as calcium channel blockers. The invention relates to a method of producing analgesia in a mammal that comprises administering an omega conopeptide having activities in (a) inhibiting electrically stimulated contraction of guinea pig ileum and (b) selectively binding to omega conopeptide WVIIA binding sites in neuronal tissue, where these activities are within the ranges of those of omega-conotoxins WVIIA and TVIA. The method is
                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Omega-conopeptide; peptide toxin; snail; calcium channel blocker; analgesia; guinea pig ileum; omega-conotoxin; pain; neuropathic.
                                                                                                                                                             Production of analgesia in mammal - by administration of omega
                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                 used for treating chronic pain, especially neuropathic pain
                                                                                                                                                                                                                                                                                                                  Justice A,
'note= "4-Hydroxyproline"
                /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "C-terminal amide"
                                                                                                                             Valentino Kü,
                                                                                                                                                                                                                                                                                                                                                     56
                                                                                                                                                                                                                                                                                                                                                             |: : : | | | | | | : | | | | CKGKGAPCRKTMYDCCSGSCGRRGKC 26
                                                                                                                                                                                                                                                                                                                                                   CXIXNOXCXOXTDDCCSXXCNXXNXC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                      Disclosure; Fig 1B; 59pp; English
                                                                                                                                                                                                                                                                                                                                                                                                             AAW95573 standard; protein; 26
                                                                                   91US-00814759
93US-00049794
                                                                   96US-00675354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    · 96US-00675354
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                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Omega-conopeptide SNX-230
                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                           Gohil KC,
                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
"Local 8; Conserve
                                                                                                           (NEUR-) NEUREX CORP.
                                                                                                                                            WPI; 1999-120002/10.
                                                                                                                                                                                                                                                                                                  Sequence 26 AA;
                                                                                                                           Miljanich GP,
        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
Modified-site
                                                                  03-JUL-1996;
                                                                                  30-DEC-1991;
15-APR-1993;
                                 US5859186-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-DEC-1991;
                                                  12-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                               29-MAR-1999
                                                                                                                                                                      peptide(s).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US5859186-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                              AAW95573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conus sp.
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Sequences AAW95564-573 represent primary sequences of natural omegaconopeptides. Omega-conopeptides are components of peptide toxins produced by marine snails of the genus Conus, and which act as calcium channel blockers. The invention relates to a method of producing analgesia in a mammal that comprises administering an omega conopeptide having activities in (a) inhibiting electrically stimulated contraction of guinea pig ileum and (b) selectively binding to omega conopeptide WIIA binding sites in neuronal tissue, where these activities are within used for treating chronic pain, especially neuropathic pain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        binding;
norepinephrine; noradrenaline;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neuropathic; pain; conotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                          omega cono-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                              Singh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Length 26;
                                                                                                                                                                                     Production of analgesia in mammal - by administration of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                            Justice A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Valentino KL, Miljanich GP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.5%; Score 69; DB 30.8%; Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Omega conopeptide, analgesic, nociceptive, marine snall, peptide toxin, inflammation, voltage-gated calcium channel; inhibition; anti-inflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12; Mismatches
                                                                                            Valentino KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CKGKGAPCRKTMYDCCSGSCGRRGKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CXIXNQXCXQXLDDCCSXXCNXXNXC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                       Disclosure; Fig 1B; 59pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Natural omega conopeptide SNX-231.
93US-00049794.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91US-00814759.
93US-00049794.
96US-00675354.
96US-00742774.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY56482 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Conservative
                                                                                            Gohil KC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ELAN-) ELAN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Justice A, Singh T,
                                              (NEUR-) NEUREX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-038270/03.
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Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 26 AA;
                                                                                         Miljanich GP,
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A method has been developed of selecting a test compound for treating inflammation. The method comprises measuring the activity of the test compound in blocking voltage-gated calcium channels, binding to the omega conopeptide binding steam of inhibiting norepinephrine (noradrenaline) release from nervous tissue. The method is useful for selecting compounds for treating inflammation. The selected compounds are capable of producing analgesia in a mammalian subject with chronic or intractable pain. Analgesic caused by selected compounds may reduce the reliance on opioid analgesic agents of the prior art which cause dependency and tolerance, requiring potentially dangerous increases in opioid doses to achieve the analgesic effect. The present sequence represents an omega conopeptide given in the present invention
test compounds in blocking voltage-gated to the omega conopeptide binding site and (noradrenaline) release for treating
                                                                                                                              Disclosure; Fig 1; 47pp; English
Measuring the activity of calcium channels, binding inhibiting norepinephrine
                                                                                inflammation
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Sequence 26 AA;

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                          Gaps
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Score 69; DB 3; Length 26; Pred. No. 22;
                         6; Indels
           ; Pred. No. 22;
11; Mismatches
                                                  CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                              |: : ||:::: ||||::| CKGKGAXCRKTMYDCCSGSCGRRGKC 26
 57.5%;
                         Conservative
            Local Similarity
nes 9; Conserv
   Query Match
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AAY5648;

AAYS6481 standard; peptide; 26 (first entry) 16-FEB-2000 AAY56481;

Natural omega conopeptide MVIIC/SNX-230.

neuropathic; pain; conotoxin; binding; norepinephrine; noradrenaline; Omega conopeptide; analgesic; nociceptive; marine snail; peptide toxin; inflammation; voltage-gated calcium channel; inhibition;

Conus

US5994305-A

98US-00138439 21-AUG-1998;

93US-00049794. 96US-00675354. 96US-00742774. 91US-00814759 30-DEC-1991; 01-NOV-1996; 15-APR-1993 03-JUL-1996

(ELAN-) ELAN PHARM INC.

Valentino KL, Miljanich GP,

WPI; 2000-038270/03

Justice A, Singh T,

Measuring the activity of test compounds in blocking voltage-gated calcium channels, binding to the omega conopeptide binding site and inhibiting norepinephrine (noradrenaline) release for treating inflammation

The present sequence represents an omega-conotoxin. Omega-conotoxins are isolated from venoms of predatory marine snalls, and have a selectivity for N-type calcium channels over P/O type channels, and so block N-type calcium channels. The omega-conotoxins of the invention can be used in any disease or disorder where blockage of N-type calcium channels is required, e.g. in the reduction of neuronal damage following ischemia, production of analgesia, or enhancement of opiate analgesia, in the treatment of schizophrenia, stimulant induced psychoses, hypertension, inflammation, and diseases which cause bronchotension, and also in the inhibition of progression of neuropathic pain. They can also be used in screen to identify compounds with activity at N-type voltage sensitive

calcium channels

Novel peptides used for the treatment of disorders and diseases where blockage of the N-type calcium channels is required.

Disclosure; Page 12; 81pp; English.

Disclosure; Fig 1; 47pp; English.

A method has been developed of selecting a test compound for treating

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inflammation. The method comprises measuring the activity of the test compound in blocking voltage-gated calcium channels, binding to the omega compound in blocking voltage-gated calcium channels, binding to the omega compopetide binding site and inhibiting norepinephrine (noradrenaline) release from nervous tissue. The method is useful for selecting compounds for treating inflammation. The selected compounds are capable of producing analgesia in a mammalian subject with chronic or intractable pain. Analgesia caused by selected compounds may reduce the reliance on
                                                                                                                                                       opioid analgesic agents of the prior art which cause dependency and tolerance, requiring potentially dangerous increases in opioid doses to achieve the analgesic effect. The present sequence represents an omega conopeptide given in the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Omega-conotoxin, venom; predatory marine snail; N-type calcium channel; neuronal damage reduction; ischemia; analgesia; opiate analgesia; schizophrenia; stimulant induced psychosis; hypertension; inflammation;
                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bronchotension; neuropathic pain; voltage sensitive calcium channel
                                                                                                                                                                                                                                                                                                                      Length 26;
                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nielsen KJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amino acid sequence of an omega-conotoxin MVIIC.
                                                                                                                                                                                                                                                                                                                        ë,
                                                                                                                                                                                                                                                                                                          DB 7
                                                                                                                                                                                                                                                                                                                                                              12; Mismatches
                                                                                                                                                                                                                                                                                                                      57.5%; Score 69; 30.8%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alewood PF,
                                                                                                                                                                                                                                                                                                                                                                                                             1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                     Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY43715 standard; peptide; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98AU-00002989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-AU000288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lewis RJ,
                                                                                                                                                                                                                                                                                                                                                                   8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QUEENSLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-013226/01.
                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                           Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drinkwater RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09954350-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-APR-1998;
01-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYQU ) UNIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY43715;
                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 89
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Gaps

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Indels

9

ed. No. 22; Mismatches

12;

Conservative

Similarity 8; Conserv

Local

Best

Matches

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26 56

1 CXIXNQXCXQXLDDCCSXXCNXXNXC

Ş

AAB14372 standard; peptide; 26

AAB14372

RESULT

(first entry)

06-DEC-2000

AAB14372;

Omega-conopeptide SNX-231

Pred. No.

30.8%;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is an omega-conopeptide from marine snails of the genus Conus. Omega-conopeptides are components of peptide toxins produced by the cone snails, and which act as calcium channel blockers. Natural omega-conopeptides and their derivatives may be useful for producing analgesia in nociceptive and neuropathic pain. The peptides bind to omega-conopeptide binding sites, which are present mainly in neuronal tissue, and inhibit norepinephrine release from nervous tissue. Conopeptides such as MVIIA and TVIA are effective as therapeutic agents for treating neurogenic conditions such as schizophrenia, tardive dyskinesia and acute dystonic reactions, inflammation and epilepsy
                                                                                                                                                                                                                                                                                               Marine snail; omega-conopeptide; calcium channel blocker; MVIIC; SNX-230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Selecting a compound for producing analgesia involves measuring activity of test compound in blocking voltage-gated calcium channels, binding to omega conopeptide binding site and inhibiting norepinephrine release.
                                                               Gaps
                                                                                                                                                                                                                                                                                                               toxin; analgesic; antiinflammatory; anticonvulsant; neuroleptic; norepinephrine release inhibitor; schizophrenia; tardive dyskinesia; acute dystonic reaction; inflammation; epilepsy.
                                                             ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Justice A;
                                DB 3; Length 26; 22;
                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Miljanich GP,
                                                            . 9
                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "C-terminal amide"
                             57.5%; Score 69;
30.8%; Pred. No. 3
                                                                                      26
                                                                                                    1 CXIXNQXCXQXLDDCCSXXCNXXNXC
                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Valentino KL,
                                                                                                                                                                                      Ā
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                                                                                                                                                                                                                                                                       Omega-conopeptide MVIIC/SNX-230.
                                                         12;
                                                                                                                                                                                  AAB14377 standard; peptide; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91US-00814759.
93US-00049794.
96US-00675354.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-00298017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96US-00742774
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                                                                                                                                                                                                                                          (first entry)
                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Selecting a compound for of test compound in block
                                                                                                                                                                                                                                                                                                                                                                                                                 1. .16
8. .20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-490177/43,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gohil KC,
                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                            Disulfide-bond
Disulfide-bond
Disulfide-bond
Sequence 26 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                           06-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-APR-1993;
03-JUL-1996;
01-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US6087091-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-DEC-1991;
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                                                                                                                                                                                                               AAB14377;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Singh T,
                                                                                                                                                                                                                                                                                                                                                                    Conus
                                                         Matches
                                                                                                                                                          RESULT 90
                                                                                                                                                                                                                                                                                                                                                                                                 ξę
                                                                                                                                                                      AAB1437
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Marine snail; omega-conopeptide; calcium channel blocker; SNX-231; toxin; analgesic; antiinflammatory; anticonvulsant; neuroleptic; norepinephrine release inhibitor; schizophrenia; tardive dyskinesia; acute dystonic reaction; inflammation; epilepsy.

Location/Qualifiers

Disulfide-bond

Key

g

Conus

Modified-site

label= 1. .16

> Disulfide-bond Disulfide-bond

Modified-site

US6087091-A. 11-JUL-2000.

/note= "C-terminal amide"

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The present sequence is an omega-conopeptide from marine snails of the genus Conus. Omega-conopeptides are components of peptide toxins produced by the cone snails, and which act as calcium channel blockers. Natural omega-conopeptides and their derivatives may be useful for producing analgesia in nociceptive and neuropathic pain. The peptides bind to omega-conopeptide binding sites, which are present mainly in neuronal tissue, and inhibit norrepinephrine release from nervous tissue. Conopeptides such as WVIIA and TVIA are effective as therapeutic agents for treating neurogenic conditions such as schizophrenia, tardive dyskinesia and acute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Selecting a compound for producing analgesia involves measuring activity of test compound in blocking voltage-gated calcium channels, binding to omega conopeptide binding site and inhibiting norepinephrine release.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     э;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dystonic reactions, inflammation and epilepsy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 69; DB
Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure, Fig 1; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 26 AA;
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Length 26;

DB 3;

57.5%; Score 69;

Sequence 26 AA?

Query Match

Justice A;

Miljanich GP,

Valentino KL,

Gohil KC,

Singh T,

WPI; 2000-490177/43.

(ELAN-) ELAN PHARM INC

21-AUG-1998; 15-APR-1993 03-JUL-1996

91US-00814759. 93US-00049794. 96US-00675354.

96US-00742774 98US-00138439

99US-00298017.

23-APR-1999;

30-DEC-1991;

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(first entry)

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Omega-conopeptide; voltage-gated calcium channel inhibitor; analgesic; peptide toxin; opiate; pain; neuronal damage; ischemic condition; schizophrenia; tardive dyskinesia; acute dystonic reaction; inflammation;
                                                                                                            Primary sequence of a natural omega-conopeptide SNX-231,
                                    AAB19450 standard; peptide; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ELAN-) ELAN PHARM INC.
                                                                                                                                                                                                                                     Disulfide-bond
                                                                                                                                                                                                                                                                                      Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                      39-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                      US6136786-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                            15-APR-1993;
                                                                                    06-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                            24-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                               30-DEC-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-JUN-1993
                                                            AAB19450;
                                                                                                                                                                           epilepsy.
                                                                                                                                                                                                   Conus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Singh T,
           RESULT 93
AAB19450
                                                             The present invention describes a modified therapeutic peptide (I)

comprising a therapeutically active amino acid region (III) and a
reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
a less therapeutically active amino acid region (IV), which covalently
conds with amino/hydroxyl/thiol groups on blood components to form a
peptidase stabilised therapeutic peptide composed of 3-50 amino acids.

(I) are useful for modifying therapeutic peptides e.g. hormones, growth
factors and neurotransmitters, to protect them from peptidase activity in
vivo for the treatment of various disorders. Endogenous therapeutic
peptides are not suitable as drug candidates as they require frequent
administration due to rapid degradation by peptidases in the body.

Modifying and attaching therapeutic peptides to albumin prevents or
reduces the action of peptidases to increase length of activity (half
IIfe) and specificity as bonding to large molecules decreases
intracellular uptake and interference with physiological processes.

AAB90829 to AAB92441 represent invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity.
 Gaps
                                                                                                                                                                                                              Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.5%; Score 69; DB 4; Length 26; 30.8%; Pred. No. 22; cive 12; Mismatches 6; Indels
Indels
 . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Holmes DL,
11; Mismatches
                       1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                    Disclosure; Page 653; 733pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Milner PG,
                                                                                                             Ą
                                                                                                            AAB92220 standard; peptide; 26
                                                                                                                                                                                                                                                                                                                                                                            99US-0134406P.
99US-0153406P.
99US-0159783P.
                                                                                                                                                                                        Toxin peptide SEQ ID NO:1396.
                                                                                                                                                                                                                                                                                                                                                      17-MAY-2000; 2000WO-US013576.
                                                                                                                                                             (first entry)
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bridon DP, Ezrin AM,
                                                                                                                                                                                                                                                                                                                                                                                                                               (CONJ-) CONJUCHEM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-112059/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 26 AA;
                                                                                                                                                                                                                                                                                                    WO200069900-A2
                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                         10-SEP-1999;
15-OCT-1999;
                                                                                                                                                               22-JUN-2001
                                                                                                                                                                                                                                                                                                                             23-NOV-2000
                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                      AAB92220;
Matches
                       8
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/note= "amidated C-terminal"

/label= Hyp /note= "hydroxyproline"

8. .20 15. .26

Location/Qualifiers

.16

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                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents an omega-conopeptide. Omega-conopeptides are components of peptide toxins which act as voltage-gated calcium channel inhibitors. The peptides are used to enhance the analgesic effect produced by an opiate in a mammalian subject. The method comprises administering to the subject an omega-conopeptide which is able to inhibit electrically stimulated contraction of the guinea pig ileum and bind to omega-conopeptide MVIA binding sites present in neuronal tissue. Omega-conopeptides are useful for enhancing the analgesic effect produced by an opiate. Omega-conopeptides may also be used in the treatment of pain, in reducting neuronal damage related to an ischemic condition in mammals, and in treating schizophrenia, tardive dyskinesia and acute dystonic reactions, inflammation and epilepsy
                                                                            Enhancing analgesia produced by opiates by administering an omega-
conopeptide that inhibits electrically stimulated contraction of guinea
pig ilium and binds to omega-conopeptide MVIIA binding sites in neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 57.5%; Score 69; DB Best Local Similarity 30.8%; Pred. No. 22; Matches 8; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                    Disclosure; Fig 1; 58pp; English.
WPI; 2001-030946/04.
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Gaps

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CXIXNOXCXQXLDDCCSXXCNXXNXC 26 |: : : |:::: | | | | | :: | :: : | CKGKGAPCRKTMYDCCSGSCGRRGKC 26

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Conservative

Justice

Miljanich GP,

Valentino KL,

Gohil KC,

93US-00049794. 93US-00081863. 96US-00675354. 96US-00138439. 99US-00298017.

99US-00392979

Gaps

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Indels

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AAB19451;

RESULT 94

ð 셤 AAB1945

Conus sp.

Key

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The invention comprises peptides having calcium channel blocking activities which are derived from the venomous saliva of assassin bugs. The calcium channel blocking peptides of the invention are useful for treating stenocardia, hypertension, myocarditis, arrhythmia and cerebral ischaemia. The present amino acid sequence represents a cone snail wconotoxin peptide
                                                                                                                                                                                                                                                                                                                                           Cone snail; venomous saliva; calcium channel blocking activity; stenocardia; hypertension; myocarditis; arrhythmia; cerebral ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conotoxin; MVIIC; peptide library; disulphide bond; biological activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A new peptide derived from venomous saliva of assassin bug, has calcium channel blocking activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57.5%; Score 69; DB 5; Length 26; 30.8%; Pred. No. 22; ive 12; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Omega-conotoxin MVIIC peptide sequence SEQ ID NO:1.
 ed. No. 22;
Mismatches
   Pred. No.
                                                                             |: : : | : : : | | | | | : : | : : | CKGKGAPCRKTMYDCCSGSCGRRGKC 26
                                                     1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CXIXNOXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cone snail w-conotoxin peptide MVIIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 4; 26pp; Japanese.
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                   12;
                                                                                                                                                                                       AAO15125 standard; peptide; 26
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 30.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-SEP-2000; 2000JP-00266187
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                                                                                                                                                                                                                                                                   (first entry)
                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           calcium channel blocker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-421068/45.
Best Local Similarity
Matches 8; Conserv
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         JP2002080499-A.
                                                                                                                                                                                                                                                                 22-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                     w-conotoxin
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                                                                                                                                                                                                                             AA015125;
                                                                                                                                                                                                                                                                                                                                                                                                                       Conus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG68252;
                                                                                                                                                   RESULT 95
                                                                                                                                                                     AA015125
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                                                                                                                                                                                                           ð
                                                                                         임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
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                                                                                                                                                                                                                                                                                             Omega-conopeptide; voltage-gated calcium channel inhibitor; analgesic; peptide toxin; opiate; pain; neuronal damage; ischemic condition; schizophrenia; tardive dyskinesia; acute dystonic reaction; inflammation; epilepsy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents an omega-conopeptide. Omega-conopeptides are components of peptide toxins which act as voltage-gated calcium channel inhibitors. The peptides are used to enhance the analgesic effect produced by an opiate in a mammalian subject. The method comprises administering to the subject an omega-conopeptide which is able to inhibit electrically stimulated contraction of the guinea pig ileum and bind to omega-conopeptide MVIA binding sites present in neuronal tissue. Omega-conopeptides are useful for enhancing the analgesic effect produced by an opiate. Omega-conopeptides may also be used in the treatment of pain, in reducing neuronal damage related to an ischemic condition in mammals, and in treating schizophrenia, tardive dyskinesia and acute dystonic reactions, inflammation and epilepsy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enhancing analgesia produced by opiates by administering an omega-
conopeptide that inhibits electrically stimulated contraction of guinea
pig illum and binds to omega-conopeptide MVIIA binding sites in neuronal
tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Justice A;
                                                                                                                                                                                                                                                         Primary sequence of a natural omega-conopeptide SNX-230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Valentino KL, Miljanich GP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "amidated C-te:rminal"
           CXIXNOXCXQXLDDCCSXXCNXXNXC 26
                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 1; 58pp; English.
                                                                                                                                           AAB19451 standard; peptide; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93US-00049794.
93US-00081863.
96US-00675354.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-00392979
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-00298017
                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ELAN-) ELAN PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Singh T, Gohil KC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-030946/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disulfide-bond
Disulfide-bond
Disulfide-bond
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 26 AA;
                                                                                                                                                                                                                   06-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US6136786-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-APR-1993
23-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-JUL-1996
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Gaps

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Indels

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Conus sp

DB 4; Length 26;

Score 69;

57.5%;

Query Match

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16-JUL-1993;
                                                                                                             16-JUL-1993;
               Conus magus.
                                     US5591821-A.
                                                              07-JAN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADP04517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                  The present invention describes a method for manufacturing a peptide library comprising a peptide (1) having 2 or more intramolecular disulphide (ID) bonds, and its variants (V). The method comprises containing two or more amino acids, for chemo-synthesising (1) and (V), where the ID bonds are formed between the peptides by air oxidation, and ID-containing peptides are separated. Also described are: (1) a peptide inbrary obtained by the above said method; (2) screening for mutant peptide with an improved biological activity than its wild type, comparising comparing the biological activity than its wild type, peptide library with a wild type peptide; (3) a mutant peptide obtained by the above said screening method; and (4) a calcium channel blocker containing Omega-conotoxin MVIIC peptide. The method is useful for synthesising a peptide library, and for screening peptides with increased biological activity than the wild type peptides. The method is suitable for producing many number of variants for a given peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents an omega-conotoxin MVIIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Omega-conotoxin; conus; Conus magus; alpha-conotoxin; mu-conotoxin; nicotinic acetylcholine receptor; venom; skeletal muscle; inhibitor; sodium ion channel; presynaptic neuronal calcium ion channel; therapy; P-like subtype; N-type channel; respiratory rhythm; respiratory control; neural developmental syndrome; respiratory crisis;
                                                                                                                                                                                                                                                                peptide mixture for synthesizing peptide of interest and its variants, forming intramolecular disulphide bonds between peptides and separating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            simultaneously. The present sequence represents an omega-conotoxin MVLI
peptide which is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                   Manufacturing peptide library, by introducing mutant amino acid in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57.5%; Score 69; DB 30.8%; Pred. No. 22; ive 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Full length omega-conotoxin MVIIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW12803 standard; peptide; 29 AA
                                                                          /note= "amidated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lambert-Eaton myasthenic syndrome
                                                                                                                                                                                                                                                                                                                Example; Fig 1; 11pp; Japanese.
                                                                                                                                                                         13-MAR-2000; 2000JP-00068023.
                                                                                                                                                 13-MAR-2000; 2000JP-00068023.
                                                                                                                                                                                                 (MITU ) MITSUBISHI CHEM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Conservative
                        1. .16
8. .20
15. .26
                                                                                                                                                                                                                          WPI; 2002-044564/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                       Disulfide-bond
Disulfide-bond
Disulfide-bond
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 26 AA;
                                                                                                JP2001253899-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-APR-1997
                                                                                                                        18-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW12803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                         them
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 97
AAW12803
ID AAW1
8
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This sequence represent omega-conotoxins isolated from Conus magus.

This sequence represents the MVIIC Conus magus omega-conotoxins. Conus verom contains three types of disulphide rich peptides, these are the alpha-conotoxins target and block the nicotinic acetylcholine receptors, the mucronotoxins target and block the nicotinic acetylcholine receptors, the mucronotoxins target and block the presynaptic neuronal calcium con channels. The omega-conotoxin peptides of the invention can target P-conotoxins target and block the presynaptic neuronal calcium con channels. The omega-conotoxin peptides of the invention can target P-conotoxins target and block the presynaptic neuronal calcium con channels are presented of calcium ion channels when the presence or absence of sites for the peptides can be used for distinguishing the types of calcium ion channel capressing calls into various types. As these sequences affect the control of respiratory rhythms in vivo, they can be used to evaluate abnormalities in respiratory control which are particularly severe in the neonatal period. The peptides can also be used for assessing neural captal period. The peptides can also be used for assessing neural captal can be used to evaluate abnormalities in respiratory control which are particularly severe in the developmental period. The peptides can also be used for assessing and can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sea squirt protein with tissue specific expression in development Seq112.
                                                                                                                                                                                                                                                                                                                                                                                                                                New omega-conotoxin peptide(s) - which target P-type and N-type calcium ion channels, used for distinguishing calcium channels or for disgnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sea squirt, regeneration medicine, gene therapy, cell proliferation, differentiation, reproduction, environmental measurement, water survey.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    used to diagnose the Lambert-Eaton myasthenic syndrome
                                                                                                                                                                                                                                                          Olivera BM, Hillyard DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.5%; Score 69; DB 30.8%; Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | : : : | : : : | | | | | : : | : : | CKGKGAPCRKTMYDCCSGSCGRRGKC 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Col 29-30; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADP04517 standard; protein; 342 AA
93US-00092215.
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                                                                                93US-00092215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-JUL-2004 (first entry)
                                                                                                                                                                                                                                                          Monje VD, Imperial JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                WPI; 1997-086679/08.
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                                                                                                                                                                     (UTAH ) UNIV UTAH.
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The invention relates to a method of inducing differentiation of at least one epithelial cell. The method involves exogenously providing at least one epithelial cell. The method involves exogenously providing at least one opithelial cell, whereby the Notch pathway is activated within at least one epithelial cell, whereby the Notch pathway is activated within at least one epithelial cell, whereby the Notch pathway is activated within at least one epithelial cell, producing differentiation of the call is induced. Methods of producing differentiation of at least one epithelial barrier cormation, for retarding progression of skin cancer and for diagnosing agreesive melanoma are also provided. The methods are useful for inducing differentiation of at least one epithelial cell e.g. a careful for inducing differentiation of epithelial cell within cutaneous epithelial tissue or dermal equivalent, or within extracutaneous epithelial tissue, gastrointestinal epithelial tissue, cornea epithelial tissue, cornea epithelial contraction of the progression of skin contraction of the progression of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer such as aggressive melanoma, aggressive cutaneous T-cell lymphoma (CTCL), aggressive squamous cell carcinoma, or aggressive basal cell carcinoma, or aggressive basal cell carcinoma, by preferably administering an antagonist of the Notch pathway such as gamma secretase inhibitor. The present sequence represents a
                                                                                                                                                                                                                                                                                              formation within epithelium for treating psoriasis, sunburn, involves exogenously providing a source of a Notch agonist to the epithelial cell.
                                                                                                                                                                                                                                                                     epithelial cell useful for inducing barrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes; inflammation; autoimmune disorder; allergy; blood disorder; acquired immunodeficiency syndrome; AIDS; obesity; asthma; immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis; Alzheimer's disease; infection; str.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56.7%; Score 68; DB 5; Length 2444; 30.8%; Pred. No. 1.58+03; ive 12; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248 GFTGQNCEENIDDCPGNNCKNGGACV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human NOVX protein homologue SegID 469.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                constitutively active notch-1 protein
                                                                                                                                                                                                                                                                                                                                                                                  Claim 10; Page 50-66; 101pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADI16933 standard; protein; 2444 AA
31-AUG-2000; 2000US-0229614P.
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                                                    (LOYO ) UNIV LOYOLA CHICAGO
                                                                                                                                                                                                                                                                  differentiation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 30.55
Best Local Similarity 30.55
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                                                                                                                Nickoloff BJ, Miele L;
                                                                                                                                                                        WPI; 2002-339659/37.
                                                                                                                                                                                                          N-PSDB; ABL40768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2444 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200268649-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-APR-2004
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8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention relates to novel genes and the encoded proteins thereof
that are derived from the sea squirt Ciona intestinalis. Specifically, it
refers to those genes that are expressed in the tissues or organs of the
cas squirt during its developmental phase. The present invention
describes the identification of these genes as useful for elucidation of
the mechanism of development and hence for developing regeneration
medicines and gene therapy techniques. Accordingly, they can be used in
the research of various genetic diseases, as well as the analysis of cell
proliferation, differentiation and reproduction. Furthermore, such
compositions can be useful for environmental measurements and water
surveys, particularly for sea water surveys, and also for the preparation
of transformed sea squirt for improving edibility of sea squirt such as
Halocynthia roretzi. This polypeptide sequence is a sea squirt protein
sequence that has tissue specific expression during development, given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7
                                                                                                                                                                                                                      Novel gene cluster which is specifically expressed in tissue or organ during developmental phase of sea squirt, useful for elucidation of mechanism of development of tissue or organ of sea squirt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cell differentiation, notch; epidermis; cytostatic; dermatological; epithelial; skin; cancer; gamma secretase; notch-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'n,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 342;
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/note= "encoded by NCC"
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                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 112; 1846pp; Japanese.
                                                                       (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
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note= "encoded by CNG"
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Matches 10, Conservative
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(CURA-) CURAGEN CORP.

Burgess CE Zerhusen BD, Patturajan M, Shimkets RA; garu M, Anderson DW, Rastelli L, Miller CE; Gusev VY, Colman SD, Wolenc AR, Pena CEA; sobrook JP, Lepley DM, Rieger DK, Burgess CE Padigaru M, Ander RJ, Gusev VY, Cc , Alsobrook JP, I ev VT, Spytek KA, Gangolli EA, Padi Taupier RJ, Li L, Gauss Gerlach VL, Taupler '' K. Grosse WM, Tchernev VT,

WPI; 2002-706998/76.

New NOVX polypeptides and nucleic acids, useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or pharmacogenomics.

Disclosure; SEQ ID NO 469; 1498pp; English.

This invention relates to a novel nucleic acids, and encoded polypeptides thereof, which have properties related to the stimulation of biochemical or physiological responses in a cell, tissue, organ or organism.

diagnostic and prognostic assays and furthermore in the treatment of diagnostic and prognostic assays and furthermore in the treatment of diagnostic and prognostic assays and furthermore in the treatment of diagnostic and diagnostic as well as methods to modulate their expression using antisense oligos, riboxymes and peptide nucleic acids.

The NOVX polypeptides, polynucleotides and antibodies are useful in the treating or preventing NoVX-associated disorders, e.g. cardiomyopathy, atherosclerosis, cancer and diabetes. Furthermore, they may be used in treating or preventing diseases such as inflammation, autoimmune treating or preventing diseases such as inflammation, autoimmune fullery, atherity, asthma, immunoglobulin (19)A nephropathy, cirrhosis, arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy and employers, the monoglopulin (19)A nephropathy, cirrhosis, and epilepsy, Accordingly, these molecules have many activities including cytostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic, hemostatic, nephrotropic, antiarthritic, hepatotropic, anorectic, cultaxant and anticonvulsant. In addition, they are useful in screening casasays to identify small molecules that modulate or inhibit, for example, neurogenesis, wound healing and angiogenesis. The nucleic acids are also the incorporation of a human NOVX protein of the angent of a human NOVX protein ö Gaps Specifically, it refers to the use of biologically active fragments ; Query Match 56.7%; Score 68; DB 5; Length 2444; Best Local Similarity 30.8%; Pred. No. 1.5e+03; Matches 8; Conservative 12; Mismatches 6; Indels 248 GFTGQNCEENIDDCPGNNCKNGGACV 273 2 XIXNOXCXOXLDDCCSXXCNXXNXCV 27 Search completed: April 18, 2005, 20:33:43 Job time : 127.5 secs Sequence 2444 AA; of the invention. 셤 8

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/cgn2 6/ptodata/1/jaa/PCTUS_COMB.pep:*
                                              GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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US-08-049-7913-19

US-08-496-847-19

US-08-75-374-19

US-08-965-918-19

US-08-965-918-19

US-08-965-918-19

US-09-398-017-19

US-09-398-017-19

US-09-392-979A-19

US-08-496-847-8

US-08-496-847-8

US-08-496-847-8

US-08-965-918-8

US-08-118-439-8

US-08-118-439-8

US-08-118-439-8

US-08-118-432-18

US-08-118-432-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-627-685A-1
120
1 CXIXNQXCXQXLDDCCSXXCNXXNXCV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 08*
Maximum Match 1008
Listing first 100 summaries
                                                                                                                                                                                                                 protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq length: 0
seq length: 200000000
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Match Length
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2523
2523
                                                                                         Copyright
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Perfect score:
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Maximum DB
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6
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Result No.

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MOLECULE TYPE: peptide HYPOTHETICAL: NO
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Best Local Similarity
Matches 9; Conserv
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RESULT 2
US-07-789-913-19
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US-08-049-794-19
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                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
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OTHER INFORMATION: /note= "Amino acid 4 may be 4-trans-hydroxyproline."
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                                                                                                                                                                     APPLICANT: Terlau, Heinrich
APPLICANT: Shon, Ki-Joon
APPLICANT: Shon, Ki-Joon
APPLICANT: Grilley, Michelle
APPLICANT: Glivera, Baldomero M.
TITLE OF INVENTION: Conctoxin Peptide PVIIA
NUMBER OF SEQUENCES:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/619,936
FILING DATE:
                ALIGNMENTS
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                                                                                                             Sequence 1, Application US/08619936
Patent No. 5672682
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 530
ATTORNEY AGENT INFORMATION:
NAME: Saxe, Stephen A.
REGISTRATION NUMBER: 38,609
REFRENCE/DOCKET NUMBER: 24266
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4848
TELEPHONE: 202-962-4848
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
ORGANISM: Conus purpurascens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                        Washington
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LOCATION:
FEATURE:
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, LOCATION:
US-08-619-936-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION:
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                                                                APPLICANT: Mijanich, George P.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Fox, James A.
APPLICANT: Valentino, Karen L.
APPLICANT: Yamashiro, Donald H.
TITLE OF INVENTION: Delayed Treatment Method of Reducing TITLE OF INVENTION: Ischemia-Related Neuronal Damage NUMBER OF SEQUENCES: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h 67.5%; Score 81; DB 1; Length 26; Similarity 34.6%; Pred. No. 0.29; 9; Conservative 13; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION NUMBER: US/07/789,913
FLLING DATE: 19911112
                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NOTE TO THE FILING DATE: 19911112
CLASSIFICATION: 514
PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: D2-AuG-1990
PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: PILING DATE: 22-NOV-1989
ATTORNEY/AGENT INFORMATION: NAME: Stratford, Carol A. REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0005. TELECOMOTUNICATION INFORMATION: TELECOMOTUNICATION INFORMATION: TELECOMOTUNICATION INFORMATION: TELECOMOTUNICATION INFORMATION: TELECOMOTUNICATION INFORMATION: TELECOMOTUNICATION OF SEQ ID NO: 19: SEQUENCE CHARACTERSFICS: LENGTH: 26 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
Sequence 19, Application US/07789913
Patent No. 5559095
GENERAL INFORMATION:
APPLICANT: Miljanich, George P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 19, Application US/08049794 Patent No. 5587454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-202
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SINGH, TEJINDER
GOHIL, KISHOR C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: JUSTICE
APPLICANT: SINGH,
APPLICANT: GOHIL,
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Gaps
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; Sequence 19, Application US/08742774
; Patent No. 5824645
; GENERAL INFORMATION:
APPLICANT: UUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
APPLICANT: WALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
NUMBER OF SQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
CITY: Palo Alto
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 67.5%; Score 81; DB 1; Length 26; Best Local Similarity 34.6%; Pred. No. 0.29; Matches 9; Conservative 13; Mismatches 4; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,774
                                                                                                                                        COMPUTER: IBM COMPACTOR.

COREATING SYSTEM: DOS

SOFTWARE: FESESEG for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,847

FILING DATE: 27-JUN-1995

CLASSIFICATION: 514

ATTORNEY FAGENT INFORMATION:
NAME: Stratford Carol A

REGISTRATION NUMBER: 34,444

REFERENCE/DOCKET NUMBER: 5865-0009.31

TELEPHONE: 650-324-0860

INFORMATION: 650-324-0860

INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTER/STICS:
LENGTH: 26 amino acids

"VIEW SECTION CAROLINGS SECONDO SECONDO
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INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
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CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION NUMBER: 08/675,354
FILING DATE: 03-UUL-196
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-APR-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein uventherICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-496-847-19
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Sequence 19, Application US/08496847

Patent No. 5795864

GENERAL INFORMATION:

APPLICANT: Ametutz, Gary A.

APPLICANT: Gohil, Kishrorchandra

APPLICANT: Adriaenseens, Peter I.

APPLICANT: Kristipati, Ramasharma

TITLE OF INVENTION: METHODS AND

TITLE OF INVENTION: FORMULATIONS FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dehlinger & Associates

STREET: 350 Cambridge Avenue, Suite 250

GITY:

CITY:

CI
APPLICANT: VALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: BETHODS OF PRODUCING ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSED: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
CONNTEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67.5%; Score 81; DB 1; Length 26; ilarity 34.6%; Pred. No. 0.29; Conservative 13; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARES DATEMENT Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 19930415
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: SELETEORY CAROL A:
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 26 amino acids TYPE: AMINO ACID
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 9; Conserva
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US-08-496-847-19
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APPLICANT: Bowersox, Stephen S.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Gohil, Kishorchandra
APPLICANT: Adrianessens, Peter I.
APPLICANT: Kristipati, Ramasharma
TITLE OF INVENTION: METHODS AND FORMULATIONS FOR PREVENTING
TITLE OF INVENTION: PROGRESSION OF NEUROPATHIC PAIN
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESSS:
STREET: 350 Cambridge & Associates
STREET: 350 Cambridge Avenue, Suite 250
                                                                       Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,918
FILING DATE: 07-NOV-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Mohr, Judy M.
REGISTRATION NUMBER: 38,563
REFERENCE/DOCKET NUMBER: 5865-0009.34
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                       67.5%; Score 81; DB 2; 34.6%; Pred. No. 0.29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67.5%; Score 81; DB 2; 34.6%; Pred. No. 0.29;
                                                                                                                 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13; Mismatches
           INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
                                                                                                                                                       1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
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Patent No. 5891849
GENERAL INFORMATION:
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Patent No. 5994305
GENERAL INFORMATION:
                                                                                                                 Conservative
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Best Local Similarity 34.6%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94306-1546
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                     Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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US-08-675-354-19
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US-09-138-439-19
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APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: GOHIL, KISHOR C
APPLICANT: WILDANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                       67.5%; Score 81; DB 2; Length 26; 34.6%; Pred. No. 0.29; 13; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORRENT APPLICATION DATA:
SOFTWAREN APPLICATION DATA:
APPLICATION NUMBER: US/08/675,354
FILING DATE: 03-UUL-1996
CLASSIFICATION 30
PRIOR APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-APR-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAMME: Stratford, Carol A.
REGISTRATION NUMBER: 5865-0009.30
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEL TYPE: protein
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
      5865-0009.30
                                                                                                                                                                                                                                                                                                                                                                                                            1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 19, Application US/08675354
Patent No. 5859186
GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
REFERENCE/DOCKET NUMBER: 586E TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 324-0880 TELEFAX: (415) 324-0960 INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS: LENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 34.69
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Palo Alto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-675-354-19
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Patent No. 6087091
GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: GOHIL, KISHOR C
APPLICANT: WALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: STATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/298,017
                                                                                             COMPUTER: IBM COMPATIONE
COMPUTER: IBM COMPATIONE
SOFTWARE: FASESE for windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/613,400A
FILING DATE: 08-MAR-1996
CLASSIFTATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTOMNEY/ABATION:
NAME: Stratford, Carol A
REGISTRATION NUMBER: 34,444
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0019
TELEPHONE: 650-124-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
US-08-613-400A-19
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/049,794
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
                           ZIP: 94306-1546
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94306
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            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY:
STATE:
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APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GGHIL, KISHOR C
APPLICANT: GGHIL, KISHOR C
APPLICANT: WILDANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 67.5%; Score 81; DB 2; Length 26; Best Local Similarity 34.6%; Pred. No. 0.29; Matches 9; Conservative 13; Mismatches 4; Indels
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Patent No. 605429
GENERAL INFORMATION:
APPLICANT: Bowersox, S. Scott
APPLICANT: Gadbois, Theresa
APPLICANT: Luther, Robert, R.
TITLE OF INVENTION: IMPROVED EPIDURAL
TITLE OF INVENTION: IMPROVED EPIDURAL
MUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Deblinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                   CUMPUTER: Lam PC Compatible
COMPRATE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/138,439
FILING DATE:
CLASSIFICATION:
PRICASSIFICATION:
PRICASSIFICATION:
PRICASSIFICATION:
PRICASSIFICATION:
PRICASSIFICATION:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1933-04-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATFORNEY/AGENT INPORMATION:
NAME: STEATEORY CANDATION:
NAME: STEATEORY CANDER: 34,444
REGISTRATION NUMBER: 34,444
REGISTRATION NUMBER: 34,444
REGISTRATION NUMBER: 34,444
RELEEPANCE: (415) 324-0960
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LEMOTH: 25 amino acids
LENGTH: 25 amino acids
LENGTH: 25 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
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                                                                                                                                                                                                                                                                                                                                             ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                     STREET: 350 Camb
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-613-400A-19
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Fatent No. 5559095
GENERAL INFORMATION:
APPLICANT: Miljanich, George P.
APPLICANT: Molanich, George P.
APPLICANT: Valentino, Karen L.
APPLICANT: Valentino, Karen L.
APPLICANT: Yamashiro, Donald H.
TITLE OF INVENTION: Delayed Treatment Method of Reducing TITLE OF INVENTION: Ischemia-Related Neuronal Damage
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 64.2%; Score 77; DB 1; Length 26; Best Local Similarity 34.6%; Pred. No. 0.65; Matches 9; Conservative 12; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTAMER Batentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 19911112
CLASSIFICATION: 514
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/561,766
FILING DATE: 02-NG-1990
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/440,094
FILING DATE: 22-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Strafford, Carol A.
REGISTRENCE/DOCKET NUMBER: 5865-0005.30
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NUMBER: 5865-0005.30
TELECOMMUNICATION NUMBER: 5865-0005.30
TELECOMMUNICATION NUMBER: 5865-0005.30
TELEFAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
FRANCENT OF APPLICATION:
NEGLEFAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
FRANCENT. 26 Amino acids
                                                                                                                                                       Query Match 67.5%; Score 81; DB 3; Best Local Similarity 34.6%; Pred. No. 0.29; Matches 9; Conservative 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Law Offices of Peter Dehlinger STREET: 350 Cambridge Avenue, Suite 300 CITY: Palo Alto STATE: CA
                                    HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
US-09-392-979A-19
                                                                                                                                                                                                                                                                                        1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide
NO
            MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE: INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: AMINO ACID TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                         US-07-789-913-8
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Patent No. 6136786

GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN'
APPLICANT: GOHIL, KISHOR C
APPLICANT: WILLIANICH, GEORGE P
ITILE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
ITILE OF INVENTION: ENHANCING OPLATE ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPLATE ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPLATE ANALGESIA
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Deblinger
STREET: 350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/392,979A
                                                                                                                                                                                                                                                                                                                                                                                                                                                67.5%; Score 81; DB 3; 34.6%; Pred. No. 0.29; tive 13; Mismatches
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELEPHONE: (415) 324-0880
TELEPHONE: (415) 324-0880
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION
FILING DATE:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-04-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        ; INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
US-09-298-017-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CXIXNOXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 34.64
Matches 9; Conservative
                                                                                                                                                                                                                               26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                 amino acid
GY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 350 Camb
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-392-979A-19
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                                                                                                                                                                                                                        LENGTH:
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Gaps

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Length 26;
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                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTESO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,847
FILING DATE: 27-JUN-1995
CLASSIFCATION: 514
ATTOMNEY/AGENT INFORMATION:
NAME: Stratford, Carol A
REGISTRATION NUMBER: 34,444
REFERRATION NUMBER: 5865-0009.31
TELEPHONE: 650-324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64.2%; Score 77; DB 1; 34.6%; Pred. No. 0.65;
APPLICANT: Adriaenseens, Peter I.
APPLICANT: Kristipati, Ramasharma
TITLE OF INVENTION: METHODS AND
TITLE OF INVENTION: FORMULATIONS FOR PREVEN
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE
US-08-496-847-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 64.2%; Score 77; DB Best Local Similarity 34.6%; Pred. No. 0.65 Matches 9; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/08742774; Patent No. 5824645; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORRATING SYSTEM: PC-DOS/MS-
SOFTWARE: Patentin Release #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPAX: 650-22.
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
'FWATH: 26 amino acids
                                                                                                                                                                                                      ZIP: US
ZIP: 94306-1546
COMPUTER READABLE FORM:
MEDIUM TYPE: Dieter
                                                                                                                                                                                                                                                                                                 Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Indels
                                                                                                                                                                                                                                                   APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: GOHIL, KISHOR C
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENFANCING OPIATE ANALGESIA AND
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRIED 94306

ZIP: 94306

COMPUTER PEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS.
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
TITING DATE: 19930415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Law Offices of Peter Dehlinger 350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 19930415
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTOWNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REPERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12; Mismatches
                                                   1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                             1 CKLKGQSCRKTSYDCCSGSCGRSGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CKLKGQSCRKTSYDCCSGSCGRSGKC 26
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US-08-496-847-8
'Sequence 8, Application US/08496847
'Patent No. 5795864
'French No. 5795864
'GENERAL INFORMATION:
                                                                                                                                                                                           Sequence 8, Application US/08049794
Patent No. 5587454
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amstutz, Gary A.
Bowersox, Stephen S.
Gohil, Kishorchandra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 9; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Palo Alto
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-049-794-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY:
STATE:
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METHODS AND
FORMULATIONS FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN
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APPLICANT: SINGH, TEJINDER
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: BNHANCING OPIATE ANALGESIA AND
TITLE OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSES: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
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Gaps

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APPLICANT: Bowersox, Stephen S.
APPLICANT: Gohll, Kishorchandra
APPLICANT: Adriaensens, Peter I.
APPLICANT: Kristipati, Ramasharma
TITLE OF INVENTION: METHODS AND FORMULATIONS FOR PREVENTING
TITLE OF INVENTION: PROGRESSION OF NEUROPATHIC PAIN
                                                                                                                                                                                                                                                                                                                                               Length 26;
                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/965,918
FILING DATE: 07-NOV-1997
CLASSIFICATION: 514
ATTORNATION: 514
ATTORNATION: MARKE: MOBER: J8,563
REGISTRATION NUMBER: 38,563
REFERRATION NUMBER: 38,563
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 34.6%; Pred. No. 0.65;
Matches 9; Conservative 12; Mismatches
                                                                                                                                                                                                                                                               • ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSES: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                          REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CKLKGQSCRKTSYDCCSGSCGRSGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                           1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/08965918
Patent No. 5891849
GENERAL INFORMATION:
                                                                                     (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Win
                                                                                                      TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                   : 26 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: US
ZIP: 94306-1546
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                          MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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                                                                                     TELEPHONE:
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                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                        US-08-675-354-8
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APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: GOHIL, KISHOR C
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1
US-08-742-774-8
                                PILLING DATE:

CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION NUMBER: 08/675,354
FILING DATE: 03-JUL-1996
APPLICATION NUMBER: 08/08/049,794
FILING DATE: 1993-APR-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATONEV/AGENT INFORMATION:
ATONEV/AGENT INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,774
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APPLICATION NUMBER: US/08/049,794
FILING DATÉ: 1993.APR-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 34.6*
...hes 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
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amino acid
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    : Patent No. 6054429
: GENERAL INFORMATION:
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                                              Gaps
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                                                                                                                                                                                                                       APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: MAINTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPLATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSE: LAW OFF:
Query Match '64.2%; Score 77; DB 2; Length 26; Best Local Similarity 34.6%; Pred. No. 0.65; Matches 9; Conservative 12; Mismatches 5; Indels
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Best Local Similarity 34.6%; Pred. No. 0.65;
Matches 9; Conservative 12; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/138,439
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 1993-04-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
APPLICATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                              1 CKLKGOSCRKTSYDCCSGSCGRSGKC 26
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CKLKGQSCRKTSYDCCSGSCGRSGKC 26
                                                                                        1 CXIXNOXCXQXLDDCCSXXCNXXNXC 26
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; Sequence 8, Application US/09138439
Patent No. 5994305
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein HYPOTHETICAL: NO
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TYPE: amino acid
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US-08-613-400A-8
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; Sequence 8, Application US/08613400A

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APPLICANT: Bowersox, S. Scott
APPLICANT: Gadbois, Theresa
APPLICANT: Petrus, Mark, R.
APPLICANT: Luther, Robert, R.
TITLE OF INVENTION: IMPROVED EPIDURAL
TITLE OF INVENTION: METHOD OF PRODUCING ANALGESIA
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/09298017
; Patent No. 6087091
; Patent No. 6087091
; GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: GOHIL, KISHOR C
APPLICANT: GOHIL, KISHOR C
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALC
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSE: Law Offices of Peter Denlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/613,400A
FILING DATE: 08-MAR-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1
                                                                                                                                                                                        ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Stratford, Carol A
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: S865-0019
TELECOMMUNICATION:
TELEPHONE: 650-324-0880
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                    ZIP: 94306-1546
ZIP: 94306-1546
COMPUTER READABLE FORM:
MEDIUM TYPE: Dieter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 650-324-0960 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                         Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein HYPOTHETICAL: NO
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APPLICANT: Artavanis-Tiakonas, Spyridon
APPLICANT: Artavanis-Tiabelle
APPLICANT: Diederich, Robert J.
APPLICANT: Xu, Tian
APPL
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,432
FILING DATE: 21-JAN-1994
CLASSIFICATION: 530
ATTONREY/AGBNT INFORMATION:
NAME: MASTOCKE S. Leslie
REGISTRATION NUMBER: 18,872
REGISTRATION NUMBER: 18,872
REGISCOMMUNICATION INFORMATION:
TELEFROMS: (212) 790-9090
TELEFRAX: (212) 780-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 34.6%; Pred. No. 0.65;
Matches 9; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1
              FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: STRATEORN (arc) A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFACE (415) 324-0860
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE GRARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acids
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: PENNIE & EDMONDS
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
US 07/814,759
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Patent No. 5750552
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1155 Aven
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
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APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: WALENTINO, KAREN L
APPLICANT: MILANICH, GEORGE P
TITLE OF INVENTION: BNHANCHOS OF PRODUCING ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
CONTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64.2%; Score 77; DB 3; Length 26; 34.6%; Pred. No. 0.65;
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                        ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BATENTIN Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/049,794
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/392,979A
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                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: SETALEGAC, CAROLA A.
REGISTRATION NUMBER: 34,44
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
TELEFAS: (415) 324-0960
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12; Mismatches
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RIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-04-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/09392979A Patent No. 6136786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 34.64
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 26 auricum
TVDE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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US-09-392-979A-8
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AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-049-794-29
                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 26
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| Sequence 3, Application US/09121457 |
| Patent No. 6699919 |
| Patent No. 6699919 |
| GENERAL INFORMATION: | APPLICANT: Arravanis-Tsakonas, S. |
| APPLICANT: Raid, M. |
| TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON |
| FILE REFERENCE: 1326-073 |
| CURRENT APPLICANTON NUMBER: US/09/121,457 |
| CURRENT APPLICANTON NUMBER: 08/899,232 |
| EARLIER PILING DATE: 1998-07-23 |
| NUMBER OF SEQ ID NOS: 4 |
| SOFTWARE: PatentIn Ver. 2.0 |
| SEQ ID NO 3 |
| LENGTH: 2523 |
                                                                                                                                                                                                                                                                APPLICANT: Artavania-Tsakonas, Spyridon
APPLICANT: Artavania-Tsakonas, Spyridon
APPLICANT: Oi, Huilin
TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON
TITLE OF INVENTION: 1366-1466
CURRENT APPLICATION NUMBER: US/08/899,232
CURRENT FILING DATE: 1997-07-23
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 2523
                                           Gaps
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0
60.0%; Score 72; DB 1; Length 2523; 34.6%; Pred. No. 1.1e+02; ive 12; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60.0%; Score 72; DB 4; I
34.6%; Pred. No. 1.1e+02;
ive 12; Mismatches 5,
                                                                                                    247 GFSGQNCEENIDDCPSNNCRNGGTCV 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               247 GFSGQNCEENIDDCPSNNCRNGGTCV 272
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                                                                              2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 XIXNOXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 21, Application US/08049794; Patent No. 5587454
                                                                                                                                                                          RESULT 23
US-08-899-232-3
; Sequence 3, Application US/08899232
; Patent No. 6436650
Query Match
Best Local Similarity 34.6'
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Xenopus sp.
US-08-899-232-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Xenopus sp.
                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 25
US-08-049-794-21
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: 7
; OTHER INFORMATION: /note= "where X is hydroxyproline"
12-08-049-794-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: BEHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
                                                                                     METHODS OF PRODUCING ANALGESIA AND ENHANCING OPIATE ANALGESIA
                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DUS/NS-DUS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 19330415
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRIONE: (415) 324-0880
TELEFRA: (415) 324-0860
INFORMATION FOR SEQ ID NO: 21: SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; DB 1;
                                                                                                                                        STREET: 350 Cambridge Avenue, Suite 300 CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57.5%; Score 69; 34.6%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNX-231, FIGURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 29, Application US/08049794; Patent No. 5587454
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: WALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF
TITLE OF INVENTION: BUHANCING C
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Pet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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Sequence 29, Application US/08496847

Sequence 29, Application US/08496847

Sequence 29, Application US/08496847

GENERAL INFORMATION:
APPLICANT: Ametutz, Gary A.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Adriaensens, Peter I.
APPLICANT: Krietipati, Ramasharma
TITLE OF INVENTION: PORMULATIONS FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Defilinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CORRESPONDENCE ABLOALTONS OF A PAIO ALCORDERS OF A PAIO A PAIO A A PAIO A PAIO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: 7; COTHER INFORMATION: /note= "where X is hydroxyproline" US-08-496-847-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,847
FILLIG DATE: 27-JUN-1995
CLASSIFCATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE: SNX-231, FIGURE 2
                                                                                                                             5865-0009.31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5865-0009.31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A
REGISTRATION NUMBER: 34,44
REFERENCE/DOCKET NUMBER: 5865
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
                                               ALIONARIA STRATEGORY

NAME: Strateford, Carol A
REGISTRATION NUMBER: 34,444
REPERENCE/DOCKET NUMBER: 586
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0960
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                           34,444
                           ATTORNEY/AGENT INFORMATION: NAME: Stratford, Carol A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
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ZIP: 94306-1546
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            650-324-0960
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JS-08-496-847-29
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Matches
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Sequence 21, Application US/08496847

Sequence 21, Application US/08496847

Seneral INFORMATION:

APPLICANT: Bowersox, Stephen S.

APPLICANT: Adriaenssens, Peter I.

APPLICANT: Kristipati, Ramasharma

TITLE OF INVENTION: PORMULATIONS FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSE: Deblinger & Associates

STREET: 350 Cambridge Avenue, Suite 250

CITY: Palo Alto
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                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 19930415
CLASSIFFICATION: DATA:
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol.A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 29:
SEQUIENCE CHARACTER LEGICS:
INFORMATION FOR SEQ ID NO: 29:
SEQUIENCE CHARACTER LEGICS:
INFORMATION FOR SEQ ID NO: 29:
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SOFTWARE: FASESEQ: for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,847
FILING DATE: 27-JUN-1995
3: Law Offices of Peter Dealinger 350 Cambridge Avenue, Suits 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-230, FIGURE 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: CA
COUNTRY: US
ZIP: 3306-1546
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 30.8%
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 26 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein HYPOTHETICAL: NO
                 STREET: 350
                                                                                                                                                                ZIP: 94306
ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-049-794-29
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                                                                                                                                    COUNTRY:
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APPLICANT: SINCH, TEJINDER
APPLICANT: SINCH, TEJINDER
APPLICANT: GOHLL, KISHOR C
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA AND
TITLE OF INVENTION: BUHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 26;
                         Length 26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57.5%; Score 69; DB 2; 30.8%; Pred. No. 3.4; tive 12; Mismatches
                         DB 2;
                         57.5%; Score 69; DB 34.6%; Pred. No. 3.4; ive 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
INDIVIDUAL įSOLATE: SNX-230, FIGURE 1
                                                                                                                                                                                    1 CKGKGAXCRKTMYDCCSGSCGRRGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |: : :|::: ||||::| :: :|
CKGKGAPCRKTMYDCCSGSCGRRGKC 26
                                                                                                                                                 1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                  Sequence 29, Application US/08742774
Patent No. 5824645
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
Query Match
Best Local Similarity 34.6*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Patent No. 5824645

GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: SINCH, TEJINDER
APPLICANT: SINCH, TEJINDER
APPLICANT: VALENTION, KAREN
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
                                                                                                                                                                                                       57.5%; Score 69; DB 1; Length 26; 30.9%; Pred. No. 3.4; Live 12; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: /note= "where X is hydroxyproline"
US-08-742-774-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Law Offices of Peter Dehlinger
350 Cambridge Avenue, Suite 300
            ) MOLECULE TYPE: protein
) HYPOTHETICAL: NO
) ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-230, FIGURE 1
US-08-496-847-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/675,354
FILING DATE: 03-ULL-1996
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-APR-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,44
REPERBENCE/DOCKET NUMBER: 5865-0009.3
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 334-0960
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                  1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                        1 CKGKGAPCRKTMYDCCSGSCGRRGKC 26
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                                                                                                                                                                                                          Query Match
Best Local Similarity 30.8%
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZUONIAL SERVICE STATE ST
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ర
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US-08-742-774-21
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57.5%; Score 69; DB 2; Length 26; 30.8%; Pred. No. 3.4; tive 12; Mismatches 6; Indels
                                  METHODS OF PRODUCING ANALGESIA AND ENHANCING OPIATE ANALGESIA
                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/675,354
FILING DATE: 03-UL-1996
CLASSIFICATION NUMBER: US/08/049,794
FILING DATE: 1993-APR-15
APPLICATION NUMBER: US/08/049,794
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: SLEAT FORM CAROL A.
REGISTRATION NUMBER: 34,444
REGISTRATION NUMBER: 34,444
REGISTRATION NUMBER: 34,444
REGISTRATION NUMBER: 34,4080
TELEPRANCK/DOCKET NUMBER: 5865-0009.30
                                                                                                                                                                            E: Law Offices of Peter Dehlinger
350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-230, FIGURE 1
US-08-675-354-29
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APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF
TITLE OF INVENTION: ENHANCING C
MUTMER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Pet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 30.8%
Them 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                   STREET: 350 Camb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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94306-1546
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                                                                                                                                                                                                                                                                                                                              COUNTRY:
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                                                                                                                       APPLICANT: UNIVERSITIE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR
APPLICANT: GOHIL, KISHOR
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: BHANCING OPIATE ANALGESIA AND
TITLE OF INVENTION: BHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57.5%; Score 69; DB 2; Length 26; 34.6%; Pred. No. 3.4; tive 11; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) LOCATION: 7
; OTHER INFORMATION: /note= "where X is hydroxyproline"
US-08-675-354-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NOTE: 03-01-1996
CLASSIFICATION: 530
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-APR-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REGISTRATION NUMBER: 34,444
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0960
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TVDEST AMINO ACID ACIDST AND ACIDST AMINO ACIDS AMINO ACIDS AMINO ACIDS AMINO ACIDS AMINO ACIDS AMINO ACIDS AMINO 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/675,354
FILING DATE: 03-JUL-1996
CLASSIFICATION: 530
                       Sequence 21, Application US/08675354; Patent No. 5859186; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 29, Application US/08675354
Patent No. 5859186
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JUSTICE, ALAN
SINGH, TEJINDER
GOHIL, KISHOR C
VALENTINO, KAREN L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 9; Conserva
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STATE: CP
COUNTRY:
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US-08-675-354-29
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Ametutz, Gary A.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Gonli, Kishorchandra
APPLICANT: Gonli, Kishorchandra
APPLICANT: Adriaensens, Peter I.
APPLICANT: Kristipati, Ramasharma
TITLE OF INVENTION: METHODS AND FORMULATIONS FOR PREVENTING
TITLE OF INVENTION: PROGRESSION OF NEUROPATHIC PAIN
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
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AUDRESSEE: Law Offices of Peter Dehlinger STREET: 350 Cambridge Avenue, Suite 300 CITY: Palo Alto
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PRIOR APPLICATION BATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-04-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                    ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-230, FIGURE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-231, FIGURE 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 21, Application US/09138439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TESTINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF
ITTLE OF INVENTION: ENHANCING OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECUMNOS. (415) 324-000
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 21
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (415) 324-0880
                                                  TYPE: amino acid
TOPOLOGY: 1:-
    TELEPHONE: 650-324-0880
TELEPAX: 650-324-0960
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 30.8%
Matches 8; Conservative
                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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US-09-138-439-21
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| US-08-965-918-29
| Sequence 29, Application US/08965918
| Patent No. 5891849
| GENERAL INFORMATION:
| APPLICANT: Bowersox, Stephen S. |
| APPLICANT: Gary A. |
| APPLICANT: Gold, Kishorchandra |
| TITLE OF INVENTION: METHODS AND FORMULATIONS FOR PREVENTING |
| TITLE OF INVENTION: METHODS AND FORMULATIONS FOR PREVENTING |
| TITLE OF INVENTION: PROGRESSION OF NEUROPATHIC PAIN |
| NUMBER OF SEQUENCES: 36 |
| CORRESPONDENCE ADDRESS: |
| ADDRESSEE: Deblinger & Associates |
| STREET: 350 Cambridge Avenue, Suite 250 |
| CITY: Palo Alto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 57.5%; Score 69; DB 2; Length 26; Best Local Similarity 34.6%; Pred. No. 3.4; Matches 9; Conservative 11; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: /note= "where X is hydroxyproline"
              COMPUTER: IBM COMPACL...
COPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for windows Version 2.0
SOFTWARE: FastSEQ for windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,918
FILING DATE: 07-NOV-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Mohr, Judy M.
REGISTRATION NUMBER: 8,865
REFERENCE/DOCKET NUMBER: 5865-0009.34
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0860
TELEFAX: 650-324-0860
TELEFAX: 650-324-0966
TELEFAX: 650-324-0966
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
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TELECOMMUNICATION:
): Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Modified-site LOCATION: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94306-1546
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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Gaps
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57.5%; Score 69; DB 2; Length 26; 30.9%; Pred. No. 3.4; tive 12; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  METHODS OF PRODUCING ANALGESIA AND ENHANCING OPIATE ANALGESIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/138,439
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Sequence 21, Application US/08613400A

Patent No. 6054429

GENERAL INFORMATION

APPLICANT: Bowersox, S. Scott

APPLICANT: Bettus, Mark, R.

APPLICANT: Luther, Robert, R.

TITLE OF INVENTION: IMPROVED EPIDURAL

TITLE OF INVENTION: METHOD OF PRODUCING ANALGESIA

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASESEO FOR Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/613,400A
FILING DATE: 08-MAR-1996
CLASSIFICATION 514
PRIOR APPLICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INDIVIDUAL ISOLATE: SNX-231, FIGURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CKGKGAXCRKTMYDCCSGSCGRRGKC 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 29, Application US/08613400A Patent No. 6054429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Stratford, Carol A
REGISTRATION UNUMBER: 34,444
REPRENCE/DOCKET NUMBER: 5865
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0860
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bowersox, S. Scott
Gadbois, Theresa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pettus, Mark, R.
Luther, Robert, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Bowerson
APPLICANT: Gadbois,
APPLICANT: Lettus,
APPLICANT: Luther,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                  Query Match 57.5%; Score 69; DB 2; Length 26; Best Local Similarity 34.6%; Pred. No. 3.4; Matches 9; Conservative 11; Mismatches 6; Indels
; NAME/KEY: Modified-site
; LOCATION: 7
; CIMER INFORMATION: /note= "where X is hydroxyproline".
US-09-138-439-21
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
CORRESPONDENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSE: LAW Offices of Peter Dehlinger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/138,439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Law Offices of Peter Dehlinger STREET: 350 Cambridge Avenue, Suite 300 CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 1993-04-15
APPLICATION NUMBER: US/08/049,794
FILING DATE: 30-DEC-1991
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRAITON NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INDIVIDUAL ISOLATE: SNX-230, FIGURE 1
                                                                                                                                                                                                                 1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                            1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                         Sequence 29, Application US/09138439
Patent No. 5994305
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (415) 324-0960
INFORMATION FOR SEQ 1D NO: SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Querỳ Match
Best Local Similarity 30.8%
Matches 8; Æonservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
GY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-138-439-29
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                                                                                                                Query Match 57.5%; Score 69; DB 3; Length 26; Best Local Similarity 34.6%; Pred. No. 3.4; Matches 9; Conservative 11; Mismatches 6; Indels
; LOCATION: 7
; OTHER INFORMATION: /note= "where X is hydroxyproline"
US-08-613-400A-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: /note= "where X is hydroxyproline"
US-09-298-017-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              METHODS OF PRODUCING ANALGESIA AND ENHANCING OPIATE ANALGESIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/298,017
   Patentin Release #1.0, Version #1.25
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Patent No. 6087091

GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: SINGH, TEJINDER
APPLICANT: OHLI, KISHOR C
APPLICANT: WALENTINO, KAREN L
APPLICANT: WALENTINO, REPROR C
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: BEHANGING OPPATE ANALG
TITLE OF INVENTION: ENHANCING OPPATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/049,794
FILING DATE: ATTORNATION:
NAME: Stratford. Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 324-0960
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-231, FIGURE 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
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APPLICATION NUMBER: US/09/298,017
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/049,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Modified-site LOCATION: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEFICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 40
US-09-298-017-29
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APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C.
APPLICANT: WILLSHING, KAREN L.
APPLICANT: WILJANICH, GEORGE P.
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
STRPETER
STRPETE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 26;
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   IMPROVED EPIDURAL
METHOD OF PRODUCING ANALGESIA
                                                                                                                                                                                   CITY:
STATE: CA
COUNTRY: US
ZIP: 94306-1546
ZIP: 94306-1546
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/613,400A
FILING DATE: 08-MAR-1996
CLASSIFFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
FILING SPETENCE/DOCKET NUMBER: 34,444
REGISTRATION NUMBER: 34,444
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0019
TELECOMONICATION INFORMATION:
TELECOMONICATION INFORMATION:
TELECOMONICATION INFORMATION:
TELECOMONICATION INFORMATION:
TELECOMONICATION SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
"NGTH: 26 amino acids
amino acids
amino acids
Innear
"TOCKEIN
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TITLE OF INVENTION: IMPROVED EPIDURAL
TITLE OF INVENTION: METHOD OF PRODUCING AL
WUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-230, FIGURE 1
US-08-613-400A-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 21, Application US/09298017
Patent No. 6087091
GENERAL INFORMATION: APPLICANT: SINGH, TEJINDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 30.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 350
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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Query Match 57.5%; Score 69; DB 3; Best Local Similarity 34.6%; Pred. No. 3.4; Matches 9; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-04-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTATION NUMBER: 34,44
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
           ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-231, FIGURE 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-230, FIGURE 1
US-09-392-979A-29
                                                                                                                                                                                                                                                                   1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                           Sequence 29, Application US/09392979A Patent No. 6136786 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (415) 324-0860
TELEFAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
                                                                           NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 30.8<sup>3</sup>
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94306
                                                                                                                                                                                                                                                                                                                                                                         RESULT 42
US-09-392-979A-29
                                                       FEATURE:
                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C.
APPLICANT: VALENTINO, KAREN L.
APPLICANT: WILJANICH, GEORGE P.
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND TITLE OF INVENTION: BNHANCING OPIATE ANALGESIA CORRESPONDENCE ADDRESS:
ADDRESSES: Law Off:
STRFF
                                                                                                                                                                                                                                                                                                                                                   57.5%; Score 69; DB 3; Length 26; 30.8%; Pred. No. 3.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/392,979A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEE: Law Offices of Peter Dehlinger: 350 Cambridge Avenue, Suite 300 Palo Alto
| REGISTRATION NUMBER: 34,444
| REFERENCE/DOCKET NUMBER: 5865-0009.30
| TELECOMMUNICATION INFORMATION:
| TELEPRANE: (415) 324-0880
| INFORMATION FOR SEQ ID NO: 29:
| SEQUENCE CHARACTERISTICS:
| LENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION
PRIOR APPLICATION
PRIOR APPLICATION DATA:
PRILING DATE: 1993-04-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             12; Mismatches
                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
MYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-230, FIGURE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-392-979A-21

Sequence 21, Application US/09392979A

Patent No. 6136786

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 21:
                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 30.89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid .
                                                                                                                                                                            amino acid
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; LOCATION: 7
; OTHER INFORMATION: /note= "where X is hydroxyproline"
0S-09-392-979A.21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

WIDDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/392,979A
FILING DATE:
CLASSIFICATION:
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Sequence 20, Application US/08083590A

Sequence 20, Application US/08083590A

Setent No. 5786158

GENERAL INFORMATION:
APPLICANT: Artavanis-Teakonas, S. et al.
APPLICANT: Artavanis-Teakonas, S. et al.
TITLE OF INVENTION: Therapeutic And Diagnostic Methods
TITLE OF INVENTION: And Compositions Based On No. 5786158ch Proteins And
TITLE OF INVENTION: Nucleic Acids
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: 0.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/083,590A

FILING DATE: 25-UM-1993

CLASSIFICATION: 435

ATTONENT/AGENT INFORMATION:

NAME: MASTOCK S. Leslie

REGISTRATION NUMBER: 18,872

REFRENCE/DOCKET NUMBER: 7326-015

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION SEQ. 12 869864/9741

TELECOMMUNICATION SEQ. 1D NO: 20:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248 GFTGQNCEENIDDCPGNNCKNGGACV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
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COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (212) 790-9090
TELERAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2556 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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Sequence 17, Application US/08185432

Patent No. 5750652

GENERAL INFORMATION:
APPLICANT: Artavanis-Teakonas, Spyridon
APPLICANT: Buseau, Isabelle
APPLICANT: Buseau, Isabelle
APPLICANT: Mateuno, Kenji
TITLE OF INVENTION: DELTEX PROTEINS, NUCLEIC ACIDS, AND
TITLE OF INVENTION: DELTEX PROTEINS, NUCLEIC ACIDS, AND
TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 1155 Avenue of the Americas
CITY: New York
CERTER: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 57.5%; Score 69; DB 1; Length 29; Best Local Similarity 30.8%; Pred. No. 3.7; Matches 8; Conservative 12; Mismatches 6; Indels
                                                                                                                                                                                             APPLICANT: Olivera, Baldomero M.
APPLICANT: Olivera, Baldomero M.
APPLICANT: Hillyard, David R.
APPLICANT: Imperial, Julita S.
APPLICANT: Monje, Virginia D.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue N.W., Suite 1000
CITY: Washington
STRTE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 2005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/092,215
FILING DATE:
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-107674
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
  1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                   1 CKGKGAPCRKTMYDCCSGSCGRRGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 CKGKGAPCRKTMYDCCSGSCGRRGKC 28
                                                                                                                                                                   Sequence 9, Application US/08092215; Patent No. 5591821; GENERAL INFORMATION: APPLICANT: Olivera, Baldomero M. APPLICANT: Hillyard, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   iryPE: amino aci
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-092-215-9
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US-08-185-432-17
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,432
FILING DATE: 21-JAN-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/POCKET NUMBER: 7326-006
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 56.7%; Score 68; DB Best Local Similarity 30.8%; Pred. No. 2.4e Matches 8; Conservative 12; Mismatches
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248 GFTGONCEENIDDCPGNNCKNGGACV 273
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Patent No. 6692919
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-33762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
US-08-899-232-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 2556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JS-09-121-457-2
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                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Areavanis-Tsakonas, S. et al.
IITLE OF INVENTION: Therapeutic And Diagnostic Methods
TITLE OF INVENTION: And Compositions Based On No. 6083904ch Proteins And
TITLE OF INVENTION: Nucleic Acids
                                                                                                                                                                  Gaps
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                                                                                                                 Query Match 56.7%; Score 68; DB 1; Length 2556; Best Local Similarity 30.8%; Pred. No. 2.4e+02; Matches 8; Conservative 12; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/532,384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Pred. No. 2.4e+02; 12; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/083,590
FILING DATE: 25-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISCHARATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-015
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 2556 amino acids
                                                                                                                                                                                                                           248 GFTGQNCEENIDDCPGNNCKNGGACV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56.7%; Score 68; 30.8%; Pred. No. 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                    2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                             Sequence 20, Application US/08532384 Patent No. 6083904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 47
US-08-899-232-2
; Sequence 2, Application US/08899232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 30.8°
Matches 8; Conservative
          STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New York
Y: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10036
                                                             , MOLECULE TYPE
US-08-083-590A-20
                                                                                                                                                                                                                                                                                                     RESULT 46
US-08-532-384-20
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US-09-270-767-33762
US-09-270-767-33762
Sequence 33762, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
JAPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 33762
LENGTH: 321
GENERAL INFORMATION:

APPLICANT: Artavanis-Teakonas, Spyridon
APPLICANT: Q1, Hullin
TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON
FILE REFERENCE: 7326-046
CURRENT APPLICATION NUMBER: US/08/899,232
CURRENT FILING DATE: 1997-07-23
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
LENGTH: 2556
TYPE: PRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Attavanis-Teakonas, S.
APPLICANT: Attavanis-Teakonas, S.
APPLICANT: Qi, H.
APPLICANT: Rand, M.
TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON
FILE REPERBURE: 7326-073
CURRENT APPLICATION NUMBER: US/09/121,457
CURRENT FILING DATE: 1998-07-23
BARLIER APPLICATION NUMBER: 08/899,232
EARLIER FILING DATE: 1997-07-23
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                      56.7%; Score 68; DB 4; Length 2556; 30.8%; Pred. No. 2.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 2556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h 56.7%; Score 68; DB 4; Length 255
Similarity 30.8%; Pred. No. 2.4e+02;
8; Conservative 12; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12; Mismatches
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Sequence 5, Application US/08981392; Patent No. 6262025; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 32,605
REGISTRATION NUMBER: 73
REPRENCE/DOCKET NUMBER: 73
TELECOMMUNICATION INFORMATION
TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                     TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , MOLECULE TYPE: peptide US-08-981-392-5
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                     RESULT 52
US-08-981-392-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                            ; MOLECULE T
US-08-872-855-7
                                                                                                                       Query Match
                                                                                                                                          Best Loc
Matches
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                                                                                                                                                                                                                                                                                                   APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PARENTIN VET. 2.0
                                                            Gaps
                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/08872855;
Patent No. 6121045;
GENERAL INFORMATION:
APPLICANT: MCCarthy, Sean
TITLE OF INVENTION: NOVEL HUMAN DELTA3 COMPOSITIONS AND
TITLE OF INVENTION: THERAPEUTIC USES THEREFOR
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 321;
                  DB 4; Length 321;
                                                        5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCENAIRS SIGNATION 1.130
SCHWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/872,855
FILING DATE: 11-JUN-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                Query Match 55.0%; Score 66; DB Best Local Similarity 33.3%; Pred. No. 58; Matches 8; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.0%; Score 66; DB 11arity 33.3%; Pred. No. 58; Conservative 11; Mismatches
                                                                                                                       165 TGKNCQHTIDDCASNPCQHGATCV 188
                                                                                                                                                                                                RESULT 50
US-09-270-767-48979
Sequence 48979, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
                                                                                                4 XNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 XNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Drosophila melanogaster US-09-270-767-48979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MAY
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          721 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Arnold, Beth E. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 48979
LENGTH: 321
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US-08-872-855-7
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APPLICANT: Henrique, Domingos Manuel Pinto
APPLICANT: Lewis, Julian Hart
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Gray, Grace
TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON
                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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     Length 721;
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/ Match 55.0%; Score 66; DB 3; Length 721
Local Similarity 32.0%; Pred. No. 1.2e+02;
nes 8; Conservative 11; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match. 55.0%; Score 66; DB 3; Length 721 Best Local Similarity 32.0%; Pred. No. 1.2e+02; Matches 8; Conservative 11; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSO Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/981,392
FILING DATE: 22-DEC-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                  36 GFSGRNCDDNLDDCTSFPCQNGGTC 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 GFSGRNCDDNLDDCTSFPCQNGGTC 460
                                                                                                                2 XIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 XIXNQXCXQXLDDCCSXXCNXXNXC 26
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1 CXIXN----OXCXQXLDDCCSXXCNXXNXCV 27
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Sequence 19, Application US/08083590A

Patent No. 5786158

GENERAL INFORMATION:
APPLICANT: Artavanis-Tsakonas, S. et al.,
TITLE OF INVENTION: Therapeutic And Diagnost TITLE OF INVENTION: And Compositions Bask;
TITLE OF INVENTION: Nucleic Acids
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STRATE: New York
COUNTRY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Artavanis-Tsakonas, S. et al
                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                     Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 25.8%
Matches 8; Conservative
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Flore:
COMPUTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            d
                                                                                                                          TITLE OF INVENTION: NUCLEOTIDE AND PROFEIN SEQUENCES OF VERTEBRATE DELTA GENE AND METHODS BASED THEREON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICAN: Xu, Tian
APPLICANT: Xu, Tian
APPLICANT: Xu, Tian
APPLICANT: Xu, Tian
APPLICANT: Xu, Tian
TITLE OF INVENTION: DELFEX PROTEINS, NUCLEIC ACIDS, AND
TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 55.0%; Score 66; DB 4; Length 721; Best Local Similarity 32.0%; Pred. No. 1.2e+02; Matches 8; Conservative 11; Mismatches 6; Indels
           No. b.co.c.

AL INFORMATION:
APPLICANT: ISh-Horowicz, David
Henrique, Domingos Manuel Pinto
Lewis, Julian Hart
Artavanis-Tsakonas, Spyridon
                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: DOS
SOFTWARE: FastSEO Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/908,322
FILING DATE: 17-Jul-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S Leslie
                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Artavanis-Tsakonas, Spyridon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
;
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-908-322-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3: PENNIE & EDMONDS
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   436 GFSGRNCDDNLDDCTSFPCQNGGTC 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 XIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 16, Application US/08185432
Patent No. 5750552
GENERAL INFORMATION:
APPLICANT: Artavanis-Teakonas, Si
APPLICANT: Busseau, Isabelle
APPLICANT: Diederich, Robert J.
                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 721 amino acids
TYPE: amino acid
STRANDEDNESS: «Unknown
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                    ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 2:
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & I
STREET: 1155 Avenue o
                                                                                                                                                                                                                                                                                           CITY: New York
                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 54
US-08-185-432-16
                         GENERAL
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Therapeutic And Diagnostic Methods
And Compositions Based On No. 5786158ch Proteins And
Nucleic Acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE PATENTIN Release #1.0, Version #1.25
SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/083,590A
FILING DATE: 25-JUN 1993
CLASSIFICATION: 435
ATTONENT/AGNET INPORMATION:
NAME: MASTOCK: S. Leslie
REGISTRATION NUMBER: 18,872
REFRENCE/DOCKET NUMBER: 18,872
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQUENCE: 12 869864/9741
TELEC: 66141 PENNIE
INPORMATION POR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,432
FILING DATE: 21-JAN-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-006
TELEPRANICATION INFORMATION:
TELECOMMUNICATION: 100-9090
TELEPRAN: (212) 790-9090
TELEPRAN: (212) 869-8864/9741
TELEX: 6614 PENNIE
SEQUENCE CHARACTERISTICS:
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Sequence 1, Application US/08899232
                                                                                                                                                                                             SEQ ID NO 1
LENGTH: 2471
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US-09-121-457-1
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And Compositions Based On No. 6083904ch Proteins And
Nucleic Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.
                                                                                                                              Length 2471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55.0%; Score 66; DB 3; Length 2471; 25.8%; Pred. No. 3.5e+02; tive 14; Mismatches 5; Indels
                                                                                                                                                                5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/532,384
                                                                                                                            55.0%; Score 66; DB 1; 1
25.8%; Pred. No. 3.5e+02;
tive 14; Mismatches 5.
                                                                                                                                                                                                                        324 CVCVNGWSGDDCSENIDDCAFASCTPGSTCI 354
                                                                                                                                                                                                                                                                                                            US-08-532-384-19

Sequence 19, Application US/08532384

Sequence 19, Application US/08532384

GENERAL INFORMATION:

APPLICANT: Artavania-Tsakonas, S. et al.

TITLE OF INVENTION: Therapeutic And Diagnos

TITLE OF INVENTION: And Compositions Based

TITLE OF INVENTION: Nucleic Acids

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                   1 CXIXN----QXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 25.8%; Preq. mc.
Watches 8; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Misrock, S. Leelle
REGISTRATION NUMBER: 18,872
REPERENCE/DOCKET NUMBER: 7226-015
TELECOMMUNICATION INFORMATION:
TELERAX: 212 869864/9741
TELERAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/083,590
FILING DATE: 25-UNW-1993
ATTORNEY/AGENT INFORMATION:
2471 amino acids
                                                                                                             Query Match
Best Local Similarity 25.89
...-rhes 8; Conservative
                                    single
                                                   TOPOLOGY: unknown; MOLECULE TYPE: peptide US-08-083-590A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: unknown
MOLECULE TYPE: peptide
                   TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: sir
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RESULT 57 US-08-899-232-1

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Sequence 19, Application US/08185432
Patent No. 5750652
GENERAL INFORMATION:
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Busseau, Isabelle
APPLICANT: Diederich, Robert J.
APPLICANT: W. Tian
APPLICANT: Mateuno, Kenji
TITLE OF INVENTION: DELTEX PROTEINS, NUCLEIC ACIDS, AND
ATTLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS
ANTANED OF COMPUNITY.
Parent No. 6436650
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Attavania-Teakonae, Spyridon
APPLICANT: Qi, Huilin Transon:
TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON
FILE REFERENCE: 7326-046
CURRENT APPLICATION NUMBER: US/08/899,232
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: ALGORITHMS.
APPLICANT: Q1, H.
APPLICANT: Rand, M.
TITLE OF INTENTION: ACTIVATED FORMS OF NOTCH. AND METHODS BASED THEREON FILE REFERENCE: 7326-073
CURRENT APPLICATION NUMBER: US/09/121,457
CURRENT FILING DATE: 1998-07-23
EARLIER FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PATENTIN Ver: 2.0
SEQ ID NOS: 4
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25.8%; Pred. No. 3.5e+02;
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Best Local Similarity 25.8%; Pred. No. 3.5e+02;
Matches 8; Conservative 14; Mismatches 5;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09121457
Patent No. 6692919
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
) ORGANISM: Homo sapiens
US-08-899-232-1
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CRGANISM: Homo sapiens
US-09-121-457-1
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Length 2703;

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APPLICANT: Rand, M.
TILLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON FILE REFERENCE: 7326-073
CURRENT APPLICATION NUMBER: US/09/121,457
CURRENT FILING DATE: 1998-07-23
EARLIER APPLICATION NUMBER: 08/899,232
RARIER FILING DATE: 1997-07-23
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                         Query Match 55.0%; Score 66; DB 4; Length 270 Best Local Similarity 29.2%; Pred. No. 3.8e+02; Matches 7; Conservative 12; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                         : |:|::||| :::|:
822 TGQKCETNIDDCVTNPCGNGGTCI 845
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Patent No. 6767895
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Shetty, Reshma
Jimenez, Elsie C.
McIntosh, J. Michael
Olivera, Baldomero M.
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ORGANISM: Conus betulinus
FEATURE:
NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Drosophila sp.
US-09-121-457-4
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US-09-894-882-168
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Sequence 4, Application US/08899232

Sequence 4, Application US/08899232

Sequence 4, Application US/08899232

Sequence 4, Application US/08899232

GENERAL INFORMATION:

APPLICANT: ALTAvanis-Tsakonas, Spyridon

TITLE OF INVENTION:

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/08/899,232

CURRENT FILING DATE: 1997-07-23

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PATENTIN Ver. 2.0
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...8e+02;
...e 5; Indels
                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,432
FILING DATE: 21-JAN-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-006
TELECOMMUNICATION INFORMATION:
MATTORNEY/AGENTION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.8e+02;
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29.2%; Pred. No. 3.8e+02
tive 12; Mismatches
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29.2%; Pred. No. 3.8e+02
tive 12; Mismatches
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TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/09121457; Patent No. 6692919; GENERAL INFORMATION: APPLICANT: Artevanis-Tsakonas, S. APPLICANT: Qi, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2703 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 29.2
Matches 7; Conservative
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Best Local Similarity 29.23
Matches 7; Conservative
                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-185-432-19
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CRGANISM: Drosophila sp.
US-08-899-232-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
               STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
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LENGTH: 2703
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US-09-121-457-4
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LOCATION: (1)...(36)
CTHER INFORMATION: Xaa at residue 10 is Glu or gamma-carboxy-Glu; Xaa at residues 18
OTHER INFORMATION: , 23 and 36 is Tyr, 1251-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulph
US-09-894-882-168
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APPLICANT: Jones, Robert M.
APPLICANT: Shen, Greg S.
ITLE OF INVENTION: I-Superfamily Conotoxins
                                                                            FILE REFERENCE: 2314-238

CURRENT APPLICATION NUMBER: US/09/894,882

CURRENT APPLICATION NUMBER: US/09/894,882

PRIOR PRIDR DATE: 2001-06-29

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-10-27

PRIOR FILING DATE: 2000-11-08

PRIOR FILING DATE: 2000-11-08

PRIOR FILING DATE: 2000-11-09

PRIOR FILING DATE: 2000-11-09

PRIOR FILING DATE: 2000-11-09

PRIOR FILING DATE: 2001-01-09

PRIOR FILING DATE: 2001-01-09

SEQ ID NOSE OF SEQ ID NOS: 506

SOFTWARE: PARENTING DATE: 2011-01-29

NUMBER OF SEQ ID NOS: 506

SEQ ID NO 168

LENGTH: 36
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Gaps
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APPLICANT: Kid, Thomas
APPLICANT: Kid, Thomas
APPLICANT: Kid, Thomas
APPLICANT: Tensie, Karija
APPLICANT: Tensier-Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REPRENCE: B98-031-3
CURRENT APPLICATION NUMBER: US/09/540, 245A
CURRENT FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 60/065,544
PRIOR FILING DATE: 1997-11-14
PRIOR FILING DATE: 1997-11-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Goodman, Corey,
APPLICANT: Rid, Thomas
APPLICANT: Brose, Kal,
Thomas
APPLICANT: Tessier, Kal,
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REPREBNCE: B98-031-3
CURRENT FILING DATE: 1998-11-13
EARLIER FILING DATE: 1998-11-14
EARLIER FILING DATE: 1997-11-14
EARLIER FILING DATE: 1997-11-14
EARLIER FILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 14
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33.3%; Pred. No. 17;
ive 12; Mismatches
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; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 167
; LENCTH: 73
                                                                                                                                                                                                                                                                                                                                                                                                   1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/09191647
Patent No. 6046015
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-191-647-9
                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 33.3*
Matches 9; Conservative
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SEQ ID NO 9
LENGTH: 735
                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Conus betulinus
US-09-894-882-167
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US-09-191-647-9
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                                                                                                                                                                               APPLICANT: University of Utah Research Foundation APPLICANT: University of Utah Research Foundation APPLICANT: Cognetix, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Shetty, Reshma APPLICANT: Jimenez, Elsie C.
APPLICANT: Jimenez, Elsie C.
APPLICANT: Olivera, Baldomero M.
APPLICANT: Watkins, Maren
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Jones, Robert M.
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: 1-Superfamily Conotoxins
FILE OF INVENTION: 1-Superfamily Conotoxins
FILE OF INVENTION: 1-Superfamily Conotoxins
FILE OF INVENTION: 1-Superfamily Conotoxins
CURRENT APPLICATION NUMBER: US 60/29
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-11-08
PRIOR PELICATION NUMBER: US 60/246,581
PRIOR PELICATION NUMBER: US 60/247,714
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-18
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: PATENTIN VETSION 3.0
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FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR PILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-37
PRIOR FILING DATE: 2000-10-27
PRIOR PLING DATE: 2000-10-27
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Best Local Similarity 33.3%; Pred. No. 9.2;
Matches 9; Conservative 12; Mismatches
  2 CLSLGQRCXRH-SDCCGXLCCFXDKCV 27
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                                                                                                              Sequence 369, Application US/09894882
Patent No. 6767895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 167, Application US/09894882
Patent No. 6767895
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McIntosh, J. Michael
Olivera, Baldomero M.
Watkins, Maren
Jones, Robert M.
Shen, Greg S.
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                                                                                                                                                               GENERAL INFORMATION:
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LENGTH: 36
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: University of Utah Research Foundation APPLICANT: Cognetix, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Shetty, Reshma
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APPLICANT: Shen, Greg S.
TITLE OF INVENTION: I-Superfamily Conotoxins
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CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR PELING DATE: 2000-10-27
PRIOR PELING DATE: 2000-11-08
PRIOR PELING DATE: 2000-11-08
PRIOR PELING DATE: 2000-11-08
PRIOR PELING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR APPLICATION NUMBER: US 60/247,714
                                                          348 GCEENLDDCAAATCAPGSTCI 368
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; Sequence 2, Application US/09230652A
; Patent No. 6537775
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McIntosh, J. Michael
Olivera, Baldomero M.
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                  GENERAL INFORMATION:
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Sequence 1, Application US/09467997

Sequence 1, Application US/09467997

Sequence 1, Application US/09467997

SENERAL INFORMATION:

APPLICANT: Kitajewski, Jan

APPLICANT: Kitajewski, Jan

APPLICANT: Witajewski, Jan

TITLE OF INVENTION: ANGIGENIC MODULATION BY NOTCH SIGNAL TRANSDUCTION

FILE REFERENCE: 53863-A-PCT-US

CURRENT FILING DATE: 1999-12-20

NUMBER OF SEQ ID NOS: 10

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 1

SEQ ID NO 1

TYPE: PRT
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APPLICANT: Kid, Thomas
APPLICANT: Kid, Thomas
APPLICANT: Kid, Thomas
APPLICANT: Brose, Katja
APPLICANT: Tessier-Lavigae, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REFERENCE: B98-031-3
CURRENT APPLICATION NUMBER: US/09/540,153
CURRENT FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: 60/081,057
PRIOR FILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                 54.2%; Score 65; DB 3; Length 735; 26.9%; Pred. No. 1.5e+02;
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                                                                                                                                                                                                                           13; Mismatches
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                                                                                                                                                                                                                                                                                                   248 GFEGDYCEKNIDDCVNSKCENGGKCV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     248 GFEGDYCEKNIDDCVNSKCENGGKCV 273
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                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/09540153
Patent No. 6270995
                                                                                    TYPE: PRT; ORGANISM: Caenorhabditis elegans
US-09-540-245A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-540-153-9
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                            Query Match
Best Local Similarity 26.94
Matches 7; Conservative
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Best Local Similarity 33.3
Matches 7; Conservative
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Best Local Similarity
Matches 7; Conserv
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       SOFTWARE: Pace
SEQ ID NO 9
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LENGTH: 735
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APPLICANT: Tournier-Lasserve, Elisabeth
APPLICANT: Joutel, Anne
APPLICANT: Joutel, Anne
APPLICANT: Bousest, Marie-Germaine
APPLICANT: Bousest, Marie-Germaine
APPLICANT: Bousest, Marie-Germaine
APPLICANT: Bousest, Marie-Germaine
TITLE OF INVENTION: THERAPEUTIC APPLICATION
TITLE OF INVENTION: THERAPEUTIC APPLICATION
FILE REFERENCE: 03715.0048-00000
CURRENT APPLICATION NUMBER: US/09/230,652A
CURRENT APPLICATION NUMBER: P9 90933
EARLIER PILING DATE: 1999-05-17
EARLIER PILING DATE: 1999-04-16
EARLIER APPLICATION NUMBER: FR 97 04680
EARLIER APPLICATION NUMBER: PCT/FF97/01433
EARLIER FILING DATE: 1997-07-31
NUMBER OF SEQ ID NOS: 163
SOFTWARE: PatentIN Ver. 2.1
SEQ ID NO 2
LENGTH: APPLICATION VER. 2.1
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Matches 9; Conservative 13; Mismatches
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APPLICANT: Waterlas, water, APPLICANT: Waterlas, APPLICANT: Shen, Greg S.
ITLE OF INVENTION: I-Superfamily Conotoxins FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US 60/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-16-30
PRIOR PILING DATE: 2000-11-08
PRIOR PLICATION NUMBER: US 60/247,714
PRIOR PILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: US 60/264,256
PRIOR PILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: PatentIn version 3.0
SEQ ID NO 119
                         McIntosh, J. Michael
Olivera, Baldomero M.
Watkins, Maren
          Jimenez, Elsie C.
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US-09-894-882-119
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US-09-894-882-324
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APPLICANT: Walker, Craig S.
APPLICANT: Shetty, Reshma
APPLICANT: Jimenez, Elsie C.
APPLICANT: McIncosh, J. Michael
APPLICANT: Olivera, Baldomero M.
APPLICANT: Watkins, Maren
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Watchins, waters
APPLICANT: Jones, Robert M.
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: 1-Superfamily Conotoxins
FILE FEFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US 60/29
FRIOR APPLICATION NUMBER: US 60/243,410
FRIOR PELING DATE: 2000-06-30
FRIOR FILING DATE: 2000-10-27
FRIOR FILING DATE: 2000-11-08
FRIOR FILING DATE: 2000-11-08
FRIOR FILING DATE: 2000-11-08
FRIOR APPLICATION NUMBER: US 60/246,581
FRIOR APPLICATION NUMBER: US 60/247,714
FRIOR APPLICATION NUMBER: US 60/247,714
FRIOR FILING DATE: 2000-11-14
FRIOR FILING DATE: 2001-11-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                  Query Match 53.8%; Score 64.5; I Best Local Similarity 33.3%; Pred. No. 10; Matches 9; Conservative 10; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 413, Application US/09894882
; Patent No. 6767895
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: PatentIn version 3.0
SEQ ID NO 364
                                                                                                                        TYPE: PRT
ORGANISM: Conus brunneus
US-09-894-882-364
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LENGTH: 35
TYPE: PRT
ORGANISM: Conus magus
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US-09-894-882-119
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Hammond, Timothy G.
APPLICANT: Verroust, Pierre J.
TITLE CANT: Verroust, Pierre J.
TITLE OF INVENTION: Cubilin Procein, DNA Sequences Encoding Cubilin TITLE OF INVENTION: and Uses Thereof
FILE REFERENCE: D6148
CURRENT APPLICATION NUMBER: US/09/341,461
CURRENT FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: PCT/US99/01259
PRIOR APPLICATION NUMBER: PCT/US99/01259
NUMBER OF SEQ ID NOS: 40
SEQ ID NO 2
LENGTH: 3623
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; OTHER INFORMATION: amino acid sequence of rat cubilin protein
US-09-141-461-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 53.3%; Score 64; DB 4; Length 3623; Best Local Similarity 29.2%; Pred. No. 7.5e+02; Matches 7; Conservative 13; Mismatches 4; Indels
  DB 4; Length 71;
                                                     Indels
Query Match 53.8%; Score 64.5; I Best Local Similarity 33.3%; Pred. No. 21; Matches 9; Conservative 11; Mismatches
                                                                                                          1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                      : |:|::::|| |::|: |: | |: | 448
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; Patent No. 6767895
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; Sequence 2, Application US/09341461
; Patent No. 6586389
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                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:

NAME/KEY: PEPTIDE

LOCATION: (1)..(36)

COTHER INFORMATION: Xaa at residue 36 is Pro or hydroxy-Pro
US-09-894-882-339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: University of Utah Research Foundation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 52.9%; Score 63.5; DB Best Local Similarity 34.6%; Pred. No. 14; Matches 9; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Jones, Robert M.
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: I-Superfamily Conotoxins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THILE REPERENCE: 2314-238
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-66-29
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-10-27
PRIOR PLING DATE: 2000-10-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-48
PRIOR PLING DATE: 2000-11-48
PRIOR PLING DATE: 2000-11-14
PRIOR PLING DATE: 2001-11-14
PRIOR PLING DATE: 2001-11-14
PRIOR PRILING DATE: 2001-11-14
PRIOR PRILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: PATENTIN VETSION 3.0
SOFTWARE: 36
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR FILING DATE: 2000-11-14
PRIOR PPLICATION NUMBER: US 60/264,256
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SSEQ ID NO 339
LENGTH: 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |: |: |: |: | CONTROL | CO
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; Sequence 441, Application US/09894882
; Patent No. 6767895
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McIntosh, J. Michael
Olivera, Baldomero M.
Watkins, Maren
                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Conus episcopatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cognetix, Inc.
Walker, Craig S.
Shetty, Reshma
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; ORGANISM: Conus episcopatus
US-09-894-882-441
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US-09-894-882-443
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OTHER INFORMATION: Xaa at residue 36 is Pro or hydroxy-Pro; Xaa at residue 23 is Tyr
OTHER INFORMATION: , 1251-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho
OTHER INFORMATION: -Ty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ij
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                           University of Utah Research Foundation
Cognetix, Inc.
Walker, Craig S.
Sherty, Reshma
Unmenez, Elsie C.
Worlnceh, J. Michael
Olivera, Baldomero M.
Watkins, Maren
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T. Cognetix, Inc.
T. Walker, Craig S.
T. Shetry, Reshma
T. Jimenez, Elsie C.
T. McIncoh, J. Michael
T. Olivera, Baldomero M.
T. Watkins, Maren
                                                                                                                                                                                                                                                                                                                             APPLICANT: Garbary Marten, APPLICANT: Grees Grees Grees Grees Grees Title OF INVENTION: 1-Superfamily Conotoxins FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US 60/9894,882
CURRENT FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 60/9810R FILING DATE: 2000-10-27
PRIOR RILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/245,581
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR PILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: Patentin version 3.0
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FILE REFERENCE: 214-218
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR APPLICATION NUMBER: US 60/245,811
PRIOR APPLICATION NUMBER: US 60/245,581
PRIOR FILING DATE: 2000-11-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Conus episcopatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jones, Robert M.
Shen, Greg S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-894-882-324
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APPLICANT:
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APPLICANT:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: University of Utah Research Foundation APPLICANT: Cognetix, Inc. APPLICANT: Walker, Craig S. APPLICANT: Shetty, Reshma
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APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: Carrier, G. Edward
APPLICANT: Watkins, Maren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Jimenez, Elsie C.
APPLICANT: McIntosh, J. Michael
APPLICANT: Olivera, Baldomero M.
APPLICANT: Jones, Robert M.
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: I-Superfamily Conotoxins
FILE REFERENCE: 2114-238
CURRENT APPLICATION INVESE: US/09/894,882
                                                                                                                                                                                                                                                                                                       10; Mismatches
                                                                                                                                                                                                                                           Query Match 52.9%; Score 63.5; I
Best Local Similarity 34.6%; Pred. No. 26;
Matches 9; Conservative 10; Mismatches
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52.9%; Score 63.5; I
Best Local Similarity 34.6%; Pred. No. 26;
Matches 9; Conservative 10; Mismatches
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PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-15
PRIOR PILING DATE: 2001-11-15
PRIOR DATE: 2001-11-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 338, Application US/09894882
Patent No. 6767895
NUMBER OF SEQ ID NOS: 506
SOFTWARE: Patentin version 3.0
SEQ ID NO 323
LENGTH: 72
                                                                                                                    ; TYPE: PRT
; ORGANISM: Conus episcopatus
US-09-894-882-323
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                                                                              APPLICANT: University of Utah Research Foundation APPLICANT: Cognetix, Inc. APPLICANT: Walker, Craig S. APPLICANT: Shetty, Reshma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: University of Utah Research Foundation APPLICANT: Cognetix, Inc. APPLICANT: Walker, Craig S.
                                                                                                                                                                                                                                                                                                                      APPLICANT: Gones, Robert M.
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: I-Superfamily Conotoxins FILE OF INVENTION: I-Superfamily Conotoxins FILE OF INVENTION: I-Superfamily Conotoxins CURRENT APPLICATION NUMBER: US/09/894,882 CURRENT FILING DATE: 2001-06-29 PRIOR PELLING DATE: 2000-06-30 PRIOR FILING DATE: 2000-10-27 PRIOR FILING DATE: 2000-11-08 PRIOR FILING DATE: 2000-11-08 PRIOR PELLING DATE: 2000-11-08 PRIOR PELLING DATE: 2000-11-08 PRIOR PELLING DATE: 2000-11-14 PRIOR PELLING DATE: 2001-11-14 PRIOR FILING DATE: 2001-11-19 PRIOR FILING DATE: 2001-11-29 NUMBER OF SEQ ID NOS: 506
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APPLICANT: Walker, Craig S.
APPLICANT: Sherty, Reshma
APPLICANT: Jimenez, Elsie C.
APPLICANT: Jimenez, Elsie C.
APPLICANT: Jimenez, Elsie C.
APPLICANT: Walkins, Maren
APPLICANT: Walkins, Maren
APPLICANT: Jones, Robert M.
BRIOR FILING DATE: 2000-10-27
PRIOR PILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-18
PRIOR FILING DATE: 2000-11-18
PRIOR FILING DATE: 2000-11-18
PRIOR FILING DATE: 2000-11-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 52.9%; Score 63.5; I
Best Local Similarity 34.6%; Pred. No. 14;
Matches 9; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
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Application US/09894882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 323, Application US/09894882; Patent No. 6767895
                                                                                                                                                                                                        Jimenez, Elsie C.
McIntosh, J. Michael
Olivera, Baldomero M.
Watkins, Maren
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US-09-894-882-323
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SOFTWARE: Pate
SEQ ID NO 443
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Sequence 2, Application US/09214278;
Patent No. 6291210;
GENERAL INPORMATION:
APPLICANT: Sakano, Seiji
APPLICANT: Icoh, Akira
TITLE OF INVENTION:
FILE REPRENCE: KP-8576;
CURRENT APPLICATION NUMBER: US/09/214,278
CURRENT FILING DATE: 1999-01-26;
NUMBER F SEQ ID NOS: 32;
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2.
LENGTH: 1055
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| Sequence 2, Application US/09855722
| Sequence 2, Application US/09855722
| Sequence 2, Application US/09855722
| Patent No. 6638741
| GENERAL INFORMATION:
| APPLICANT: SAKANO, Seiji
| APPLICANT: Itch, Akira
| TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
| FILE REFERENCE: KP-8576
| CURRENT APPLICATION NUMBER: US/09/855,722
| CURRENT FILING DATE: 2001-05-16
| PRIOR APPLICATION NUMBER: 09/214,278
| PRIOR FILING DATE: 1999-01-26
| NUMBER OF SEQ ID NOS: 32
| SOFTWARE: PatentIn Ver: 2.1
| SEQ ID NO 2
| LENGTH 1055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52.5%; Score 63; DB 3; Length 1055; larity 23.1%; Pred. No. 3.18+02; Conservative 13; Mismatches 7; Indels
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                                                                                                                                                                             Length 585;
                                                                                                                                                                         12.5%; Score 63; DB 4; Length 585
ilarity 30.8%; Pred. No. 1.8e+02;
Conservative 10; Mismatches 8; Indels
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Best Local Similarity 23.1%; Pred. No. 3.1e+02;
Matches 6; Conservative 13; Mismatches 7; Indels
                                                                                                                                                                                                                                                                              380 GFAGPRCEHDLDDCAGRACANAGTCV 405
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                                                                                                LOCATION: (1)...(585)
CTHER INFORMATION: Xaa
US-09-641-612-5
                        TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1055
TYPE: PRT
ORGANISM: Homo sapiens
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US-09-855-722-2
                                                                                                                                                                                             Best Local Similarity
Matches 8; Conserv
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Matches 6; Conserv
                                                          FEATURE:
NAME/KEY: VARIANT
      LENGTH: 585
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US-09-214-278-2
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APPLICANT: Vivien Chan et al.
TITLE OF INVENTION: NOTCH RECEPTOR LIGANDS AND USES THEREOF
FILE REPERENCE: PPO-1602.002 / 200130.458
CURRENT APPLICATION NUMBER: US/09/641,612
CURRENT PILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/09641612
PREMENT NO. 6703221
GENERAL INFORMATION:
APPLICANT: Vivien Chan et al.
TITLE OF INVENTION: NOTCH RECEPTOR LIGANDS AND USES THEREOF
FILLS REPERENCE: PPO-1602.002 / 201030.498
CURRENT APPLICATION NUMBER: US/09/641,612
CURRENT FILING DATE: 0000-08-17
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FASELSEQ for Windows Version 4.0
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                                            12; Mismatches
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Pred. No.
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; Sequence 2, Application US/09641612
; Patent No. 6703221
Hillyard, David R.
McIntosh, J. Michael
Layer, Richard T.
Jones, Robert M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52.5%;
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Best Local Similarity 35.73
Matches 10; Conservative
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LENGTH: 583
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-749-637A-207
                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 207
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US-09-641-612-5
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Gaps

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NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815
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                                                                                                                                                                                                   ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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STATE: California
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
   CORRESPONDENCE ADDRESS:
                                           Abbarrers 43.v. STREET: 43.v. CITY: San Diego STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                         APPLICANT: Hehrique, Domingos M.P.
APPLICANT: Henrique, Domingos M.P.
APPLICANT: Henrique, Domingos M.P.
APPLICANT: Henrique, Domingos M.P.
APPLICANT: Mari, Anna M.
APPLICANT: Mari, Robert J.
APPLICANT: Artavanis-Teakonas, Spyridon
APPLICANT: Artavanis-Teakonas, Artavanis-Teakonas, Art
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APPLICANT: Hood, Leroy
APPLICANT: Hood, Leroy
APPLICANT: Spinner, Nancy B.
APPLICANT: Spinner, Nancy B.
TITLE OF INVENTION: Human Jagged Polypeptide, Encoding
TITLE OF INVENTION: Nucleic Acids and Methods of Use
NUMBER OF SEQUENCES: 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPTRE: BAC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/400,159
FILING DATE: 07-MAR-1995
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457 GFTGTYCHENIDDCLGQPCRNGGTCI 482
601 GFTGTYCHENIDDCLGQPCRNGGTCI 626
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NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFRENCE/DOCKET NUMBER: 7326
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/08882046
Patent No. 6136952
GENERAL INFORMATION:
APPLICANT: Li, Linheng
                                                                                                                                                                      Sequence 8, Application US/08400159
Patent No. 5869282
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TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1065 amino acids
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Best Local Similarity 23.1%
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STRANDEDNESS:
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: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-400-159-8
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US-08-882-046-4
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STATE:
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Krantz, Ian D.
Spinner, Nancy B.
TITLE OF INVENTION: Methods of Diagnosing Alagille Syndrome
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.25
    CURRENT APPLICATION DATE:
    FILING DATE: 05-May-2000
    CLASSIFICATION: CURROWN>
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STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,046
FILING DATE: 25-JUM-1997
CLASSIFICATION: 536
ATTONREY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKFY NUMBER: 9-UW 2637
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ 10 NO: 4:
SEQUENCE (619) 535-8949
INFORMATION FOR SEQ 1D NO: 4:
SEGUENCE FIRRACTERISTICS:
LENGTH: 1148 amino acide
E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/882,046
FILING DATE: 25-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          538 GFTGTYCHENIDDCLGQPCRNGGTCI 563
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Indels

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13; Mismatches
      Conservative
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Best Local Similarity 23.1%
Matches 6; Conservative
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ORGANISM: Homo sapiens
US-09-214-278-5
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LENGTH: 1238
      9
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US-08-882-046-6
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      Matches
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Fatent No. 6291210
GENERAL INPORMATION:
APPLICANT: Sakano, Seiji
APPLICANT: Itch, Akira
TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
FILE REFERENCE: KP-8576
CURRENT APPLICATION NUMBER: US/09/214,278
CURRENT APPLICATION NUMBER: 1999-01-26
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 1212
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| Sequence 3, Application US/09855722
| Patent No. 6638741
| GABREAL INFORMATION:
| APPLICANT: Sakano, Seiji
| APPLICANT: Itch, Akira
| TILLO FOR INVENTION: DIFFERENTIATION-SUPFRESSIVE POLYPEPTIDE
| TILLO FOR INVENTION: DIFFERENTIATION-SUPFRESSIVE POLYPEPTIDE
| CURRENT APPLICATION NUMBER: US/09/855,722
| CURRENT FILING DATE: 1999-01-26
| PRIOR APPLICATION NUMBER: 09/214,278
| PRIOR APPLICATION NUMBER: 09/214,278
| PRIOR FILING DATE: 1999-01-26
| NUMBER OF SEQ ID NOS: 32
| SEQ ID NO 3
| SEQ ID NO 3
| LENGTH: 1212
                                                                                                                                                                                                                                                                            Query Match 52.5%; Score 63; DB 4; Length 1148; Best Local Similarity 23.1%; Pred. No. 3.3e+02; Matches 6; Conservative 13; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52.5%; Score 63; DB 3; Length 1212; 23.1%; Pred. No. 3.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 23.1%; Pred. No. 3.5e+02;
Matches 6; Conservative 13; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 63; DB 4; 1
Pred. No. 3.5e+02;
REFERENCE/DOCKET NUMBER: P-UW 4164
                                                                                                                                                   TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-566-047-4
                                                                                                                                                                                                                                                                                                                                                                                        538 GFTGTYCHENIDDCLGQPCRNGGTCI 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
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                                                                             INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1148 amino acids
                   TELECOMMUNICATION INFORMATION TELEPHONE: (858) 535-900.
                                                             TELEFAX: (858) 535-8949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52.5%;
23.1%;
                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-722-3
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Best Local Similarity
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US-09-214-278-3
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US-09-855-722-3
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                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Sakano, Seiji
APPLICANT: Troh, Akira
TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
FILE REFERENCE: KP-8576
CURRENT APPLICATION NUMBER: US/09/214,278
CURRENT FILING DATE: 1999-01-26
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.5%; Score 63; DB 4; Length 1238; 23.1%; Pred. No. 3.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE FILE REFERENCE: KP-8576
CURRENT APPLICATION NUMBER: US/09/855,722
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 09/214,278
PRIOR FILING DATE: 1999-01-26
NUMBER OF SEQ ID NOS: 32
SEQ ID NO 5
LENGTH: 1238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Indels
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                                 601 GFTGTYCHENIDDCLGOPCRNGGTCI 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      627 GFTGTYCHENIDDCLGQPCRNGGTCI 652
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
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                                                                                                                                                                      Sequence 5, Application US/09214278 Patent No. 6291210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/09855722
Patent No. 6638741
GENERAL INFORMATION:
APPLICANT: Sakano, Seiji
APPLICANT: Itch, Akira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/08882046
Patent No. 6136952
GENERAL INFORMATION:
APPLICANT: Li, Linheng
APPLICANT: Hood, Lercy
APPLICANT: Krantz, Ian D.
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TYPE: amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECTLE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-566-047-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       628 GFTGTYCHENIDDCMGQPCRNGGTCI 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7326-037
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/08611729A
Patent No. 6004924
GENERAL INFORMATION:
         FILING DATE: 25-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (212) 790-9090
(212) 869-9741/8864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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Hodd, Lercy
Krantz, Ian D.
Spinner, Nancy B.
TITLE OF INVENTION: Methods of Diagnosing Alagille Syndrome NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.5%; Score 63; DB 3; Length 1248; 23.1%; Pred. No. 3.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Indels
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MEDIUM TYPE: FOCOMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICANT: Spinner, Nancy B.
TITLE OF INVENTION: Human Jagged Polypeptide, Encoding
TITLE OF INVENTION: Nucleic Acids and Methods of Use
                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                  NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STREET: COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13; Mismatches
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REPLICATION NUMBER: US/09/566,047
FILING DATE: 05-May-2000
CLASSIPICATION: «UNKNOWN»
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                                                                                                                                                                                                                                                                                                                                                                          CURENT AFFLICATION DATE:

CLASSIFICATION: 536
FILING DATE: 25-JUN-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 9-UW 2637
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-8949
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTER/STICS:
LENGTH: 1248 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             628 GFTGTYCHENIDDCMGQPCRNGGTCI 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 23.13
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                           92122
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Gaps
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APPLICANT: Henrique, Domingos M.P.
APPLICANT: Lewis, Ullian H.
APPLICANT: Eleming, Robert J.
APPLICANT: Pleming, Robert J.
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Mann, Robert S.
APPLICANT: Gray, Grace E.
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF THE
TITLE OF INVENTION: SERRATE GENE AND METHODS BASED THEREON
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 52.5%; Score 63; DB 4; Length 1248; Best Local Similarity 23.1%; Pred. No. 3.6e+02; Matches 6; Conservative 13; Mismatches 7; Indels
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APPLICATION NUMBER: US/08/611,729A FILING DATE: CASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cabiryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UW 4164
TELEPHONE: (858) 535-9001
TELEPHONE: (858) 535-9001
TELEPAX: (658) 535-9049
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1248 amino acids
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Sequence 210, Application US/09894882
Patent No. 6767895
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Shetty, Reshna
Jimenez, Blasie C.
McIntosh, J. Michael
Olivera, Baldomero M.
Watkins, Maren
Jones, Robert M.
Shen, Greg S.
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APPLICANT:
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APPLICANT:
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                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Ish-Horowicz, David
APPLICANT: Henrique, Domingos M.P.
APPLICANT: Henrique, Domingos M.P.
APPLICANT: Lewis, Julian H.
APPLICANT: Fleming, Robert J.
APPLICANT: Artavanis-Tsakonas, Spyridon
APDRESSES: Pennie & Edmonds
                                                                                                            .
Query Match 52.5%; Score 63; DB 3; Length 1257; Best Local Similarity 23.1%; Pred. No. 3.68+02; Matches 6; Conservative 13; Mismatches 7; Indels
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23.1%; Pred. No. 3.6e+02;
Live 13; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
CITY: New York
CONTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: BM PC COMPATIBLE
COMPUTER: DATE COMPATIBLE
COMPUTER: DATE COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/195,524
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457 GFTGTYCHENIDDCLGQPCRNGGTCI 482
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/611,729
FILING DATE: 06-WAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
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Patent No. 6703489
GENERAL INFORMATION:
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(212) 869-9741/8864
5141 PENNIE
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FELECOMMUNICATION INFORMATION: TELEPHONE: (212) 790-9090
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 23.1%
Matches 6; Conservative
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RESULT 96 US-09-894-882-433 ; Sequence 433, Application US/09894882

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APPLICANT: University of Utah Research Foundation APPLICANT: Cognetix, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: University of Utah Research Foundation APPLICANT: Cognetix, Inc.
                                    APPLICANT: Cognetrx, inc.
APPLICANT: Malker, Craig S.
APPLICANT: Malker, Craig S.
APPLICANT: Sheetty, Reshma
APPLICANT: Jimenez, Elsie C.
APPLICANT: Malnesh, J. Michael
APPLICANT: Markins, Maren
APPLICANT: Makkins, Maren
APPLICANT: Makkins, Maren
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: I-Superfamily Conotoxins
FILE REFERENCE: 2314-238
FILE REFERENCE: 2314-238
FILE REFERENCE: 2314-238
FILE REFERENCE: 2300-06-29
FRIOR FILING DATE: 2000-16-29
FRIOR FILING DATE: 2000-16-29
FRIOR FILING DATE: 2000-11-08
FRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SSCO ID NOS: 506
SSCO ID NOS: 506
FRIOTH OF ASS
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CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-110-27
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2001-10-19
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          University of Utah Research Foundation
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APPLICANT: Warkins, waren
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: I-Superfamily Conotoxins
FILE REFRENCE: 2314-238
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT APPLICATION NUMBER: US 60/29
PRIOR APPLICATION NUMBER: US 60/43,410
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR PILING DATE: 2000-11-18
SPRIOR PILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SEQ ID NO 209
LENGTH: 70
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APPLICANT: Shen, Greg S.
TITLE OF INVENTION: I-Superfamily Conotoxins
FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-10-27
PRIOR PLILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/245,581
PRIOR PILING DATE: 2000-11-08
PRIOR PILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR PILING DATE: 2001-10-19
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McIntosh, J. Michael
Olivera, Baldomero M.
Watkins, Maren
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McIntosh, J. Michael
Olivera, Baldomero M.
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Walker, Craig S.
Shetty, Reshma
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US-09-894-882-209
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LOCATION: (1)..(36)
OTHER INFORMATION: Xaa at residues 2 and 4 is Trp or bromo-Trp; Xaa at residue 25 is OTHER INFORMATION: Tyr, 1251-Tyr, mono-lodo-Tyr, di-lodo-Tyr, O-sulpho-Tyr or O-pho OTHER INFORMATION: spho-Ty
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F. Cognetix, Inc.
F. Wakker, Craig S.
F. Shetty, Reshma
Jimenez, Elsie C.
F. McIncosh, J. Michael
Olivera, Baldomero M.
F. Watkins, Maren
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FILE REFERENCE: 2314-238
FILE REFERENCE: 2314-238
FILE OF SUPERIOR NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR PAPLICATION NUMBER: US 60/246,581
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR FILING DATE: 2000-11-18
PRIOR FILING DATE: 2001-11-18
PRIOR FILING DATE: 2001-11-19
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: PALENTIN VERSION 3.0
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37.0%; Pred. No. 17;
tive 10; Mismatches
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Sequence 209, Application US/09894882

Patent No. 6767895

; GENERAL INFORMATION:
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SOFTWARE: Patentin version 3.0 SEQ ID NO 210
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Shen, Greg S.
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Best Local Similarity 33.3%
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Best Local Similarity 37.0%
Matches 10; Conservative
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US-09-894-882-404
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; LENGTH: 71
; TYPE: PRT
; ORGANISM: Conus striatus
US-09-894-882-74
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Query Match 52.1%; Score 62.5; DB 4; Length 71; Best Local Similarity 33.3%; Pred. No. 31; Matches 9; Conservative 10; Mismatches 7; Indels à

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Search completed: April 18, 2005, 20:39:51 Job time: 32.5 secs

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Sequence 258, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 268, App
Sequence 268, App
Sequence 468, App
Sequence 12, Appl
Sequence 12, Appl
Sequence 134, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 29, Appl
Sequence 470, Appl
Sequence 470, Appl
Sequence 470, Appl
Sequence 470, Appl
Sequence 149, Appl
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118, Appl
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Sequence 4, Appli
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OTHER INFORMATION: at residue 4 may be Pro or Hyp; Xaa at residue 9 and OTHER INFORMATION: at an abe Phe.Tyr. meta-Tyr. orthor-Tyr. nor-Tyr.
OTHER INFORMATION: O-phospho-Tyr, di-halo-Tyr, O-sulpho-Tyr,
PEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(27)
OTHER INFORMATION: neo-Trp,halo-Trp (D or L) or any synthetic aromatic amino OTHER INFORMATION: acid; Xaa at residue 11 is His or halo-His
                                                         Sequence 27, Appl
Sequence 27, Appl
Sequence 23, Appl
Sequence 57, Appl
Sequence 73, Appl
Sequence 723, Appl
Sequence 168, App
Sequence 167, Appl
Sequence 167, Appl
Sequence 167, Appl
Sequence 167, Appl
Sequence 6999, Appl
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US-10-352-254-1

Sequence 1, Application US/10352254

Publication No. US20030224343A1

GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: University of Utah Research Foundation
APPLICANT: Temple, Davis
APPLICANT: Pemberton-Goodman, Karen
APPLICANT: Pemberton-Goodman, Karen
APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REPERENCE: 2314-254

CURRENT FILING DATE: 2003-01-28

PRIOR FILING DATE: 2003-01-29

NUMBER OF SEQ ID NOS: 28

SOFTWARE: PatentIn Ver. 2.0

LENGTH: 27

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SEQ ID NO 1

LENGTH: 27
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NAME/KEY: PEPTIDE
LOCATION: (1)..(27).
COTHER INFORMATION: Xaa at residue 2, 7, 18, 19, 22 and 25 may be Arg,
OTHER INFORMATION: homoarginine, ornithine, Lys, N-methyl-Lys,
OTHER INFORMATION: N.N-dimethyl-Lys, N.N.N-trimethyl-Lys, any
OTHER INFORMATION: synthetic basic amino acid, His or halo-His; Xaa
FEATURE:
NAME/KEX: PEPTIDE
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US-10-765-727-23

T US-10-764-989-57

US-10-322-281-723

US-09-894-882-168

US-09-894-882-169

US-09-894-882-167

US-09-894-882-167

US-09-894-882-167

US-09-894-882-167

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APPLICANT: Cognetix, Inc.
APPLICANT: Cognetix, Inc.
APPLICANT: Cognetix, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: Pemberton-Goodman, Karen
APPLICANT: Jones, Robert M.
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: Olivera, Baldomero M.
ITILE OF INVENTION: Kappa PVIIA-Related Conotoxins as Organ Protectants
FILE REFERENCE: 2314-254
CURRENT APPLICATION NUMBER: US /10/352,254
CURRENT FILING DATE: 2003-01-29
PRIOR FILING DATE: 2003-01-29
PRIOR FILING DATE: 2002-01-29
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.0
LENGTH: 27
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APPLICANT: Cognetix, Inc.
APPLICANT: Cognetix, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: University of Utah Research Foundation
APPLICANT: Pember. Cooledman, Karen
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: Olivers, Baldomero M.
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REFERENCE: 2314-254
CURRENT APPLICATION NUMBER: US/10/352,219
PRIOR PLILING DATE: 2003-01-29
PRIOR FILING DATE: 2003-01-29
PRIOR FILING DATE: 2002-01-29
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 27
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NAME/KEY: PEPTIDE
LOCATION: (1) . (27)
OTHER INFORMATION: Xaa is Hyp
US-10-352-254-2
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, LOCATION: (1)..(27)
, OTHER INFORMATION: Xaa is Hyp
US-10-352-254-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Conus purpurascens
IS-10-352-254-2
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Sequence 7, Application US/1035254

Fublication No. US2003022434341

GENERAL INFORMATION:
APPLICANT: Cognetix, Inc.
APPLICANT: Objectiv, Inc.
APPLICANT: Demberton-Goodman, Karen
APPLICANT: Temple, Davis
APPLICANT: McIntosh, J. Michael
APPLICANT: McIntosh, J
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APPLICANT: Cognetix, Inc.
APPLICANT: Cognetix, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: Pemberton-Goodman, Karen
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: McIntosh, J. Michael
CURRENT FILING DATE: 2013-01-28
FRIOR APPLICATION NUMBER: US 60/352,219
FRIOR APPLING DATE: 2002-01-29
NUMBER OF SEQ ID NOS: 28
SEQ ID NO 8
LENGTH: 27
LENGTH: 27
                               Length 27;
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                           ; Score 120; DB 15;
Pred. No. 4.7e-05;
9; Mismatches 0;
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100.0%; Score 120; DB 15;
Best Local Similarity 66.7%; Pred. No. 4.7e-05;
Matches 18; Conservative 9; Mismatches 0;
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                           Query Match
Best Local Similarity 66.7%; Matches 18; Conservative 9;
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LOCATION: (1)..(27)
CTHER INFORMATION: Xaa is Hyp
US-10-352-254-7
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ORGANISM: Conus purpurascens
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APPLICANT: Cognetix, Inc.

APPLICANT: University of Utah Research Foundation

APPLICANT: University of Utah Research Foundation

APPLICANT: Jones, Robert M.

APPLICANT: Temple, Baise

APPLICANT: Temple, Davis

APPLICANT: Temple, Davis

APPLICANT: Temple, Davis

APPLICANT: McIntosh, J. Michael

APPLICANT: Winder: 2314-254

CURRENT APPLICATION NUMBER: US 60/352,219

PRIOR PILING DATE: 2002-01-29

NUMBER OF SEQ ID NOS: 28

SEQ ID NO 6

LENGTH: 27
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100.0%; Score 120; DB 15; Length 27;

Best Local Similarity 66.7%; Pred. No. 4.7e-05;

Matches 18; Conservative 9; Mismatches 0; Indels 0
                                  1 CRIXNOKCFQHLDDCCSRXCNAFNKCV 27
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COTHER INFORMATION: Xaa is Hyp
US-10-352-254-6
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CTHER INFORMATION: Xaa is Hyp
US-10-352-254-5
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ORGANISM: Conus purpurascens
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Score 120; DB 15;
Pred. No. 4.7e-05;
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66.7%; Pred. No. 4.7e-05;
tive 9; Mismatches 0;
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9; Mismatches
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Best Local Similarity 66.7%;
Matches 18; Conservative 9
               SEQ ID NO 10
LENGTH: 27
TYPE: PRT
ORGANISM: Conus purpurascens
FEATURE:
NAME/KEY: PEPTIDE
                                                                                                                                                                ; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-10
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; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-11
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ORGANISM: Conus purpurascens
SOFTWARE: PatentIn Ver. 2.0
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Best Local Similarity 66.7
Matches 18; Conservative
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APPLICANT: Cognetix, Inc.

APPLICANT: University of Utah Research Foundation
APPLICANT: University of Utah Research Foundation
APPLICANT: University of Utah Research Foundation
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: McInted, J. Michael
APPLICANT: McInted, J. Michael
APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REFERENCE: 2314-224
CURRENT APPLICATION NUMBER: US 60/352,219
PRIOR APPLICATION NUMBER: US 60/352,219
PRIOR APPLICATION NUMBER: US 60/352,219
PRIOR APPLICATION NUMBER: US 60/352,219
NUMBER OF SEQ ID NOS: 28
SSOTWARE: PatentIn Ver. 2.0

SEQ ID NO 9

LENGTH: 27
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Sequence 10, Application US/10352254

Sequence 10, Application US/10352254

Publication No. US2000224343A1

GENERAL INFORMATION:
APPLICANT: Cognetix, Inc.
APPLICANT: Pemberton-Goodman, Karen
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: APPLICANT: Aldomero M.
TATHE OF INVENTION: ABJOOMER. US. Michael
APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REFERENCE: 2314-254

CURRENT APPLICATION NUMBER: US/10/352,254

CURRENT FILING DATE: 2003-01-28

PRIOR APPLICATION NUMBER: US 60/352,219

PRIOR FILING DATE: 2002-01-29
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                                                                                                                          Query Match 100.0%; Score 120; DB 15
Best Local Similarity 66.7%; Pred. No. 4.7e-05;
Matches 18; Conservative 9; Mismatches 0
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          ; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-8
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; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-9
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ORGANISM: Conus purpurascens
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US-10-352-254-11

Sequence 11, Application US/10352254

Publication No. US20030224343A1

SEQUENAL INFORMATION:

APPLICANT: COSNELX, Inc.

APPLICANT: University of Utah Research Foundation

APPLICANT: University
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Publication No. US20030224343A1

GENERAL INFORMATION:
APPLICANT: Cognetix, Inc.
APPLICANT: Demberton-Goodman, Karen
APPLICANT: Pemberton-Goodman, Karen
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: McIntosh, J. Michael
APPLICANT: McIntosh, J. Michael
APPLICANT: OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REPERENCE: 2314-254
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Length 27;
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Lemple, Davis
APPLICANT: McIntosh, J. Michael
APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REPERBENCE: 2314-254
CURRENT APPLICATION NUMBER: US/10/352,254
CURRENT FILING DATE: 2003-01-28
FRIOR PPLICATION NUMBER: US 60/352,219
FRIOR FILING DATE: 2002-01-29
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
LENGTH: 27
TYPE: ...
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APPLICANT: Cognetix, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: Pemberton-Goodman, Karen
APPLICANT: Pemple, Davis
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REFERENCE: 2314-254
CURRENT PAPLICANTION NUMBER: US/10/352,254
CURRENT FILING DATE: 2003-01-28
PRIOR FILING DATE: 2002-01-29
PRIOR FILING DATE: 2002-01-29
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US-10-627-685-1
Sequence 1, Application US/10627685
Publication No. US20040092447A1
GENERAL INFORMATION:
APPLICANT: COTROLL-Bell, Ann H.
APPLICANT: Pemberton, Karen E.
APPLICANT: Temple Jr., Davis L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: PEPTIDE

LOCATION: (1)..(27)

CHER INFORMATION: Xaa is Hyp
US-10-352-254-14
                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Conus purpurascens FEATURE:
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SEQ ID NO 24
LENGTH: 27
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Matches 17; Conservative
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| Sequence 13, Application US/10352254
| Publication No. US20030224343A1
| Sequence 13, Application US/10352254
| Publication No. US20030224343A1
| GENERAL INPORMATION:
| APPLICANT: Cognetix, Inc.
| APPLICANT: Cognetix, Inc.
| APPLICANT: Pemberton-Goodman, Karen
| APPLICANT: Pemberton-Goodman, Karen
| APPLICANT: Temple, Davis
| APPLICANT: Temple, Davis
| APPLICANT: Olivera, Baldomero M.
| TILLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
| FILE REFERENCE: 2314-254
| CURRENT APPLICATION NUMBER: US/10/352,254
| CURRENT FILING DATE: 2003-01-28
| PRIOR APPLICATION NUMBER: US 60/352,219
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APPLICANT: University of Utah Research Foundation APPLICANT: Pemberton-Goodman, Karen APPLICANT: Jones, Robert M.
                                                                                      CURRENT APPLICATION NUMBER: US/10/352,254
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US 60/352,219
PRIOR FILING DATE: 2002-01-29
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PARENTIN Ver. 2.0
SEQ ID NO 12
LENGTH: 27
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                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (1)..(27)
OTHER INFORMATION: Xaa is Hyp
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; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-13
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ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                              ORGANISM: Conus purpurascens
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SOFTWARE: PatentIn Ver. 2.0
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Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: PEPTIDE
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LENGTH: 27
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PUblication No. US20040092447A1
GENERAL INFORMATION:
APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: Layer, Richard T.
APPLICANT: Ones, R. Tyler
APPLICANT: Connetix, Inc.
TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-FVIIA
FILE REFERENT : CONNER: Kappa-FVIIA
CURRENT APPLICANT: USes of Kappa-FVIIA
FILE REFERENT : 12003-07128
                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 120; DB 15; Best Local Similarity 66.7%; Pred. No. 4.7e-05; Matches 18; Conservative 9; Mismatches 0;
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PRIOR PLING DATE: 2003-07-28

PRIOR FILING DATE: 2000-09-21

PRIOR PLING DATE: 2000-09-21

PRIOR PLING DATE: 2000-09-20

PRIOR PLING DATE: 2000-07-20

PRIOR PLING DATE: 2000-07-20

PRIOR PLING DATE: 1999-09-22

NUMBER OF SEQ ID NOS: 25

SOFTWARE: PATENTIN VEY: 2.0

SEQ ID NO 3

LENGTH: 27
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Publication No. US20040092447A1
GENERAL INFORMATION:
APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Pemberton, Karen E.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: MCCabe, R. Tyler
                                                                                                                                                           , LOCATION: (1) ----;
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-2
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LOCATION: (1)...(27)
LOCATER INFORMATION: Xaa is Hyp
US-10-627-685-3
                                                                                                ORGANISM: Conus purpurascens
PRATURE:
PAME/KEY: PEPTIDE
LOCATION: (1)...(27)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Conus purpurascens
SOFTWARE: Patentin Ver. 2.0
                     SEQ ID NO 2
LENGTH: 27
TYPE: PRT
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OTHER INFORMATION: Asa at residue 2, 7, 18, 19, 22 and 25 may be Arg, OTHER INFORMATION: homoarginine, ornithine, Lyss, N-methyl-Lys, OTHER INFORMATION: N.M-dimethyl-Lys, N.M. hrimethyl-Lys, any OTHER INFORMATION: Synthetic basic amino acid, His or halo-His; Xaa at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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NAMES/KEX: PEPTIDE
LOCATION: (1)...(27)
OTHER INFORMATION: halo-Trp (D or L) or any synthetic aromatic amino OTHER INFORMATION: acid; Xaa at residue 11 is His or halo-His
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (1)...(27)
OTHER INFORMATION: residue 4 may be Prc or Hyp; Xaa at residue 9 and OTHER INFORMATION: 23 may be Phe,Tyr, meta-Tyr, ortho-Tyr, nor-Tyr, OTHER INFORMATION: mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, OTHER INFORMATION: O-phospho-Tyr, nitrc-Tyr, Trp (D or L), neo-Trp,
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     APPLICANT: McCabe, R. Tyler
APPLICANT: Jones, Robert M.
APPLICANT: Jones, Robert M.
APPLICANT: Cognetix, Inc.
TITLE OF INVENTION: Uses of Kappa-Conotcxin PVIIA
FILE REFERENCE: Kappa-PVIIA
CURRENT APPLICATION NUMBER: US/10/627,685
CURRENT FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US/09/666,837
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-07-20
PRIOR FILING DATE: 1209-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
SEQ ID NO 1
SEQ ID NO 1
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APPLICANT: Pemberton, Karen E.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: Layer, Richard T.
APPLICANT: Mocabe, R. Tyler
APPLICANT: Jones, Robert M.
APPLICANT: Cognetix, Inc.
TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REPRENCE: Kappa-PVIIA
CURRENT APPLICATION NUMBER: US/10/627,685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 120; DB 15;
100.0%; Pred. No. 4.7e-05;
iive 0; Mismatches 0;
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PRIOR APPLICATION WUMBER: US/09/666,837
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-07-20
PRIOR PLICATION NUMBER: US 60/155,135
PRIOR PLING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
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Publication No. US20040092447A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 27; Conservative
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US-10-627-685-2
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1 CAIXNOKCFOHLDDCCSRKCNRFNKCV 27

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Jones, Robert M.

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APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: Layer, Richard T.
APPLICANT: Layer, Richard T.
APPLICANT: Jones, Robert M.
APPLICANT: Cognetix, Inc.
APPLICANT: Cognetix, Inc.
APPLICANT: Cognetix, Inc.
APPLICANT: WIRE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
FILE REFERENCE: Kappa-PVIIA
FILE REFERENCE: Cognetix, 1000-09-20
FRIOR APPLICATION NUMBER: US 60/219,438
FRIOR FILING DATE: 2000-09-20
FRIOR APPLICATION NUMBER: US 60/154,135
FRIOR PILING DATE: 1999-09-22
NUMBER OF EEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
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Publication No. US20040092447A1

GENERAL INPORMATION:

APPLICANT: Cornell-Bell, Ann H.

APPLICANT: Pemberton, Karen E.

APPLICANT: Temple Jr., Davis L.

APPLICANT: McCabe, R. Tyler

APPLICANT: McCabe, R. Tyler

APPLICANT: McCabe, R. Tyler

APPLICANT: McCabe, R. Tyler

APPLICANT: Cognetix, Inc.

TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA

FILE REFERENCE: Kappa-PVIIA

CURRENT PLING DATE: 2003-07-28

PRIOR FILING DATE: 2000-07-21

PRIOR FILING DATE: 2000-07-21

PRIOR FILING DATE: 2000-07-21

PRIOR FILING DATE: 2000-07-20

PRIOR FILING DATE: 1999-09-22

NUMBER OF SEQ ID NOS: 25
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Publication No. US20040092447A1
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; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-7
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                                                                                                                                                   GENERAL INFORMATION
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LENGTH: 27
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APPLICANT: Pemberton, Karen E.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: McCabe, R. Tyler
APPLICANT: Cognetix, Inc.
TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
CURRENT PPLICATION NUMBER: US/10/627,685
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66.7%; Pred. No. 4.7e-05;
tive 9; Mismatches 0;
APPLICANT: Cogĥetix, Inc.
TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
                                                                 CURRENT APPLICATION NUMBER: US/10/627,685
CURRENT FILING DATE: 2003-07-28
PRIOR APPLICATION NUMBER: US/09/666,837
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-07-20
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VET: 2.0
SOFTWARE: PATENTIN VET: 2.0
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PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/219,438
PRIOR FILING DATE: 2000-07-20
PRIOR PPLIANG DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATCHIN VET: 2.0
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; OTHER INFORMATION: Xaa is HypUS-10-627-685-5
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COTHER INFORMATION: Xaa is Hyp
US-10-627-685-6
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ORGANISM: Conus purpurascens
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Best Local Similarity 66.7
Matches 18; Conservative
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NAME/KEY: PEPTIDE
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66.7%; Pred. No. 4.7e-05;
tive 9; Mismatches 0;
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Pred. No. 4.7e-05;
9; Mismatches 0;
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APPLICANT: Pemberton, Karen E.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: Jones, R. Tyler
APPLICANT: Jones, Robert M.
APPLICANT: Cognetix, Inc.
TILLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
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CURRENT FILING DATE: 2003-07-28
PRIOR PRILOR APPLICATION NUMBER: US/09/666,837
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-07-20
PRIOR FILING DATE: 2000-07-20
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VET. 2.0
SSOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 11
LENGTH: 27
                      CURRENT FILING DATE: 2003-07-28
PRIOR APPLICATION NUMBER: US/09/666,837
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-07-20
PRIOR FILING DATE: 2000-07-20
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOFWARE: Patentin Ver: 2.0
SEQ ID NO 10
LENGTH: 27
TYPE: PRT
CORMANIEM: CONUS PURPURABCENS
         CURRENT APPLICATION NUMBER: US/10/627,685
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Publication No. US20040092447A1
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Best Local Similarity 66.7%;
Matches 18; Conservative 9
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COTHER INFORMATION: Xaa is Hyp.
US-10-627-685-10
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; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-11
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ORGANISM: Conus purpurascens
FEATURE:
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Best Local Similarity
Matches 18; Conserv
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APPLICANT: Pemberton, Karen E.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: Layer, Richard T.
APPLICANT: McCabe, R. Tyler
APPLICANT: Gones, Robert M.
APPLICANT: Cognetix, Inc.
TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
CURRENT APPLICATION NUMBER: US/09/666,837
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VET: 2.0
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Pred. No. 4.7e-05;
9; Mismatches 0;
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APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Temple Jr., Davis L.
APPLICANT: McCabe, R. Tyler
APPLICANT: Jones, Robert M.
APPLICANT: Cognetix, Inc.
TILLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
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Publication No. US20040092447A1
GENERAL INFORMATION:
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66.7%; P
                                         NAME/KEY: PEPTIDE
LOCATION: (1)...(27)
CTHER INFORMATION: Xaa is Hyp
US-10-627-685-8
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; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-9
ORGANISM: Conus purpurascens
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                                                                                                                                                                                                Conservative
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Matches 18; Conservative
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Best Local Similarity
Matches 18; Conserv
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APPLICANT: Pemberton, Karen E.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: Capmes, Robert M.
APPLICANT: Cognetix, Inc.
ITTLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
CURRENT APPLICATION NUMBER: US/09/666,837
FRICR PELING DATE: 2000-09-21
PRIOR PPLICATION NUMBER: US 60/219,438
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: US 60/155,135
                                                                                    Query Match 100.0%; Score 120; DB 15; Best Local Similarity 66.7%; Pred. No. 4.7e-05; Matches 18; Conservative 9; Mismatches 0;
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Pred. No. 4.7e-05;
9; Mismatches 0;
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PRIOR APPLICATION NUMBER: US/09/666,837
PRIOR FILING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                                                                                                  US-10-627-685-14
; Sequence 14, Application US/10627685
; Publication No. US20040092447A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 24, Application US/10627685 Publication No. US20040092447A1
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Best Local Similarity 66.7%;
Matches 18; Conservative 9
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, OTHER INFORMATION: Xaa is Hyp
US-10-627-685-14
; OTHER INFORMATION: Xaa is Hyp US-10-627-685-13
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APPLICANT:
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                                                                                                     APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: Layer, Richard T.
APPLICANT: Gones, Robert M.
APPLICANT: Cognetix, Inc.
TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
FILE REFERENCE: Kappa-PVIIA
FILE REFERENCE: Kappa-PVIIA
FILE REFELICATION NUMBER: US/09/666,837
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR PPLICATION NUMBER: US 60/159,135
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATCHTIN VET. 2.0
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APPLICANT: Temple Jr., Davis L.
APPLICANT: Temple Jr., Davis L.
APPLICANT: McCabe, R. Tyler
APPLICANT: Jones, Robert M. APPLICANT: Cognetix, Inc., TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA CURRENT APPLICANTON NUMBER: US/10/627,685
CURRENT APPLICATION NUMBER: US/09/666,837
PRIOR PRILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/219,438
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-07-20
PRIOR PRILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13
LENGTH: 27
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                             Sequence 12, Application US/10627685
Publication No. US20040092447A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: PEPTIDE
LOCATION: (1)..(27)
CTHER INFORMATION: Xaa is Hyp
US-10-627-685-12
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LOCATION: (1)..(27)
                                                                                 GENERAL INFORMATION
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SEQ ID NO 12
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APPLICANT: University of Utah Research Foundation

APPLICANT: University of Utah Research Foundation

APPLICANT: University of Utah Research Foundation

APPLICANT: Pemberton-Goodman, Karen

APPLICANT: Temple, Davis

APPLICANT: Temple, Davis

APPLICANT: Moritocsh, J. Michael

APPLICANT: Moritocsh, J. Michael

TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants

FILE REFERENCE: 2314-254

CURRENT APPLICATION NUMBER: US/10/352,254

CURRENT APPLICATION NUMBER: US/10/352,254

CURRENT FILING DATE: 2003-01-29

PRIOR FILING DATE: 2002-01-29

NUMBER OF SEQ ID NOS: 28

SOFTWARE: Patentin Ver. 2.0

LENOTH: 27

TYPP:
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97.5%; Score 117; DB 15; Length 27;
Best Local Similarity 63.0%; Pred. No. 9.1e-05;
Matches 17; Conservative 10; Mismatches 0; Indels
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    FILE REFERENCE: Kappa-PVIIA
CURRENT APPLICATION NUMBER: US/10/627,685
CURRENT FILING DATE: 2003-07-28
FRIOR APPLICATION NUMBER: US 69/666,837
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-07-20
PRIOR FILING DATE: 2000-07-20
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
NUMBER OF SEQ ID NOS: 25
SECTIANE: PATENTIN Ver: 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-18
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NAME/KEY: PEPTIDE
LOCATION: (1)..(27)
OTHER INFORMATION: Xaa is Hyp
                                                                                                                                                                                                                                                                                                                                              ORGANISM: Conus purpurascens
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US-10-627-685-23
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APPLICANT: Cognetix, Inc.
APPLICANT: Cognetix, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: Demberton-Goodman, Karen
APPLICANT: Demberton-Goodman, Karen
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: McIncosh, J. Michael
APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REFERENCE: 2314-254
CURRENT APPLICATION NUMBER: US/10/352,254
CURRENT FILING DATE: 2003-01-29
PRIOR FILING DATE: 2003-01-29
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 18
LENGTH: 27
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Best Local Similarity 63.0%; Pred. No. 4.7e-05;
Matches 17; Conservative 10; Mismatches 0; Indels C
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APPLICANT: Layer, Richard T.
APPLICANT: McCabe, R. Tyler
APPLICANT: Jones, Robert M.
APPLICANT: Cognetix, Inc.
TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
                                                                                                                                                                                                                                                                                                                                                                                   1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
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                      PRIOR FILING DATE: 2000-07-20
PRIOR PEDLICATION NUMBER: US 60/155,135
PRIOR FILING DATE: 1990-09-22
NUMBER OF SEQ ID NOS: 25
SPETWARE: PALENTIN Ver. 2.0
SEQ ID NO 24
LENGTH: 27
PRIOR APPLICATION NUMBER: US 60/219,438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 18, Application US/10352254; Publication No. US20030224343A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 18, Application US/10627685; Publication No. US20040092447A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Cornell-Bell, Ann H. APPLICANT: Pemberton, Karen E.
                                                                                                                                                                                         TYPE: PRT
CRGANISM: Conus purpurascens
US-10-627-685-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Conus purpurascens
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APPLICANT:
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Gaps

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Gaps

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Sequence 20, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix. Inc.
; APPLICANT: Cognetix. Inc.
; APPLICANT: Davis
; APPLICANT: Davis
; APPLICANT: Temple, Davis
; APPLICANT: Mointoch, J. Michael
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
; TITLE OF INVENTION NUMBER: US/10/352,254
; CURRENT APPLICATION NUMBER: US 60/352,219
; PRIOR APPLICATION NUMBER: US 60/352,219
; RIUNG APPLICATION NUMBER: US 60/352,219
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.0
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
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APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: McCabe, R. Tyler
APPLICANT: Gorgetix, Inc.
TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
CURRENT APPLICATION NUMBER: US/09/666, 837
FILE REFERENCE: CO03-07-28
PRIOR APPLICATION NUMBER: US 60/219, 438
PRIOR PILING DATE: 2000-09-20
PRIOR PILING DATE: 2000-07-20
PRIOR PILING DATE: 1999-09-22
PRIOR APPLICATION NUMBER: US 60/155,135
PRIOR PILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
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63.0%; Pred. No. 0.00014;
tive 9; Mismatches 1;
                                             1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
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NAME/KEY: PEPTIDE

LOCATION: (11..(27)

CTHER INFORMATION: Xaa is Hyp
US-10-352-254-20
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ORGANISM: Conus purpurascens
FEATURE:
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Best Local Similarity 63.0°
Matches 17; Conservative
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                                                                                      APPLICANT: Femple Jr., Davis L.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: McCabe, R. Tyler
APPLICANT: Gonetix, Inc.
TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE Kappa-PVIIA
CURRENT APPLICATION NUMBER: US/10/627,685
CURRENT FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US/09/666,837
PRIOR APPLICATION NUMBER: US 60/219,438
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-07-20
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO S: 23
LENGTH: 27
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Publication No. US20030224343A1
GENERAL INFORMATION:
APPLICANT: Cognetix, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: University of Utah Research Foundation
APPLICANT: Venberton-Goodman, Karen
APPLICANT: Temple, Davis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 96.7%; Score 116; DB 15; Best Local Similarity 65.4%; Pred. No. 0.00011; Matches 17; Conservative 9; Mismatches 0;
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63.0%; Pred. No. 0.00014;
tive 9; Mismatches 1;
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       Cornell-Bell, Ann H.
Pemberton, Karen E.
Temple
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LOCATION: (1)..(27)
CTHER INFORMATION: Xaa is Hyp
US-10-352-254-4
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LOCATION: (1)..(27)
JUSTION: (1)..(27)
US-10-627-685-23
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ORGANISM: Conus purpurascens
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Best Local Similarity 63.0
Matches 17; Conservative
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1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
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  PRIOR APPLICATION NUMBER: US 60/352,219
PRIOR FILING DATE: 2002-01-29
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 16
LENGTH: 27
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Publication No. US20030224343A1
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Publication No. US20040092447A1
GENERAL INFORMATION:
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APPLICANT: Pemberton, Karen E.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: McCabe, R. Tyler
APPLICANT: Jones, Robert M.
                                                                                                                                                                                                NAME/KEY: PEPTIDE
LOCATION: (1)..(27)
CTHER INFORMATION: Xaa is Hyp
US-10-352-254-16
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NAME/KEY: PEPTIDE
LOCATION: (1)..(27)
CTHER INFORMATION: Xaa is Hyp
US-10-352-254-22
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Best Local Similarity 63.09
Matches 17; Conservative
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Best Local Similarity 63.09
warches 17; Conservative
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                                                                                                                                    TYPE: PRT
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APPLICANT: Dones, Robert M.
APPLICANT: Jones, Robert M.
APPLICANT: Temple, Davis Baldomero M.
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REFERENCE: 2314-254
CURRENT APPLICATION NUMBER: US/10/352,254
                                                                                                                                                           Gaps
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                                                                                                           Score 115; DB 15; Length 27;
Pred. No. 0.00014;
9; Mismatches 1; Indels
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63.0%; Pred. No. 0.00014;
ive 9; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cognetix, Inc.
TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REPERENCE: Kappa-PVIIA
FILE REPERENCE: Kappa-PVIIA
CURRENT PPLICATION NUMBER: US/10/627,685
CURRENT FILING DATE: 2003-07-28
PRIOR REPLICATION NUMBER: US/09/666,837
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-07-20
PRIOR PPLICATION NUMBER: US 60/159,135
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VOICE: 200
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APPLICANT: Universalty of Utah Research Foundation APPLICANT: Pemberton-Goodman, Karen APPLICANT: Jones, Robert M.
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Publication No. US20040092447A1
GENERAL INFORMATION:
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Publication No. US20030224343A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Pemberton, Karen E.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: McCabe, R. Tyler
APPLICANT: Jones, Robert M.
                    ; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-4
                                                                                                      Query Match
Best Local Similarity 63.0%;
Matches 17; Conservative
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OTHER INFORMATION: Xaa is Hyp
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Matches 17; Conserva
NAME/KEY: PEPTIDE
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US-10-627-685-20
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APPLICANT: Cognetix, Inc.
APPLICANT: Cognetix, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: Demberton-Goodman, Karen
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: McIntosh, J. Michael
APPLICANTON NUMBER: US/10/352,254
CURRENT APPLICATION NUMBER: US 60/352,219
PRIOR FILING DATE: 2003-01-29
PRIOR FILING DATE: 2002-01-29
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 22
                                                           Gaps
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95.0%; Score 114; DB 15; Length 27; 63.0%; Pred. No. 0.00018; ive 9; Mismatches 1; Indels
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63.0%; Pred. No. 0.00018;
tive 9; Mismatches 1;
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APPLICANT: Cognetia, Inc.
APPLICANT: Cognetia, Inc.
APPLICANT: Cognetia, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: University of Utah Research Foundation
APPLICANT: University of Utah Research Foundation
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: McIntosh, J. Michael
APPLICANT: McIntosh, J. Michael
APPLICANT: McIntosh, J. Michael
APPLICANT: McIntosh, J. Michael
APPLICANT: Musers, Baldomero M.
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REFERENCE: 2314-254
CURRENT APPLICATION NUMBER: US/10/352,254
CURRENT APPLICATION NUMBER: US 60/352,219
PRIOR FILING DATE: 2002-01-29
NUMBER OF SEQ ID NOS: 28
SOFTHARE: Patentin Ver. 2.0
SEQ ID NO 17
LENGTH: 27
                                                                                                                                                                                              APPLICANT: Cognetix, Inc.
APPLICANT: Cognetix, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: Pemberton-Goodman, Karen
APPLICANT: Pemple, Davis
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REFERENCE: 2314-254
CURRENT APPLICANTION NUMBER: US/10/352,254
CURRENT PILING DATE: 2003-01-28
PRIOR FILING DATE: 2002-01-29
PRIOR FILING DATE: 2002-01-29
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63.0%; Pred. No. 0.00028;
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                                                                                                               Sequence 15, Application US/10352254 Publication No. US20030224343A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 17, Application US/10352254
Publication No. US20030224343A1
GENERAL INFORMATION:
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COTHER INFORMATION: Xaa is Hyp
US-10-352-254-15
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COTHER INFORMATION: Xaa is Hyp
US-10-352-254-17
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FEATURE:
NAME/KEY: PEPTIDE
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ORGANISM: Conus purpurascens
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
LENGTH: 27
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Best Local Similarity
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NAME/KEY: PEPTIDE
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Pred. No. 0.00018;
9; Mismatches 1; Indels
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APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: Layer, Richard T.
APPLICANT: Layer, Richard T.
APPLICANT: Cognetix, Inc.
ITILE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
CURRENT APPLICATION NUMBER: US/09/666,837
FILE REPERENCE: 2000-09-21
PRIOR APPLICATION NUMBER: US/09/666,837
PRIOR RILING DATE: 2000-09-21
PRIOR PLLING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: US 60/19,438
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO SEQ ID NOS: 25
LENGTH: 27
APPLICANT: Cognetix, Inc.

TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
CURRENT APPLICATION NUMBER: US/10/627,685
CURRENT FILING DATE: 2003-07-28
PRIOR APPLICATION NUMBER: US/09/666,837
PRIOR PLILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/219,438
PRIOR APPLICATION NUMBER: US 60/219,438
PRIOR APPLICATION NUMBER: US 60/155,135
PRIOR APPLICATION UND S: 25
SOFTWARE: PATENTIN VET: 2.0
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Sequence 2.5 Application US/10627685
Publication No. US20040092447A1
GENERAL INFORMATION:
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COTHER INFORMATION: Xaa is Hyp. US-10-627-685-16
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; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-22
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Best Local Similarity 63.0%;
Matches 17; Conservative
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ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Conus purpurascens
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Best Local Similarity 63.0
Matches 17; Conservative
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Gaps

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APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: Morticosh, Michael
APPLICANT: Morticosh, Michael
APPLICANT: Morticosh, Baldomero M.
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REPERENCE: 2314-254
CURRENT FILING DATE: 2002-01-28
PRIOR PAPLICATION NUMBER: US 60/352,219
PRIOR PAPLICATION NUMBER: US 60/352,219
PRIOR FILING DATE: 2002-01-29
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Ratentin Ver. 2.0
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APPLICANT: Cognetix, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: Pemberton-Goodman, Karen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93.3%; Score 112; DB 15;
63.0%; Pred. No. 0.00028;
                                                                     Score 112; DB 15;
Pred. No. 0.00028;
9; Mismatches 1;
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APPLICANT: Layer, Richard T.
APPLICANT: McCabe, R. Tyler
APPLICANT: Jones, Robert M.
APPLICANT: Cognetix, Inc.
AITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
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CURRENT FILING DATE: 2003-07-28
PRIOR APPLICATION NUMBER: US/09/666,837
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-07-20
PRIOR PLICATION NUMBER: US 60/219,438
PRIOR PLICATION NUMBER: US 60/219, PRIOR APPLICATION NUMBER: US 60/155,135
PRIOR FILING DATE: 1999-09-22
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APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Pemberton, Karen E.
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (1)..(27)
OTHER INFORMATION: Xaa is Hyp
                                                                     Query Match 93.3%;
Best Local Similarity 63.0%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Conus purpurascens
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Best Local Similarity 63.0°
Matches 17; Conservative
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APPLICANT: Cognetix, Inc.
APPLICANT: Cognetix, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: University of Utah Research Foundation
APPLICANT: Demberton-Goodman, Karen
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: McIntosh, J. Michael
APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REFERENCE: 2314-254
CURRENT FILING DATE: 2003-01-28
PRIOR PILING DATE: 2003-01-29
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 19
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APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: McIntosh, J. Michael
APPLICANT: Olivera, Baldomero M.
APPLICANT: Olivera, Baldomero M.
FILLE REFERENCE: 2314-254
CURRENT APPLICATION NUMBER: US/10/352,254
CURRENT FILING DATE: 2003-01-28
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     Indels
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PRELICANT: University of Utah Research Foundation APPLICANT: Pemberton-Goodman, Karen APPLICANT: Jones, Robert M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93.3%; Score 112; DB ilarity 63.0%; Pred. No. 0.00 Conservative 9; Mismatches
  9; Mismatches
                                                   1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
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                                                                               1 CRIXNOKCFQHLDDCCSRKCARFNKCV 27
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PRIOR FILING DATE: 2002-01-29
                                                                                                                                                                                                                       ; Sequence 19, Application US/10352254; Publication No. US20030224343A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 21, Application US/10352254; Publication No. US20030224343A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (1)..(27)
COTHER INFORMATION: Xaa is Hyp
US-10-352-254-19
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 21
LENGTH: 27
  17; Conservative
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Best Local Similarity
Matches 17; Conserv
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LOCATION: (1)..(27)
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US-10-352-254-19
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  Matches
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93.3%; Score 112; DB 15;
Best Local Similarity 63.0%; Pred. No. 0.00028;
Matches 17; Conservative 9; Mismatches 1;
                                                                       TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA FILE REFERENCE: Kappa-PVIIA CURRENT APPLICATION NUMBER: US/10/627,685 CURRENT FILING DATE: 2003-07-28
                                                                                           THILE REFERENCE: Kappa-PVIIA
CURRENT APPLICATION NUMBER: US/10/627,685
CURRENT FILING DATE: 2003-07-28
PRIOR PAPLICATION NUMBER: US/09/666,837
PRIOR FILING DATE: 2000-09-21
PRIOR PLING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: US 60/219,438
PRIOR PLING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 19
LENTH: 27
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PRIOR APPLICATION NUMBER: US/09/666,837
PRIOR APPLICATION NUMBER: US/09/666,837
PRIOR APPLICATION NUMBER: US 60/219,438
PRIOR PILING DATE: 2000-07-20
PRIOR PELING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN UNMBER: US 60/155,135
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 21
LENGTH: 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: PEPTIDE
LOCATION: (1)..(27)
OTHER INFORMATION: Xaa is Hyp
US-10-627-685-19
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; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-21
                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Conus purpurascens
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APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: McCabe, R. Tyler
APPLICANT: McCabe, R. Tyler
APPLICANT: Cognetix, Inc.
TITLE OF INVENTION: Ubes of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
CURRENT APPLICATION NUMBER: US/10/627,685
CURRENT FILING DATE: 2003-07-28
PRIOR PILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/219,438
PRIOR FILING DATE: 2000-07-20
PRIOR FILING DATE: 2000-07-20
PRIOR FILING DATE: 1099-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VOR: 25
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                               1 CXIXNOXCXQXLDDCCSXXCNXXNXCV 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17, Application US/10627685
Publication No. US20040092447A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Cornell-Bell, Ann H. APPLICANT: Pemberton, Karen E.
                                                                                                                                                                       NAME/KEY: PEPTIDE
LOCATION: (1)..(27)
OTHER INFORMATION: Xaa is Hyp
US-10-627-685-15
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LOCATION: (1)..(27)
OTHER INFORMATION: Xaa is Hyp
US-10-627-685-17
                                                                                                   TYPE: PRT
ORGANISM: Conus purpurascens
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Best Local Similarity 63.0'
Matches 17; Conservative
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver.
SEQ ID NO 15
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Ouery Match 67.5%; Score 81; DB 10; Length 26; Best Local Similarity 34.6%; Pred. No. 0.28; Matches 9; Conservative 13; Mismatches 4; Indels

; LENGTH: 26
; TYPE: PRY
CORGANISM: Conus striatus
US-09-910-082A-395

1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26 | ::: | :| ::: | | | | | :: | 1 CKLKGQSCRRTMYDCCSGSCGRRGKC 26

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APPLICANT: Cornell-Bell, Ann H.

APPLICANT: Pemberton, Karen E.

APPLICANT: Temple Jr., Davis L.

APPLICANT: Temple Jr., Davis L.

APPLICANT: McCabe, R. Tyler

APPLICANT: Ones, Robert M.

APPLICANT: Ognetix, Inc.

TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA

FILE REFERENCE: Kappa-PVIIA

CURRENT APPLICATION NUMBER: US/09/666,837

PRIOR APPLICATION NUMBER: US/09/666,837

PRIOR APPLICATION NUMBER: US 60/219,438

PRIOR APPLICATION NUMBER: US 60/155,135

PRIOR FILING DATE: 2000-07-20

PRIOR FILING 
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Pred. No. 0.00028;
9; Mismatches 1;
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APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Machael
APPLICANT: Watkins, Maren
APPLICANT: Watkins, Maren
APPLICANT: Shon, Ki-Joon
APPLICANT: Shon, Ki-Joon
APPLICANT: Jacobsen, Richard
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APPLICANT: Cartier, G. Edward
FILE REFERENCE: 2314-241
CURRENT APPLICATION NUMBER: US/09/910,082A
FILE REFERENCE: 2001-07-23
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SEQ ID NO 395
1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
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                                                                                                                                                                                                                                ; Sequence 25, Application US/10627685; Publication No. US20040092447A1; GENERAL INFORMATION:
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63.0%;
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; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-25
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ORGANISM: Conus purpurascens
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Best Local Similarity 63.0%
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US-10-755-926-395

Sequence 395, Application US/10765926

Sequence 395, Application US/10765, 205

Sequence 395, Application US/10765, 205

Sequence 396, Application US/10765, 306

Sequence 396, Application US/10761, Application US/10765, 306

Sequence 396, Application US/10765, App
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atkins, Maren
arrett, James E.
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ORGANISM: Conus striatus
FEATURE:
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APPLICANT: Octobe, J. Michael
APPLICANT: Morthcobh, J. Michael
APPLICANT: Matkins, Maren
APPLICANT: Garrett, James E.
APPLICANT: Jacobsen, Richard
TITLE OF INVENTION: Omega-Conopeptides
TITLE OF INVENTION NUMBER: US 09/910,082
RRIOR FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 60/265,888
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: PatentIn version 3.0
SEQ ID NO 252
LENGTH: 30
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                                                                                                                                                                                                                                                                                                                                                             Query Match 67.5%; Score 81; DB 10
Best Local Similarity 34.6%; Pred. No. 0.31;
Matches 9; Conservative 13; Mismatches
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34.6%; Pred. No. 0.31;
tive 13; Mismatches
CURRENT APPLICATION NUMBER: US/09/910,082A
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                     CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR FILING DATE: 2000-07-21
PRIOR PLILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: Patentin version 3.0
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US-09-910-082A-258
Sequence 258, Application US/09910082A
Publication No. US20030119731A1
GENERAL INFORMATION:
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Olivera, Baldomero M.
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Best Local Similarity 34.6
Matches 9; Conservative
                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Conus striatus
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US-10-765-926-257
                                                                                                                                                                                                 SEQ ID NO 257
LENGTH: 30
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TYPE: PRT
ORGANISM:
COND STRIAGE
SEATURE:
NAME/KEY: PEPTIDE
COCATION: (1)...(26)
OTHER INFORMATION: Xaa at residue 13 is Tyr, 1251-Tyr, mono-iodo-Tyr, di-iodo-Tyr, OTHER INFORMATION: -sulpho-Tyr or O-phospho-Tyr
US-09-910-082A-258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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LOCATION: (1)..(26)
OTHER INFORMATION: Xaa at residue 13 is Tyr, 1251-Tyr, mono-iodo-Tyr,
OTHER INFORMATION: di-iodo-Tyr, 0-sulpho-Tyr or 0-phospho-Tyr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 61.7%; Score 74; DB 10; Length 26; Best Local Similarity 34.6%; Pred. No. 1.3; Matches 9; Conservative 13; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. SEREMAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: Marinos, March
APPLICANT: Markinos, Maren
APPLICANT: Garrett, James E.
APPLICANT: Shon, Ki-Joon
APPLICANT: Jacobsen, Richard
APPLICANT: Jones, Robert M.
APPLICANT: Jones, Robert M.
APPLICANT: Cartier, G. Edward
ITILE OF INVENTION: Omega-Conopeptides
APPLICANT: Shon, Ki-Joon
APPLICANT: Shon, Ki-Joon
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Cartier, G. Edward
TITLE OF INVENTION: Omega-Conopeptides
FILE REFERENCE: 2314-241
CURRENT PPLICATION NUMBER: US/09/910,082A
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR PILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: PATENTIN VETSION 3.0
SEQ ID NO 258
LENGTH: 26
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CURRENT APPLICATION NUMBER: US/10/765,926
CURRENT FILING DATE: 2004-01-29
PRIOR APPLICATION NUMBER: US 09/910,082
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR APPLICATION NUMBER: US 60/265,888
PRIOR PILING DATE: 2000-07-21
PRIOR FILING DATE: 2001-05-65
NUMBER OF SEQ ID NOS: 413
SEQ ID NO 258
LENTH: 26
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Sequence 258, Application US/10765926
Publication No. US20040132663A1
GENERAL INFORMATION:
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US-10-765-926-258

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SOFTWARE: CuraSeqList version 0.1./
SEQ ID NO 25
LENGTH: 2524
NUMBER OF SEQ ID NOS: 136
                                                                           ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-190-115-25
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                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F: VOSB, Edward Z.
INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
SRENCE: 21402-050 CIP
                                                            .
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     61.7%; Score 74; DB 16; Length 26; 34.6%; Pred. No. 1.3;
                                                            4; Indels
                                                 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/190,115
CURRENT FILING DATE: 2003-02-10
PRIOR APPLICATION NUMBER: 60/303,168
PRIOR FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 60/368,996
                                                                                                   1 CXIXNOXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                      PRIOR APPLICATION NUMBER: 60/366,996
PRIOR FILING DATE: 2002-04-01
PRIOR PELING DATE: 2002-04-01
PRIOR PELING DATE: 2002-06-07
PRIOR PILING DATE: 2002-66-07
PRIOR FILING DATE: 2000-07-03
PRIOR APPLICATION NUMBER: 60/215,856
PRIOR FILING DATE: 2000-07-03
PRIOR PILING DATE: 2000-07-03
PRIOR FILING DATE: 2000-07-03
PRIOR PELING DATE: 2000-07-07
PRIOR PELING DATE: 2000-07-07
PRIOR PELING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2001-07-07
PRIOR PILING DATE: 2001-07-07
PRIOR PILING DATE: 2001-07-07
PRIOR PILING DATE: 2000-07-07
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Shimkets, Richard A.
Spaderna, Steven K.
Spytek, Kimberly A.
Szekeres, Edward S. Jr.
Taupier, Raymond J. Jr.
                                                                                                                                                                                                                                                                              Sequence 25, Application US/10190115
Publication No. US20030207394A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mezick, Amanda J.
Padigaru, Muralidhara
Patturajan, Meera
Rastelli, Luca
Shen, Lei
                                                                                                                                                                                                                                                                                                                                                     Alsobrook, John P. II
Boldog, Ferenc L.
Burgess, Catherine E.
Casman, Stacie J.
Grosse, William M.
Gusev, Vladimir Y.
Ji, Weizhen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pley, Denise M.
Query Match
Best Local Similarity 34.6
Matches 9; Conservative
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APPLICANT: Burgess, Catherine E
APPLICANT: Shimkets, Richard
APPLICANT: Shimkets, Richard
APPLICANT: Padigaru, Muralidhara
TITLE OF INVENTION No. US20040014081A1el Proteins and Nucleic Acids Encoding Same
FILE REPERENCE: 21402-050 CON2
CURRENT APPLICATION NUMBER: US/10/369,072
CURRENT PILING DATE: 2003-02-18
PRIOR APPLICATION NUMBER: 10/174,372
PRIOR FILING DATE: 2003-04-1
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PRIOR APPLICATION NUMBER: 60/218,622
PRIOR FILING DATE: 2000-07-17
SEQ ID NOS: 100
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 25
LINGTH: 2524
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                             Indels
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  34.6%; Pred. No. 1.4e+02;
tive 12; Mismatches 5;
                                                                                               248 GFSGQNCEENIDDCPSNNCRNGGTCV 273
                                                               2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
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PRIOR APPLICA.

PRIOR PILING DATE:

PRIOR FILING DATE:

PRIOR FILING DATE:

PRIOR FILING DATE:

PRIOR FILING DATE: 2000-07-v.

PRIOR APPLICATION NUMBER: 60/216,-7

PRIOR PLING DATE: 2000-07-07

PRIOR FILING DATE: 2000-07-07

APPLICATION NUMBER: 60/218,622

"NG DATE: 2000-07-17

"NG DATE: 2000-07-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OR FILING DATE: 2002-06-17
OR APPLICATION NUMBER: 09/898,994
OR FILING DATE: 2001-07-03
OR APPLICATION NUMBER: 60/215,854
OR FILING DATE: 2000-07-03
OR APPLICATION NUMBER: 60/215,856
OR FILING DATE: 2000-07-03
OR APPLICATION NUMBER: 60/215,902
OR PILING DATE: 2000-07-03
OR PILING DATE: 2000-07-03
OR PILING DATE: 2000-07-03
OR PILING DATE: 2000-07-07
OR APPLICATION NUMBER: 60/216,585
OR FILING DATE: 2000-07-07
OR APPLICATION NUMBER: 60/216,586
                                                                                                                                                                                                                                Sequence 25, Application US/10369072
Publication No. US20040014081A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                     APPLICANT: Alsobrook II, John p
APPLICANT: Spaderna, Stephen K
APPLICANT: Tchernev, Velizar
APPLICANT: Liu, Xiaohong
APPLICANT: Shenoy, Suresh
APPLICANT: Spytek, Kimberly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                zerkeres, Edward S
epley, Denise M
                                                                                                                                                                                                                                                                                                                                                                                                                                             Zerhusen, Bryan
Patturajan, Meera
Taupier, Raymond
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Grosse, William M
Best Local Similarity 34.6
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Xenopus laevis
US-10-369-072-25
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Best Local Similarity
Matches 9; Conserv
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PRIOR
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60.0%; Score 72; DB 15; Length 2524;

Query Match

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APPLICANT: Miele, Lucio
TITLE OF INVENTION: METHOD AND REAGENTS FOR EPITHELIAL BARRIER FORMATION AND TREATMENTITLE OF INVENTION: METHOD AND REAGENTS FOR EPITHELIAL BARRIER FORMATION AND TREATMENTITLE OF INVENTION: MALIGNANT AND BENIGN SKIN DISORDERS BY MODULATING THE NOTCH PATH FILE REFERENCE: 212583
CURRENT APPLICATION NUMBER: US/09/944,849
CURRENT APPLICATION NUMBER: US 60/229,614
PRIOR APPLICATION NUMBER: US 60/229,614
PRIOR FILING DATE: 2000-08-31
NUMBER OF SEQ 1D NOS: 18
SOFTWARE: PATENTIN VERSION 3.1
SEQ 1D NO 2
LENGTH: 2444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: misc_feature
LOCATION: (891).
OTHER INFORMATION: The 'Xaa' at location 891 stands for Gly, or Ala.
NAME/KEY: misc_feature
LOCATION: (1763)...(1763)
OTHER INFORMATION: The 'Xaa' at location 1763 stands for Gln, Arg, Pro, or Leu.
NAME/KEY: misc_feature
LOCATION: (1787)...(1787)
OTHER INFORMATION: The 'Xaa' at location 1787 stands for Thr, Ala, Pro, or Ser.
OTHER INFORMATION: Constitutively Active No. US20020151487Alch-1
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                                                  ; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(26)
; OTHER INFORMATION: Xaa at residue 13 is Tyr, 1251-Tyr, mono-iodo-Tyr,
; OTHER INFORMATION: di-iodo-Tyr, O -sulpho-Tyr or O-phospho-Tyr
US-10-765-926-268
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                                                                                                                                                                                                                               Length 26;
                                                                                                                                                                                                                               DB 16;
                                                                                                                                                                                                                            Query Match 58.3%; Score 70; DB 1
Best Local Similarity 34.6%; Pred. No. 3.2;
Matches 9; Conservative 12; Mismatches
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Publication No. US20040033493A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09944849
Patent No. US20020151487A1
GENERAL INFORMATION:
APPLICANT: Nickoloff, Brian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gangolli, Esha
Padigaru, Muralidhara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: TChernev, Velizar
APPLICANT: Spytek, Kimberly
APPLICANT: Zerhueen, Bryan
APPLICANT: Patturajan, Meera
APPLICANT: Shimkets, Richard
TYPE: PRT
ORGANISM: Conus striatus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (1)..(26)
; OTHER INFORMATION: Xaa at residue 13 is Tyr, 1251-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
; OTHER INFORMATION: -sulpho-Tyr or O-phospho-Tyr
US-09-910-082A-268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.3%; Score 70; DB 10; Length 26; illarity 34.6%; Pred. No. 3.2; Conservative 12; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: University of Utah Research Foundation
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Matches, J. Michael
APPLICANT: Watkins, Maren
APPLICANT: Garrett, James E.
APPLICANT: Shon, Ki-Joon
APPLICANT: Jacobeen, Richard
APPLICANT: Jones, Robert M.
                                                                                          APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIns, Maren
APPLICANT: Watkins, Maren
APPLICANT: Garrett, James E.
                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Omega-Conopeptides
TITLE OF INVENTION: Omega-Conopeptides
FILE REPERENCE: 2314-241
CURRENT APPLICATION NUMBER: US/09/910,082A
CURRENT FILING DATE: 2001-07-23
PRIOR PAPLICATION NUMBER: US 60/219,616
PRIOR PILING DATE: 2000-07-21
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: PatentIn version 3.0
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CURRENT FILING DATE: 2004-01-29
PRIOR APPLICATION NUMBER: US 09/910,082
PRIOR FILING DATE: 2001-07-23
PRIOR FILING DATE: 2000-07-21
PRIOR PILING DATE: 2000-07-21
PRIOR PILING DATE: 2000-07-21
PRIOR FILING DATE: 2001-06-65
NUMBER OF SEQ ID NOS: 413
SOFTWARE: Patentin Version 3.0
LENGTH: 26
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TITLE OF INVENTION: Omega-Conopeptides
FILE REFERENCE: 2314-241
Sequence 268, Application US/09910082A Publication No. US20030119731A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 268, Application US/10765926; Publication No. US20040132663Al; GENERAL INFORMATION:
                                                                                                                                                                                                                                                      Shon, Ki-Joon
Jacobsen, Richard
Jones, Robert M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Conus striatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 9; Conserva
US-09-910-082A-268
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US-10-765-926-268
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LENGTH: 26
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APPLICANT: Padgatu, Muralidhara
APPLICANT: Addaran, David M.
APPLICANT: Addaran, David M.
APPLICANT: Madaran, David M.
APPLICANT: Miler, Charles E.
APPLICANT: Grace, Miler, Charles E.
APPLICANT: Colman, Steven D.
APPLICANT: Grace, Milliam
APPLICANT: Grace, Millia
                                                                                                                                                                                       Patturajan, Meera
Shimkets, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT PRENENCE: 21402-258

CURRENT PILLOR DATE: 2002-01-31

PRIOR PAPLICATION NUMBER: 60/265,102

PRIOR PELING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-31

PRIOR PELING DATE: 2001-02-32

PRIOR PELING DATE: 2001-02-32

PRIOR PELING DATE: 2001-02-05

PRIOR PELING DATE: 2001-02-05

PRIOR PELING DATE: 2001-02-07

PRIOR PELING DATE: 2001-02-07
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56.7%; Score 68; DB 15; Length 2444;

Best Local Similarity 30.8%; Pred. No. 3.4e+02;

Matches 8; Conservative 12; Mismatches 6; Indels
                                                                                                                                                                                                                                                                               APPLICANT: Wolenc, Adam R.
APPLICANT: Pena, Carol E. A
APPLICANT: Pena, Carol E. A
APPLICANT: Gross, Milliam M.
APPLICANT: Alsobrook II, John P.
APPLICANT: Lepley, Denise M.
APPLICANT: Burgest, Catherine E.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME,KEY: VARIANT
LOCATION: (891)
OTHER INFORMATION: Wherein Xaa is any amino acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (1763)
OTHER INFORMATION: Wherein Xaa is any amino acid.
FEATURE:
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (1787)
OTHER INFORMATION: Wherein Xaa is any amino acid
                              Ratelli, Luca
Miller, Charles E.
Gerlach, Valerie
Taupier Jr, Raymond J.
Gusev, Vladimir Y.
Colman, Steven D.
Anderson, David W.
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: VARIANT
LOCATION: (1763)
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TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: VARIANT
COCATION: (890)
OTHER INFORMATION: Wherein Xaa is any amino acid.
FEATURE:
CATION: (1762)
OTHER INFORMATION: Wherein Xaa is any amino acid.
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1762)
OTHER INFORMATION: Wherein Xaa is any amino acid.
LocATION: (1786)
COCATION: (1786)
COCATION: Wherein Xaa is any amino acid.
US-10-072-012-468
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 30.8<sup>3</sup>
Matches 8; Conservative
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RESULT 63 US-10-072-012-468 ; Sequence 468, Application US/10072012 ; Publication No. US20040033493A1

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PRIOR FILING DATE: 2001-01-31

PRIOR FILING DATE: 2001-01-31

PRIOR PELICATION NUMBER: 60/266,406

PRIOR PELICATION NUMBER: 60/266,406

PRIOR PELICATION NUMBER: 60/266,767

PRIOR PELING DATE: 2001-02-05

PRIOR PELING DATE: 2001-02-06

PRIOR PILING DATE: 2001-02-07

PRIOR FILING DATE: 2001-02-07

PRIOR FILING DATE: 2001-02-07

PRIOR FILING DATE: 2001-02-08

PRIOR PILING DATE: 2001-02-08

PRIOR PLING DATE: 2001-02-08

PRIOR PLING DATE: 2010-02-08

PRIOR 
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APPLICANT: Rieger, Daniel K.
APPLICANT: Burges, Catherine E.
IITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 56.7%; Score 68; DB 15; L. Best Local Similarity 30.8%; Pred. No. 3.5e+02; Matches 8; Conservative 12; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  248 GFTGQNCEENIDDCPGNNCKNGGACV 273
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CURRENT FILING DATE: 2002-01-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                             PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/265,514
PRIOR FILING DATE: 2001-01-31
PRIOR PLING DATE: 2001-01-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 467, Application US/10072012
Publication No. US20040033493A1
GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 60/265,102
PRIOR FILING DATE: 2001-01-30
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Padigaru, Muralidhara
Anderson, David W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spytek, Kimberly
Zerhusen, Bryan
Patturajan, Meera
Shimkets, Richard
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Grosse, William M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Colman, Steven D. Wolenc, Adam R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carol E. A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rastelli,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-072-012-134
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APPLICANT: Wehrman, Tom
APPLICANT: Wehrman, Tom
APPLICANT: Wehrman, Tom
TITLE OF INVENTION: No. USCO040013657Alel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 21272-029CIP2H-PCT
CURRENT APPLICATION NUMBER: US/10/294,006
CURRENT FILING DATE: 2002-11-12
PRIOR PILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PL. Genes Version 2.0
SEQ ID NO 12
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 56.7%; Score 68; DB 15; Length 2556; Best Local Similarity 30.8%; Pred. No. 3.5e+02; Matches 8; Conservative 12; Mismatches 6; Indels
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                                         248 GFTGQNCEENIDDCPGNNCKNGGACV 273
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2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
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                                                                                                                                                                                             US-10-294-006-12
Sequence 12, Application US/10294006
Publication No. US20040013657A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gerlach, Valerie
Taupier Jr, Raymond J.
Gusev, Vladimir Y.
Colman, Steven D.
Wolenc, Adam R.
Pena, Carol E. A
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Padigaru, Muralidhara
Anderson, David W.
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Patturajan, Meera
Shimkets, Richard
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Grosse, William M
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Spytek, Kimberly
                                                                                                                                                                                                                                                                                                                         APPLICANT: Tang, Y. Tom
APPLICANT: Zhou, Ping
APPLICANT: Goodrich, Ryle
APPLICANT: Asundi, Vinod
APPLICANT: Yang, Yonghong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lepley, Denise M
Rieger, Daniel K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Luca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rastelli,
                                                                                                                                                                                                                                                                                                GENERAL INFORMATION
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Gaps

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Indels

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US-10-764-415B-39

| Sequence 39, Application US/10764415B
| Sequence 39, Application No. US2005005903A1
| Publication No. US2005005903A1
| GENERAL INFORMATION:
| APPLICART: LOCAINTS LEG.
| TITLE OF INVENTION: Modulations of Notch signalling for use in Immunotherapy
| TITLE OF INVENTION: Modulations of Notch signalling for use in Immunotherapy
| FILE REFRENCE: PO11073US
| CURRENT APPLICATION NUMBER: US/10/764,415B
| CURRENT APPLICATION NUMBER: GB01181536
| PRIOR FILING DATE: 2001-07-01
| PRIOR FILING DATE: 2002-04-05
| PRIOR FILING DATE: 2002-04-05
| PRIOR FILING DATE: 2002-05-28
                                                                                                                                                                                                                      Gaps
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                                                                                                                        56.7%; Score 68; DB 17; Length 2556; allarity 30.8%; Pred. No. 3.5e+02; Conservative 12; Mismatches 6; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: BODMER, MARK WILLIAM
APPLICANT: BRIEND, EMMANUEL CYRILLE PASCAL
APPLICANT: CHAMPION, BRIAN ROBERT
APPLICANT: CHAMPION, BRIAN ROBERT
APPLICANT: LENNARD, ANDREW CHRISTOPHER
APPLICANT: RAGNO, SILVIA
APPLICANT: RAGNO, SILVIA
APPLICANT: ROGNO, SILVIA
APPLICANT: YOUNG, LESLEY LYNN
ITLE OF INVENTION: MEDICAL TREATMENT
FILE REFERENCE: 65452-2012
CURRENT APPLICATION NUMBER: US/10/846,989
CURRENT FILING DATE: 2004-05-14
PRIOR PILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: GB 0127271.5
PRIOR PILING DATE: 2002-11-13
PRIOR PILING DATE: 2002-11-14
PRIOR PILING DATE: 2002-10
NUMBER OF SEQ ID NOS: 68
SOFTWARE: PATCHIN VET: 3.2
SEQ ID NO 56
TANDE: DATE: 2566
                                                                                                                                                                                                                                                                                                                                          248 GFTGQNCEENIDDCPGNNCKNGGACV 273
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                                                                                                                                                                                                                                                                                      2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
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| NAME/KEY: MOD RES | LOCATION: (891) | OTHER INFORMATION: Variable amino acid US-10-846-989-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 56, Application US/10846989 Publication No. US20050026831A1 GENERAL INFORMATION:
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ORGANISM: Homo sapiens
                                                                                                               Query Match
Best Local Similarity
Matches 8; Conserv
                                      US-10-765-727-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 69
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Publication No. US20050025751A1

GRENEAL INFORMATION:

APPLICANT: BODMER, MARK WILLIAM
APPLICANT: GHAMPION, BRIAN ROBERT
APPLICANT: GHAMPION, BRIAN ROBERT
APPLICANT: GHAMPION, BRIAN ROBERT
APPLICANT: CHAMPION, BRIAN ROBERT
APPLICANT: CHAMPION, BRIAN ROBERT
CURRENT: CHAMPION, BRIAN ROBERT
APPLICANT: OF INVENTION: MODULATORS OF NOTCH SIGNALLING FOR USE IN IMMUNOTHERAPY
ITILE OF INVENTION: MODULATORS OF NOTCH SIGNALLING FOR USE IN IMMUNOTHERAPY
CURRENT APPLICATION NUMBER: US/10/65,727
CURRENT PILING DATE: 2002-01-23
FRIOR PELICATION NUMBER: GB 0118153.6
FRIOR APPLICATION NUMBER: GB 021783.6
FRIOR APPLICATION NUMBER: GB 021783.6
FRIOR APPLICATION NUMBER: GB 0212283.6
FRIOR APPL
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PRIOR APPLICATION NUMBER: 60/265,514
PRIOR FILING DATE: 2001-01-31
PRIOR PLING DATE: 2001-01-31
PRIOR PLING DATE: 2001-01-31
PRIOR PLING DATE: 2001-03-31
PRIOR PLING DATE: 2001-02-02
PRIOR PLING DATE: 2001-02-02
PRIOR PLING DATE: 2001-02-02
PRIOR PLING DATE: 2001-02-02
PRIOR PLING DATE: 2001-02-05
PRIOR PLING DATE: 2001-02-06
PRIOR PLING DATE: 2001-02-07
PRIOR PLING DATE: 2001-02-08
PRIOR PLING DATE: 2010-02-07
PRIOR PLING DATE: 2010-02-07
PRIOR PLING DATE: 2010-02-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: VARIANT
CCATION: (891)
COTHER INFORMATION: Wherein Xaa is any amino acid.
US-10-072-012-467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            248 GFTGQNCEENIDDCPGNNCKNGGACV 273
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OTHER INFORMATION: Variable amino acid
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ORGANISM: Homo sapiens
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LOCATION: (891)
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US-10-190-115-29
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FILE REFERENCE: 21402-050 CIP
CURRENT APPLICATION NUMBER: US/10/190,115
CURRENT FILING DATE: 2003-02-10
PRIOR APPLICATION NUMBER: 60/303,168
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                                                                                                                                      REFLING DATE: 2001-07-05
R APPLICATION NUMBER: 60/368,996
R FILING DATE: 2002-04-01
R APPLICATION NUMBER: 60/386,816
R FILING DATE: 2002-06-07
R APPLICATION NUMBER: 60/215,854
R FILING DATE: 2000-07-03
R APPLICATION NUMBER: 60/215,856
R FILING DATE: 2000-07-03
R APPLICATION NUMBER: 60/215,956
R APPLICATION NUMBER: 60/215,902
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FILING DATE: 2001-07-07
APPLICATION NUMBER: 60/216,722
ELING DATE: 2000-07-07
APPLICATION NUMBER: 60/218,622
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APPLICATION NUMBER: 60/216,585,
FILING DATE: 2000-07-07
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Publication No. US20030207394A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Alsobrook, John P. II
APPLICANT: Boldog, Ferenc L.
APPLICANT: Burgess, Catherine E.
APPLICANT: Casman, Stacie J.
APPLICANT: Grosse, William M.
APPLICANT: Gusev, Vladimir Y.
APPLICANT: Ji, Weizhen
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Szekeres, Edward S. Jr.
Taupier, Raymond J. Jr.
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Patturajan, Meera
Rastelli, Luca
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Zerhusen, Bryan D.
Voss, Edward Z.
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NUMBER OF SEQ ID NOS: 40,
SOFTWARE: Patentin version 3.0
SEQ ID NO 39
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Liu, Xiaohong
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                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                               LENGTH: 2556
                                                                                                                          FEATURE:
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APPLICANT: Burgess, Catherine E
APPLICANT: Burgess, Catherine E
APPLICANT: Shimkets, Richard
APPLICANT: Shimkets, Richard
APPLICANT: Shimkets, Richard
APPLICANT: Shimkets, Richard
TITLE OF INVENTION: NO. US20040014081Alel Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-050 CON2
CURRENT APPLICATION NUMBER: 10/174,372
PRIOR APPLICATION NUMBER: 001-07-03
PRIOR FILING DATE: 2000-07-03
PRIOR APPLICATION NUMBER: 00/215,854
PRIOR APPLICATION NUMBER: 60/215,856
PRIOR FILING DATE: 2000-07-03
PRIOR FILING DATE: 2000-07-03
PRIOR FILING DATE: 2000-07-03
PRIOR FILING DATE: 2000-07-03
PRIOR PRILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/215,965
PRIOR PRILING DATE: 2000-07-07
PRIOR PRILING DATE: 2000-07-17
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Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 136
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 29
LENGTH: 2531
TYPE: PRT
ORGANISM: Homo sapiens
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NUMBER OF SEQ ID NOS: 100
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 29
LENGTH: 2531
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Publication No. US20040014081A1
GENERAL INFORMATION:
APPLICANT: Alsobrook II, John P
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Patturajan, Meera
Taupier, Raymond T
Rastelli, Luca
Grosse, William M
Szerkeres, Edward S
Lepley, Denise M
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Tchernev, Velizar
Liu, Xiaohong
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Best Local Similarity 30.8*
Matches 8; Conservative
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Spytek, Kimberly
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US-10-369-072-29
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248 GFAGQNCEENVDDCPGNNCKNGGACV 273
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                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :: Gerlach,
:: Taupier Jr. L.
T. Gusev, Indianir 1.
T. Gusev, Indianir 1.
T. Gusev, Indianir 1.
T. Collann, Steven D.
MT: Wolanc, Adam R.
ANT: Pena, Caroll E. A
ANT: Pera, Caroll E. A
ANT: Pera, Caroll E. A
ANT: Reges, Villiam M.
.CANT: Alsobrook II, John P.
.ICANT: Rieger, Daniel M.
.ICANT: Rieger, Daniel M.
.ICANT: Rieger, Daniel M.
.ICANT: Burgeso, Catherine E.
.LIG OF INVENTION: Processis and Nucleic Acids Encoding Same
LE REFRENCE: 21402-28

LIRENT FELICATION NUMBER: 60/265,102

PRIOR APPLICATION NUMBER: 60/265,112

PRIOR PILING DATE: 2001-01-31
PRIOR PILING DATE: 2001-02-37
PRIOR PILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/266,767
PRIOR PILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/266,767
PRIOR PELING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/266,767
PRIOR PILING DATE: 2001-02-07
PRIOR PELING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/266,767
PRIOR PELING DATE: 2001-02-07
PRIOR PELING DATE: 2001-02-08
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NUMBER OF SEQ ID NOS: 1391
SOFTWARE: PatentIn Ver. 2.1
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Query Match 55.8%; Score 67; DB 15; Length 2531; Best Local Similarity 30.8%; Pred. No. 4.3e+02; Matches 8; Conservative 12; Mismatches 6; Indels C
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                                                                                                                           2 XIXNOXCXQXLDDCCSXXCNXXNXCV 27
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Publication No. US20040033493A1
GENERAL INFORMATION:
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Padigaru, Muralidhara
Anderson, David W.
Rastelli, Luca
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Patturajan, Meera
Shimkets, Richard
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CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: 60/265,102
PRIOR APPLICATION NUMBER: 60/265,102
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-31
PRIOR PILING DATE: 2001-01-31
PRIOR PILING DATE: 2001-01-31
PRIOR PELING DATE: 2001-01-31
PRIOR PELING DATE: 2001-01-31
PRIOR PELING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,395
PRIOR PELING DATE: 2001-02-02
PRIOR PELING DATE: 2001-02-02
PRIOR PELING DATE: 2001-02-06
PRIOR PELING DATE: 2001-02-07
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APPLICANT: Rieger, Daniel K.
APPLICANT: Burges, Catherine E.
IIILE OF INVENTION: Proteins and Nucleic Acids Encoding Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 21402-258
CURRENT APPLICATION NUMBER: US/10/072,012
CURRENT FILING DATE: 2002-01-31
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Sequence 471, Application US/10072012
Publication No. US20040033493A1
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Padigaru, Muralidhara
Anderson, David W.
Rastelli, Luca
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Taupier Jr, Raymond J.
Gusev, Vladimir Y.
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Patturajan, Meera
Shimkets, Richard
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Wolenc, Adam R.
Pena, Carol E. A
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                                                                                                         APPLICANT: Tchernev, Velizar
APPLICANT: Spytek, Kimberly
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TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF
VERTEBRATE DELTA GENE AND METHODS BASED THEREON
NUMBER OF SEQUENCES: 94
                                                                                                                                                                                                                  LOCATION: (1)...(29)
CTHER INFORMATION: Xaa at residue 4 and 7 is Pro or Hyp; Xaa at
OTHER INFORMATION: xesidue 22 and 29 is Tyr, 1251-Tyr, mono-iodo-Tyr,
OTHER INFORMATION: di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr
US-10-765-926-149
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APPLICANT: Cimbora, Daniel M.
APPLICANT: Cimbora, Daniel M.
APPLICANT: Heichman, Karen
APPLICANT: Barrel, Paul L.
TITLE OF INVENTION: Protein-Protein Interactions
FILE REFERENCE: 2318-278-11
FULRENT APPLICATION NUMBER: US/10/024,599
CURRENT APPLICATION NUMBER: US 60/256,986
PRIOR APPLICATION NUMBER: US 60/256,986
PRIOR PILING DATE: 2001-12-21
PRIOR PILING DATE: 2001-12-21
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
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Henrique, Domingos Manuel Pinto
Lewis, Julian Hart
Artavanis-Tsakonas, Spyridon
                                                                                                                                                                                                                                                                                                                                                                  Query Match 55.0%; Score 66; DB 16
Best Local Similarity 38.5%; Pred. No. 8.7;
Matches 10; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 CVCVNGWSGDDCSENIDDCAFASCTPGSTCI 39
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Best Local Similarity 25.8%; Pred. No. 46;
Matches 8; Conservative 14; Mismatches
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; OTHER INFORMATION: Xaa is Gly or Cys
US-10-024-599-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/10024599 Publication No. US20020165352A1 GENERAL INFORMATION:
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Patent No. US20020107194A1
GENERAL INFORMATION:
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: PatentIn version 3.0
                                                                                                                       TYPE: PRT ORGANISM: Conus geographus FEATURE: NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: PEPTIDE
                                                                         SEQ ID NO 149
LENGTH: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-024-599-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: PEPTIDE
LOCATION: (1)..(29)
OTHER INFORMATION: Xaa at residue 4 and 7 is Pro or Hyp; Xaa at residue 22 and 29 is
OTHER INFORMATION: Tyr, 1251-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-pho
OTHER INFORMATION: spho-Tyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: University of Utah Research Foundation APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: Watkins, Maren
                                                                                                                                                                                   APPLICANT: University of Utah Research Foundation APPLICANT: Cognetix, Inc.
Dilvers, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: Watkins, Maren
                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 2314-241
CURRENT APPLICATION NUMBER: US/09/910,082A
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: Patentin version 3.0
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Best Local Similarity 38.5%; Pred. No. 8.7;
Matches 10; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Garrett, James E.
APPLICANT: Garrett, James E.
APPLICANT: Shon, Ki-Joon
APPLICANT: Jacobsen, Richard
APPLICANT: Jones, Robert M.
APPLICANT: Cartier, G. Edward
TITLE OF INVENTION: Omega-Conopeptides
TITLE OF INVENTION: Omega-Conopeptides
CURRENT FILING DATE: 2004-01-29
PRIOR PELING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: US 60/219,616
  248 GFAGGNCEENVDDCPGNNCKNGGACV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |: | ||:::: |||::: ||:|:|| CKSXGTXCSRGMRDCCTSCLSXSNKC 26
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                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Jones, Robert M.
APPLICANT: Cartier, G. Edward
TITLE OF INVENTION: Omega-Conopeptides
                                                                                             Sequence 149, Application US/09910082A; Publication No. US20030119731A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 149, Application US/10765926; Publication No. US20040132663A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                  Garrett, James E.
Shon, Ki-Joon
Jacobsen, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Conus geographus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-910-082A-149
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APPLICANT:
APPLICANT:
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: MILIDANIUM Pharmaceuticals, Inc.
APPLICANT: MICLALLY, Sean
APPLICANT: MICLALLY, Sean
APPLICANT: Gearing, David
ITILE OF INVENTUON: HUMAN DELTA3 AND USES THEREOF
FILE REFERENCE: MBIO1997-002CP2M
CURRENT APPLICATION NUMBER: US/10/417,719
CURRENT FILING DATE: 2003-04-17
PRIOR PELICATION NUMBER: US/09/568,218
PRIOR FILING DATE: 2000-05-09
PRIOR FILING DATE: 1997-06-11
PRIOR FILING DATE: 1997-06-11
PRIOR FILING DATE: 1997-06-11
PRIOR FILING DATE: 1997-06-11
SPRIOR FILING DATE: 1997-06-11
SPRIOR FILING DATE: 1997-06-11
SPRIOR FILING DATE: 1997-06-11
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Best Local Similarity 32.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 11; Mismatches 6.
                                                                                        PRIOR AFFLICATION DIALR

PRIOR AFFLICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997

ATTORNEY/AGRYT INFORMATION:

NAME: ALLIET, Adriane M.

REGISTRATION NUMBER: 32,605

REFERENCE/DOCKET NUMBER: 7326-122

TELEPAN: 212-790-9090

TELEPAN: 212-790-9090

TELEPAN: 212-2869-8864

TELEPAN: 212-2869-8864

TELEPAN: 212-2869-8864

TELEPAN: 212-2869-8864

TELEPAN: 212-300-9090

TELEPAN: 212-300-9090

TELEPAN: 212-300-9090

TELEPAN: 212-300-9090

TELEPAN: 212-300-9090

TELEPAN: 212-790-9090

TELEPAN: 212-300-9090

TELEPAN: 212-300-9
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36 GFSGRNCDDNLDDCTSFPCQNGGTC 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 XIXNOXCXQXLDDCCSXXCNXXNXC 26
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                                              CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 109, Application US/10042865;
Publication No. US20040029216A1
GENERAL INFORMATION:
APPLICANT: Padigaru, Muralidhara
                 FILING DATE: 15-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/10417719
Publication No. US20030180784A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 8; Conserva
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TITLE OF INVENTION: ANTIBODIES TO VERTEBRATE DELTA PROTEINS
AND FRAGMENTS
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32.0%; Pred. No. 1.7e+02;
tive 11; Mismatches 6; Indels
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Publication No. US20030073620A1
GENERAL INFORMATION:
APPLICANT: ISh-Horowicz, David
Henrique, Domingos Manuel Pinto
Lewis, Julian Hart
Artavanis-Teakonas, Spyridon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:

NAME: Misrock, & Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1326-123
TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-790-9090
TELEFAX: 212-869-864
TELEXX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/908,322
FILING DATE: 17-Jul-2001
CLASSIFICATION: <Unknown>
                               ADDRESSEE: Pennie & Edmonds LLP .
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
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APPLICATION NUMBER: US/09/783,931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-908-322-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : :: | | | | | :: | :: | 436 GFSGRNCDDNLDDCTSFPCQNGGTC 460
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
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TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                               COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 32.0%
Matches 8; Conservative
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ZIP: 10036/2711
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RESULT 82
US-10-369-072-4
Sequence 4, Application US/10369072
Publication No. US20040014081A1
GENERAL INFORMATION:
APPLICANT: Alsobrook II, John P
APPLICANT: Tchernev, Velizar
APPLICANT: Tchernev, Velizar
APPLICANT: Liu, Xiaohong
APPLICANT: Liu, Xiaohong
APPLICANT: Spatek, Kimberly
APPLICANT: Spatek, Kimberly
APPLICANT: Spatek, Kimberly
APPLICANT: Taupier, Rayan
APPLICANT: Taupier, Rayan
APPLICANT: Rastelli, Luca
Liu, Xiaohong
Mezick, Amanda J.
Padigaru, Muralidhara
                                                                                                                                                                                                                                                                                                               Shenoy, Suresh G.
Shimkets, Richard A.
Spaderna, Steven K.
Spytek, Kimberly A.
                                                                                                                                                             Patturajan, Meera
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APPLICANT: Boldog, Ference L
APPLICANT: Boldog, Ference L
APPLICANT: Alebrock II, John P
APPLICANT: Action Valerie L
APPLICANT: Edinger, Shlomit R
APPLICANT: Edinger, Shlomit R
APPLICANT: Blerman, Karen
APPLICANT: MacDougall, John
APPLICANT: Mallet, Isabelle
APPLICANT: Millet, Isabelle
APPLICANT: Smithson, Glennda
APPLICANT: Smithson, Glennda
APPLICANT: Stone, David
TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
TITLE OF INVENTION: David
FITLE OF INVENTION: David
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Best Local Similarity 32.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 11; Mismatches 6; Indels
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US-10-190-115-4
Sequence 4, Application US/10190115
Publication No. US20030207394A1
GENERAL INFORMATION:
APPLICANT BAIGODOOK, JOHN P. II
APPLICANT BOLGOG, Ferenc L.
APPLICANT BUTGES, Catherine E.
APPLICANT:
APP
                                                                                                                                                                                                                                                                                                   Gangolli, Esha A
Burgess, Catherine E
Patturajan, Meera
Vernet, Corine A.M
Taylor, Sarah
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Miller, Charles E
Guo, Xiaojia
                Zerhusen, Bryan D
                                                                                               Casman, Stacie J
Shenoy, Suresh G
Spytek, Kimberly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-042-865-109
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PRIOR PILING DATE: 2003-02-10
PRIOR FILING DATE: 2001-07-05
PRIOR PLING DATE: 2001-07-06
PRIOR FILING DATE: 2001-07-06
PRIOR FILING DATE: 2002-06-07
PRIOR PLING DATE: 2002-06-07
PRIOR PLING DATE: 2002-06-07
PRIOR PLING DATE: 2000-07-03
PRIOR PLING DATE: 2000-07-07
PRIOR PLING 
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APPLICANT: Szekeres, Edward S. Jr.
APPLICANT: Taupier, Raymond J. Jr.
APPLICANT: Tenernev, Velizar T.
APPLICANT: Zerhusen, Bryan D.
APPLICANT: Zerhusen, Bryan D.
APPLICANT: Voss, Edward Z.
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME FILE REFERENCE: 2140-050 CIP
CURRENT APPLICATION NUMBER: US/10/190,115
CURRENT FILING DATE: 2003-02-10
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Best Local Similarity 25.8%; Pred. No. 3.3e
Matches 8; Conservative 14; Mismatches
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TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REPERENCE: 21402-050 CIP
GURRENT PAPLICATION NUMBER: US/10/190,115
CURRENT FILING DATE: 2001-07-05
FRIOR APPLICATION NUMBER: 60/346,996
FRIOR APPLICATION NUMBER: 60/346,996
FRIOR APPLICATION NUMBER: 60/346,916
FRIOR APPLICATION NUMBER: 60/346,916
FRIOR FILING DATE: 2002-04-01
FRIOR PILING DATE: 2000-07-03
FRIOR PELING DATE: 2000-07-03
FRIOR PELING DATE: 2000-07-03
FRIOR APPLICATION NUMBER: 60/215,856
FRIOR APPLICATION NUMBER: 60/215,856
FRIOR PILING DATE: 2000-07-03
FRIOR PILING DATE: 2000-07-03
FRIOR PELING DATE: 2000-07-07
FRIOR PELING DATE: 2000-07-07
FRIOR APPLICATION NUMBER: 60/216,586
FRIOR PELING DATE: 2000-07-07
FRIOR PELING DATE: 2000-07-07
FRIOR PELING DATE: 2000-07-07
FRIOR PELING DATE: 2000-07-07
FRIOR FILING DATE: 2000-07-07
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FRIOR PILING DATE: 2000-07-07
FRIOR PILING DATE: 2000-07-07
FRIOR PILING DATE: 2000-07-07
FRIOR PILING DATE: 2000-07-07
FRIOR APPLICATION NUMBER: 60/218,622
FRIOR PILING DATE: 2000-07-07
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NUMBER OF SEQ ID NOS: 136
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                     78 CVCVNGWSGDDCSENIDDCAFASCTPGSTCI 108
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Shanoy, Suresh G.
Shaders, Richard A.
Spaderna, Steven K.
Syytek, Kimberly A.
Szekeres, Edward S. Jr.
Taupier, Raymond J. Jr.
Tcherney, Velizar T.
Zerhusen, Bryan D.
Voss, Edward Z.
                                                                                                                                                                                                                  Sequence 28, Application US/10190115
Publication No. US20030207394A1
                                                                                                                                                                                                                                                                                                                                                                                                                        Burgess, Catherine E. Casman, Stacie J. Grosse, William M. Gusev, Vladimir Y. Ji, Weizhen.
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Padigaru, Muralidhara
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SEQ ID NO 28
LENGTH: 2447
                                                                                                                                                                                                                                                                                                                                                APPLICANT: Alsobrook, John P. II
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Rastelli, Luca
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Liu, Xiaohong
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; ORGANISM: Homo sapiens
US-10-190-115-28
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Best Local Similarity
Matches 9; Conserv
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APPLICANT: Szerkeres, Edward S
APPLICANT: Lepley, Denise M
APPLICANT: Show Lester, Relater, Relater, Richard
APPLICANT: Shimkers, Richard
APPLICANT: Padigaru, Muralidhara
TITLE OF INVENTION: No. US20040014081A1=1 Proteins and Nucleic Acids Encoding Same FILE REFRENCE: 21402-050 CONZ
CURRENT APPLICATION NUBER: US/10/369,072
CURRENT FILING DATE: 2003-02-18
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PRIOR PLING DATE: 2003-06-17
PRIOR PLING DATE: 2002-06-17
PRIOR PLING DATE: 2001-07-03
PRIOR FILING DATE: 2001-07-03
PRIOR PLING DATE: 2000-07-03
PRIOR PLING DATE: 2000-07-03
PRIOR PELING DATE: 2000-07-03
PRIOR APPLICATION NUMBER: 60/215,856
PRIOR PELING DATE: 2000-07-03
PRIOR PELING DATE: 2000-07-03
PRIOR PELING DATE: 2000-07-03
PRIOR PELING DATE: 2000-07-07
PRIOR PELING DATE: 2000-07-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 726, Application US/1032281
Publication No. US20040126762A1
GENERAL INFORMATION:
APPLICANT: David W. Morris
APPLICANT: Marc S. Malandro
ITILE OF INVENTION: Novel Compositions and Methods in Cancer FILE REPERENCE: 52945201010 NOVEL COMPOSITION APPLICATION NUMBER: US/10/322,281
UUMBERT PILING DATE: 2002-12-17
NUMBER OF SEQ ID NOS: 866
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 726
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Best Local Similarity 25.8%
Matches 8; Conservative
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens US-10-369-072-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ••
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CURRENT APPLICATION NUMBER: US/10/190,115
CURRENT FILING DATE: 2003-02-10
PRIOR APPLICATION NUMBER: 60/303,168
PRIOR APPLICATION NUMBER: 60/303,168
PRIOR PELING DATE: 2001-07-05
PRIOR PELING DATE: 2002-04-01
PRIOR PELING DATE: 2002-06-07
PRIOR PELING DATE: 2002-06-07
PRIOR PELING DATE: 2000-07-03
PRIOR PELING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/216,586
PRIOR PELING DATE: 2000-07-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME FILE REFERENCE: 21402-050 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55.0%; Score 66; DB 15; Lo
25.8%; Pred. No. 5.3e+02;
tive 14; Mismatches 5;
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Publication No. US20040014081A1
GENERAL INFORMATION:
APPLICANT: Alsobrook II, John P
APPLICANT: Spaderna, Stephen K
APPLICANT: Tchernev, Velizar
APPLICANT: Liu, Xiaohong
APPLICANT: Shenoy, Suresh
APPLICANT: Shenoy, Suresh
APPLICANT: Spenoy, Suresh
APPLICANT: Schusen, Bryan
                                                                                                                                                                                                                                                                                                                                                                Shenoy, Suresh G.
Shimkets, Richard A.
Spaderna, Steven K.
Syttek, Kimberly A.
Szekeres, Edward S. Jr.
Taupier, Raymond J. Jr.
Tchernev, Velizar T.
Zerhusen, Bryan D.
Voss, Edward Z.
                                                                                                                                                                                  Mezick, Amanda J.
Padigaru, Muralidhara
Grosse, William M. Gusev, Vladimir Y.
                                                                                                                                                                                                                                                            Pattūrajan, Meera
Rastelli, Luca
                                                                                                                Lepley, Denise M.
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Best Local Similarity 25.8*
Matches 8; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-190-115-2
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US-10-369-072-2
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TITLE OF INVENTION: No. US20040014081Alel Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-050 CON2
CURRENT APPLICATION NUMBER: US/10/369,072
CURRENT FILING DATE: 2003-02-18
PRIOR PELING DATE: 2001-07-03
PRIOR FILING DATE: 2001-07-03
PRIOR PELING DATE: 2000-07-03
PRIOR PELING DATE: 2000-07-07
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NUMBER OF SEG ID NOS: 100

SECTION 28

LENGTH: 2447

TYPE: PRT

ORGANISM: Takifugu rubripes
US-10-369-072-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       279 CVCVNGWSGLDCSENIDDCDTAACSPGSTCV 309
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                                                                 Sequence 28, Application US/10369072
Publication No. US20040014081A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rastelli, Luca
Grosse, William M
Szerkerse, Edward S
Lepley, Denise M
Shen, Lei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Burgess, Catherine E
                                                                                                                                                                              APPLICANT: Alsobrook II, John P
APPLICANT: Spaderna, Stephen K
APPLICANT: Tchernev, Velizar
APPLICANT: Liu, Xiaohong
                                                                                                                                                                                                                                                                                                                          Shenoy, Suresh
Spytek, Kimberly
Zerhusen, Bryan
Patturajan, Meera
Taupier, Raymond T
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Best Local Similarity 29.0%
Matches 9; Conservative
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Gaps

us-10-627-685a-1.rapb

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APPLICANT: Shimkets, Richard
APPLICANT: Padigaru, Muralidhara
TITLE OF INVENTION: No. US20040014081Alel Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-050 CON2
APPLICANT: Spytek, Kimberly A.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Techernev, Velizar T.
APPLICANT: Jesusen, Bryan D.
APPLICANT: Velizar T.
APPLICANT: Velizar T.
APPLICANT: Velizar T.
APPLICANT: Velizar T.
APPLICANT: Volument C.
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME FILE OF INVENTION DATE: 2001-01-05
FRIOR APPLICATION NUMBER: 06/303,168
FRIOR APPLICATION NUMBER: 60/308,996
FRIOR APPLICATION NUMBER: 60/308,996
FRIOR APPLICATION NUMBER: 60/318,896
FRIOR PILING DATE: 2002-04-01
FRIOR APPLICATION NUMBER: 60/215,856
FRIOR APPLICATION NUMBER: 60/215,902
FRIOR APPLICATION NUMBER: 60/215,902
FRIOR PILING DATE: 2000-07-03
FRIOR PILING DATE: 2000-07-03
FRIOR PILING DATE: 2000-07-03
FRIOR PILING DATE: 2000-07-07
FRIOR APPLICATION NUMBER: 60/216,586
FRIOR FILING DATE: 2000-07-07
FRIOR PILING DATE: 2000-07-07
FRIOR PILING DATE: 2000-07-07
FRIOR PILING DATE: 2000-07-07
FRIOR FILING DATE: 2000-07-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4
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Publication No. US20040014081A1
GENERAL INFORMATION:
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Taupler, Raymond T
Rastelli, Luca
Grosse, William M
Szerkeres, Edward S
Lepley, Denise M
Shen, Lei
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Tchernev, Velizar
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Shenoy, Suresh
Spytek, Kimberly
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Best Local Similarity 25.84
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-190-115-27
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                                                                                                                                                               APPLICANT: Shimkets, Richard
TITLE OF INVENTION: No. US20040014081A1e1 Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-050 CON2
CURRENT APPLICATION NUMBER: 105/10/369,072
CURRENT FILING DATE: 2003-06-18
PRIOR APPLICATION NUMBER: 60/218,994
PRIOR PILING DATE: 2000-07-03
PRIOR PILING DATE: 2000-07-03
PRIOR PELLING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/216,585
PRIOR PELLING DATE: 2000-07-07
PRIOR PELLING DATE: 2000-07-17
PRIOR PELLING DATE: 2000-07-17
PRIOR PELLING DATE: 2000-07-17
PRIOR PELLING DATE: 2000-07-17
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323 CVCVNGWSGDDCSENIDDCAFGACTPGSTCI 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 100 SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Burgess, Catherine E. Casman, Stacie J. Grose, William M. Gusev, Vladimir Y. Ji, Weizhen Lepley, Denise M. Liu, Xaohong Mezick, Amanda J. Padigaru, Muralidhara Patturajan, Weera Rastelli, Luca
                                                      Grosse, William M
Szerkeres, Edward S
Lepley, Denise M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shenoy, Suresh G.
Shimkets, Richard A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 25.8%
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-369-072-2
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LENGTH: 2469
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Sequence 40, Application US/10764415B

Sequence 40, Application US/20050059093A1

GENERAL INFORMATION:

TITLE OF INVENTION: Modulations of Notch signalling for use in Immunotherapy
FILE REFERENCE: PO11073U3

CURRENT APPLICATION NUMBER: US/10/764,415B

CURRENT PILING DATE: 2004-01-23

PRIOR APPLICATION NUMBER: GB0118153.6

PRIOR PILING DATE: 2001-07-01

PRIOR FILING DATE: 2002-04-05

PRIOR FILING DATE: 2002-04-05

PRIOR FILING DATE: 2002-05-28

PRIOR FILING DATE: 2002-05-28

PRIOR FILING DATE: 2002-05-28

NUMBER OF SEQ ID NOS: 40

SSOFTARE: PATCHIN VERSION 3.0

LENGTH: 2471
    Gaps
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; Pred. No. 5.3e+02;
14; Mismatches 5; Indels 4
  Indels
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در
                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: BODMER, MARK WILLIAM
APPLICANT: BRIEND, EMMANUEL CYRILLE PASCAL
APPLICANT: CHAMPION, BRIAN ROBERT
APPLICANT: LENNARD, ANDREW CHRISTOPHER
APPLICANT: RAGNO, SILVIA
APPLICANT: RAGNO, SILVIA
APPLICANT: TOUNG, LESLEY LYNN
ITILE OF INVENTION: MEDICAL TREATMENT
FILE REFERENCE: 65455-2012
CURRENT APPLICANTION WUMBER: US/10/846,989
CURRENT FILING DATE: 2004-05-14
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: GB 0127271.5
PRIOR PILING DATE: 2001-11-14
PRIOR PLING DATE: 2002-10
NUMBER: OF SEQ ID NOS: 68
SOFTWARE: PALENTIN VOWER: 33.2
SEQ ID NO 57
LENGTHARE: PALENTIN VOWE: 33.2
                                                                          324 CVCVNGWSGDDCSENIDDCAFASCTPGSTCI 354
                                               1 CXIXN----QXCXQXLDDCCSXXCNXXNXCV 27
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  14; Mismatches
                                                                                                                                                                                                             Sequence 57, Application US/10846989
Publication No. US20050026831A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55.0%;
25.8%;
  8; Conservative
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Best Local Similarity 25.8*
Matches 8; Conservative
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JS-10-846-989-57
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PRIOR PILING DATE: 2002-06-17
PRIOR PILING DATE: 2001-07-03
PRIOR FILING DATE: 2001-07-03
PRIOR PILING DATE: 2000-07-03
PRIOR PILING DATE: 2000-07-03
PRIOR PILING DATE: 2000-07-03
PRIOR PILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/215,902
PRIOR APPLICATION NUMBER: 60/215,902
PRIOR APPLICATION NUMBER: 60/216,585
PRIOR APPLICATION NUMBER: 60/216,585
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-07
PRIOR PELING DATE: 2000-07-07
PRIOR PELING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/216,722
PRIOR APPLICATION NUMBER: 60/218,622
PRIOR PILING DATE: 2000-07-17
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324 CVCVNGWSGDDCSENIDDCAFASCTPGSTCI 354
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CURRENT APPLICATION NUMBER: US/10/369,072
                                          PRIOR APPLICATION NUMBER: 10/174,372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Drosophila melanogaster
US-10-369-072-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patentin Ver. 3.2
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US-10-765-727-23
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Best Local Similarity
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SEQ ID NO 23
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US-10-765-727-23
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Gaps
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) Patent No. US2002010260/AL
) GENERAL INFORMATION:

APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Shetty, Reshma
APPLICANT: Jimenez, Elsie C.
APPLICANT: McIntosh, J. Michael
             ; LOCATION: (1)...(36)
; OTHER INFORMATION: Xaa at residue 10 is Glu or ga; OTHER INFORMATION: , 23 and 36 is Tyr, 1251-Tyr, ; OTHER INFORMATION: o-Tyr or O-phospho-Ty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: University of Utah Research Foundation APPLICANT: Cognetix, Inc. APPLICANT: Walker, Craig S. APPLICANT: Shetty, Reshma
                                                                                                                                                                                           Ouery Match

54.6%; Score 65.5; I

Best Local Similarity 44.4%; Pred. No. 12;

Matches 12; Conservative 9; Mismatches
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APPLICANT: Shen, Greg S.
TITLE OF INVENTION: 1-Superfamily Conotoxins
FILE REFERENCE: 2314-238
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Best Local Similarity 33.3%; Pred. No. 12;
Matches 9; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2001-01-29
PRIOR FILING DATE: 2001-01-29
PRIOR FILING DATE: 2001-01-29
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: Patentin version 3.0
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CURRENT FILING DATE: 2001-06-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 369, Application US/09894882
Patent No. US20020102607A1
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Patent No. US20020102607A1
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McIntosh, J. Michael
Olivera, Baldomero M.
Watkins, Maren
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US-09-894-882-167
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Sequence 723, Application US/10322281

Sequence 723, Application US/10322281

Sequence 723, US2040126762A1

SERERAL INFORMATION:

APPLICANT: David W. Morris

APPLICANT: David W. Morris

TITLE OF INVENTION: Novel Compositions and Methods in Cancer

TITLE OF INVENTION: Novel Compositions and Methods in Cancer

FILE REFERENCE: 529452001000

CURRENT PILING DATE: 2002-12-17

NUMBER OF SEQ ID NOS: 866

SOFTWARE FEASESE FEASESE FOR Windows Version 4.0
  55.0%; Score 66; DB 17; Length 2471; 25.8%; Pred. No. 5.3e+02; Live 14; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Shetty, Reshma
APPLICANT: Jimenez, Elsie C.
APPLICANT: McIncosh, J. Michael
APPLICANT: Olivera, Baldomero M.
APPLICANT: Watkins, Maren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 25.8%; Pred. No. 5.4e+02;
Matches 8; Conservative 14; Mismatches 5.
                                                                                                                                        324 CVCVNGWSGDDCSENIDDCAFASCTPGSICI 354
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                                                                                                          1 CXIXN----QXCXQXLDDCCSXXCNXXNXCV 27
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PRIOR PILING DATE: 2000-06-30
PRIOR PELING DATE: 2000-10-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: PATENTIN VETSION 3.0
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CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 168, Application US/09894882
Patent No. US20020102607A1
GENERAL INFORMATION:
Query Match
Best Local Similarity 25.8<sup>†</sup>
Matches 8<sup>†</sup>, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jones, Robert M.
Shen, Greg S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
CRGANISM: Mus musculus
US-10-322-281-723
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LENGTH: 2503
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                                        APPLICANT: R.O., incursos, APPLICANT: Brose, Katigae, Marc APPLICANT: Tessier-Lavigne, Marc TILLE OF INVENTION: Modulating Robo: Ligand Interactions FILE REFERENCE: B98-031-3 CURRENT APPLICATION NUMBER: US/10/289,776 CURRENT FILING DATE: 2002-11-06 PRIOR APPLICATION NUMBER: US/09/540,245 PRIOR APPLICATION NUMBER: G0/065,544 PRIOR FILING DATE: 1090-03-31 PRIOR PLICATION NUMBER: G0/061,057 PRIOR PLICATION NUMBER: G0/081,057 PRIOR PLICATION OF SEQ ID NOS: 20

SEQ ID NO 9

LENGTH: 735
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 54.2%; Score 65; DB 14; Best Local Similarity 26.9%; Pred. No. 2.2e+02; Matches 7; Conservative 13; Mismatches 6
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Publication No. US20030207394A1
GENERAL INFORMATION:
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Burgess, Catherine E.
Casman, Stacie J.
Grosse, William M.
Gusev, Vladimir Y.
Ji, Weizhen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) ORGANISM: Caenorhabditis elegans US-10-289-776-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              adigaru, Muralidhara
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Liu, Xiaohong
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Rastelli, Luca
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; Sequence 6999, Application US/10369493
; Bedication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Gldman, Barry S.
APPLICANT: Gldman, Barry S.
APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: DLANTS WITH IMPROVED PROPERTIES
; TITLE OF INVENTION: BLANTS WITH IMPROVED PROPERTIES
; TITLE OF INVENTION: BLANTS WITH IMPROVED
; TITLE OF INVENTION: UNMBER: US 60/360,039
; PRIOR PELLING DATE: 2003-02-28
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6999
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                                                                                                                                    TITLE OF INVENTION: 1-Superfamily Conotoxins FILE REFERENCE: 2314-239
FILE REFERENCE: 2314-239
FUNERNT APPLICATION NUMBER: US/09/894,882
CURRENT APPLICATION NUMBER: US 60/
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: US 60/264,256
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ 1D NOS: 506
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 54.6%; Score 65.5; E
Best Local Similarity 33.3%; Pred. No. 23;
Matches 9; Conservative 12; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39 CLSLGQRCERH-SDCCGYLCCFYDKCV 64
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; ORGANISM: Caenorhabditis elegans
US-10-369-493-6999
Olivera, Baldomero M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 26.9%
                                                            Jones, Robert M.
Shen, Greg S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Conus betulinus
US-09-894-882-167
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LENGTH: 73
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301 CVCVNGWTGESCSQNIDDCATAVCFHGATC 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature; DCATION: (440); OTHER INFORMATION: Wherein Xaa may be any naturally occurring amino acid 1S-10-19-115-26
        PRIOR PILING DATE: 2000-07-03
PRIOR PILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-17
PRIOR PILING DATE: 2000-07-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 136
SOFTWARE: CuraSequist version 0.1
LENGTH: 2317
LENGTH: 2317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 54.2%; Score 65: DB 15; Length 2317; Best Local Similarity 30.0%; Pred. No. 6.2e+02; Matches 9; Conservative 13; Mismatches 4; Indels
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CURRENT FILING DATE: 2003-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2003-02-18
PRIOR APPLICATION NUMBER: 10/174,372
PRIOR FILING DATE: 2002-06-17
PRIOR FILING DATE: 2001-07-03
PRIOR PELICATION NUMBER: 09/898,994
PRIOR FILING DATE: 2001-07-03
PRIOR FILING DATE: 2000-07-03
PRIOR PELICATION NUMBER: 60/215,854
PRIOR PELING DATE: 2000-07-03
PRIOR PELING DATE: 2000-07-03
PRIOR APPLICATION NUMBER: 60/215,902
PRIOR APPLICATION NUMBER: 60/215,902
PRIOR APPLICATION NUMBER: 60/216,585
PRIOR PILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/216,585
PRIOR PILING DATE: 2000-07-07
60/215,902
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Publication No. US20040014081A1
GENERAL INFORMATION:
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Shimkets, Richard
Padigaru, Muralidhara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Alsobrook II, John P
APPLICANT: Spaderna, Stephen K
APPLICANT: Tchernev, Velizar
APPLICANT: Liu, Xiaohong
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Grosse, William M
Szerkeres, Edward S
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Taupier, Raymond
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Spytek, Kimberly
Zerhusen, Bryan
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US-10-369-072-26
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PRIOR APPLICATION NUMBER: 60/218,622

PRIOR FILING DATE: 2000-07-17

PRIOR PEDICATION NUMBER: 60/218,992

PRIOR FILING DATE: 2000-07-17

PRIOR PILING DATE: 2000-07-17

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEO ID NOS: 100

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 26

LENGTH: 2317

TYPE: PRT

ORGANISM: Drosophila melanogaster

FEATURE:

NAME/KEY: VARIANT

LOCATION: (440)

COCATION: (440)

SOFTWARIANT

COCATION: (440)

SOFTWARIANT

COCATION: (440)
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on 5.1.6 is Compugen Ltd.	ng sw model	20:23:04 ; Search time 26.5 Seconds (without alignments) 98.032 Million cell updates/sec	-10-627-685A-1 0 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27	Gapext 0.5	residues	chosen parameters: 283416	0	0% 100% 100 summaries		results predicted by chance to have a il to the score of the result being printed, of the total score distribution.		Description	kappa-conotoxin PV omega-conotoxin SV	Xotch protein - Af	notch protein homo	neurogenic repetit crumbs protein - f	transmembrane prot	notch-1 protein -	omega-conotoxin GV Motch B protein -	cell-fate determin	nocch procein - ir hypothetical prote	protein F40E10.4 (notch4 - mouse	notch 3 protein - notch3 protein - h	notch homolog - se hypothetical prote		metallothionein - fibronellin C prec	EGF repeat transme	DELTA-like 1 - mou fibropellin Ia - s
GenCore version (c) 1993 - 2005					96216763 ree						SUMMARIES	1	A58997 C44379	A35844	A40043	B26637 A35672	842612	A46019	B43620	A49128	A24420 T22025	D89711 T09059	S45306 S78549	T31070 T25933	T30201	S18174	T30176	148324 A40136
Gen (c)	using	'n.	A-1	Gap	962		0000	44. H		of squa		BB :																0 00
Copyright	protein search,	April 18, 200	US-10-627-685A- 120 1 CXIXNQXCXQXLD	BLOSUM62DX Gapop 10.0 ,	seda,	satisfying	ength: 0 ength: 2000000000	um Match um Match ng first	PIR 79:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*	the number of r than or equal d by analysis c		Length	27 26	2524	2555	293 2139	2437	2531	1203	2471	601	601 1964	2318	2531	2352	43	1687	722 1064
			US-10- 120 1 CXIX		283416	hits s		Minimum Maximum Listing		o. is the nu reater than derived by a	* Query	Match	100.0	60.0	56.7	55.8 55.8	55.8	55.8	55.0	55.0	54.0 54.2	54.2	54.2	54.2	53.3	52.5	52.5	51.7 51.7
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	OM protein	Run on:	Title: Perfect Sequence	Scoring	Searched	Total nu	Minimum Maximum	Post-processing	Database	9 P P C C C C C C C C C C C C C C C C C	Result	No.	7 7	m	* W	9 ~	ω (10	11	12:	14 15	16 17	118	20	55	. 22 c	52	28 28 28

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ALIGNMENTS

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A; Reference number: Universy; RULL: 323/324; FRILD: 13322700
A; Accession: JH0699
A; Molecule type: mRNA
A; Residues: 1-29 **HIL>
A; Cross references: UNIPROT: P37300; GB: 540826; NID: 9252126; PIDN: AAB22674.1; PID: 9252127
B; Nemoto, N.; Kubo, S.; Yoshida, T.; Chino, N.; Kimura, T.; Sakakibara, S.; Kyogoku, Y.; Biochem. Blophys. Res. Commun. 207, 695-700, 1995
A; Title: Solution structure of omega-conotoxin MVIIC determined by NMR.
A; Reference number: PC2380, MUID: 95169113; PMID: 7864862
A; Molecule type: protein
A; Residues: 3-28 **ARM>
A; Molecule type: protein
A; Reference number: A66297; PDB: 10MN
A; Reference number: A66297; PDB: 10MN
A; Reference number: A66297; PDB: 10MN
A; Reference number: A665982; MUID: 95248339; PMID: 7731037
A; Csuperfamily: omega-conotoxin
C; Meywords: acetylcholine release inhibition; amidated carboxyl end; calcium channel inhum
C; Keywords: acetylcholine release inhibition; amidated carboxyl end; calcium channel inhum
C; Keywords: acetylcholine release inhibition; amidated carboxyl end; A; B-18-10-22,17-28/Disulfide bonds: #status experimental
F; 3-28 /*Modified site: amidated carboxyl end (Cys) (amide in mature form from following glyc
                                                                                                                                                                                                                                                                         A;Status: preliminary, nucleic acid sequence not shown; not compared with conceptual trans, A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Species: Conus magus (magus cone)
C; Date: 17-Apr-1993 #sequence_revision 11-Apr-1997 #text_change 09-Jul-2004
C; Date: 17-Apr-1993 #sequence_revision 11-Apr-1997 #text_change 09-Jul-2004
C; Accession: JH699; PC2380
R; Hillyard, D.R.; Monje, V.D.; Mintz, I.M.; Bean, B.P.; Nadasdi, L.; Ramachandran, J.; M. Neuron 9, 69-77, 1992
A; Title: A new conus peptide ligand for mammalian presynaptic Ca2+ channels.
A; Reference number: JH0699; MUID:92337922; PMID:1352986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               omega-conotoxin MVIIC precursor [validated] - cone shell (Conus magus) (fragment)
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Xotch protein - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 12-Oct-1990 #sequence_revision 12-Oct-1990 #text_change 16-Aug-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                        A;Residues: 1-224 <CCP>
C;Superfamily: Notch protein; ankyrin repeat homology; EGF homology
C;Keywords: transmembrane protein
F;146-177/Domain: EGF homology <EGF1>
F;184-215/Domain: EGF homology <EGF1>
F;222-254/Domain: EGF homology <EGF>
F;557-788/Domain: EGF homology <EGF>
F;577-788/Domain: EGF homology <EGF>
F;577-788/Domain: EGF homology <EGF>
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                                                                                                                                                                                  A;Title: Xotch, the Xenopus homolog of Drosophila notch. A;Reference number: A35844; MUID:90385285; PMID:2402639 A;Accession: A35844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F,1025-1056/Domain: EGF homology «EGX3»
F,1934-1956/Domain: ankyrin repeat homology «F;1957-1989/Domain: ankyrin repeat homology «F;1991-2023/Domain: ankyrin repeat homology F;2024-2056/Domain: ankyrin repeat homology F;2057-2089/Domain: ankyrin repeat homology v
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                                                                                          C, Accession: A35844
R; Coffman, C.; Harris, W.; Kintner, C.
Science 249, 1438-1441, 1990
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Best Local Similarity
Matches 9; Conserv
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RiTerlau, H.; Shon, K.J.; Grilley, M.; Stocker, M.; Stuehmer, W.; Olivera, B.M.
Nature 381, 148-151, 1996
A;Title: Strategy for rapid immobilization of prey by a fish-hunting marine snail.
A;Reference number: AS8997
A;Stetus: preliminary
A;Stetus: preliminary
A;Molecule type: protein
A;Residues: 1-27 <TER>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:P56633
C;Comment: This conotoxin blocks conductance of the Shaker potassium channel.
C;Keywords: hydroxyproline; neurotoxin; venom
F;4/Modified site: 4-hydroxyproline (Pro) #status experimental
                                                                    Kappa-conotoxin PVIIA - cone shell (Comus purpurascens)
N;Alternate names: fin-popping peptide
C;Species: Conus purpurascens (purple cone)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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; Pred. No. 0.43;
12; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 120; DB 2; 63.0%; Pred. No. 4.3e-05;
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100.0%; Score 120; D
Best Local Similarity 63.0%; Pred. No. 4.3e
Matches 17; Conservative 10; Mismatches
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Best Local Similarity 34.6%;
Matches 9; Conservative 1:
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R;Tepass, U.; Theres, C.; Knust, E.
Cell 61, 787-799, 1990
A;Title: crumbs encodes an EGF-like protein expressed on apical membranes of Drosophila & A;Reference number: A35672, MUID:90263104; PMID:2344615
A;Accession: A35672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:P10040; GB:M33753
A;Note: the authors translated the codon GGC for residue 1928 as Cys, and TAT for residu<sup>k</sup>
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A;Molecule type: mRNA
A;Residues: 1-2437 <BIE>
A;Cross-references: UNIPROT:P46530; EMBL:X69088; NID:g433866; PIDN:CAA48831.1; PID:g43389
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology
F;755-786/Domain: EGF homology <EGFI>
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Mech. Dov. 43, 87-100, 1993
A;Title: A zebrafish homologue of the Drosophila neurogenic gene Notch and its pattern
A;Reference number: S42612; MUID:94128602; PMID:8297791
                                                                                                                                                                                                                       crumbs protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 21-Sep-1990 #sequence_revision 18-Nov-1992 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Brachydanio_rerio (zebra fish)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S42612
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76;
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1826 GFEGQHCEQNIDECADQPCHNGGNC 1850
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164 GFEGQHCEQNIDECADQPCHNGGNC 188
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A;Cross-references: FlyBase:FBgn0000368
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F;352-385/Domain: EGF homology «EGX1»
F;392-424/Domain: EGF homology «EGF1»
F;691-722/Domain: EGF homology «EGF3»
F;767-799/Domain: EGF homology «EGF3»
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Best Local Similarity 28.0%
Best Local 7; Conservative
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Best Local Similarity 30.0°
Matches 9; Conservative
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A;Molecule type: mRNA
A;Residues: 1-2139 <TEP>
                                                                                                                                                                                                                                                                                                                                 C; Accession: A35672
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C;Species: Drosophila melanogaster
B;Knust, E.; Dietrich, U.; Tepass, U.; Bremer, K.A.; Weigel, D.; Vaessin, H.; Campos-Ort
B;Knust, E.; Dietrich, U.; Tepass, U.; Bremer, K.A.; Weigel, D.; Vaessin, H.; Campos-Ort
A;Title: EGF homologous sequences encoded in the genome of Drosophila melanogaster, and
A;Reference number: A91081; MUID:87218837; PMID:3107986
A;Accession: B26637
A;Molecule type: mRNA
A;Residues: 1-293 <a href="https://doi.org/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1009/10.1
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A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: A40043
R;Ellisen, L.W.; Bird, J.; West, D.C.; Soreng, A.L.; Reynolds, T.C.; Smith, S.D.; Sklar, Cell 66, 649-61, 1991
A;Title: TAN-1, the human homolog of the Drosophila Notch gene, is broken by chromosomal A;Reference number: A40043; MUID:91347367; PMID:1831692
A;Accession: A40043
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                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Homo sapiens (man)
C;Date: 21-Apr 1992 #sequence_revision 21-Apr-1992 #text_change 16-Aug-2004
                                                                               Gaps
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A;Cross-references: GB:M73980
C;Superfamily: Notch protein; ankyrin repeat homology; EGF homology F:261-292/Domain: EGF homology <EGX1>
F;494-525/Domain: EGF homology <EGF1>
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       Length 29;
                                                                               Indels
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Query Match 57.5%; Score 69; DB 2; Best Local Similarity 30.8%; Pred. No. 2.5; Matches 8; Conservative 12; Mismatches 6
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                                                                                                                                                                                                                                                                                                                                                                                              protein homolog TAN-1 precursor - human
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F;1960-1992/Domain: ankyrin repeat homology
F;1994-2026/Domain: ankyrin repeat homology
F;2027-2059/Domain: ankyrin repeat homology
F;2060-2092/Domain: ankyrin repeat homology
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                                                                                                                                                   1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
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F;1149-1180/Domain: EGF homology <EGF>
F;1187-1218/Domain: EGF homology <EGF3
F;1233-1264/Domain: EGF homology <EGF3
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F:177-208/Domain: EGF homology <EGF1>
F:216-252/Domain: EGF homology <EGF>
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Best Local Similarity 28.0%
T; Conservative
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Best Local Similarity
Matches 8; Conserv
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2 XIXNQXCXQXLDDCCSXXCNXXNXC 26

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,1935-1937,'L',1938-1967,'I',1969-2044,'IE',2047-2052,'S',2054-
                                                                                                                A, Experimental source: embryo
A,Note: sequence extracted from NCBI backbone (NCBIN:131246, NCBIP:131247)
C,Comment: This protein has many BGF repeats and lin-12[#1172]/Notch repeats.
C,Comment: This protein is one of the neurogenic proteins controlling the decision between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Omega-conotoxin GVIIB - cone shell (Conus geographus)

NyAlternate names: shaker peptide GVIIB

Sisternate names: shaker peptide GVIIB

Cispecies: Conus geographus (geography cone)

Cispecies: Conus geographus (geography cone)

Cispecies: Day, N.S. Seay, W.S. Zeikus, R.; McIntosh, J.M.; Varga, J.; Rivier, J.; de Santos

Sicience 230, 1338-1343, 1985

A;Title: Peptide neurotoxins from fish-hunting cone snails.
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C;Keywords: acetylcholine release inhibition; calcium channel inhibitor; hydroxyproline;
F;1-16,8-19,15-26/bisulfide bonds: #status predicted
F;4,7/Modified site: 4-hydroxyproline (Pro) #status experimental
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repeat homology; EGF homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <AN3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55.8%; Score 67; DB 30.8%; Pred. No. 78; iive 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         248 GFAGQNCEENVDDCPGNNCKNGGACV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;1917-1948/Domain: ankyrin repeat homology F;1949-1981/Domain: ankyrin repeat homology F;1983-200-Domain: ankyrin repeat homology F;2016-2048/Domain: ankyrin repeat homology F;2049-2081/Domain: ankyrin repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1233-1264/Domain: EGF homology <EGF4>
1352-1383/Domain: EGF homology <EG19>
1391-1425/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       987-1018/Domain: EGF homology <EG14>
                                                                                                                                                                                                                                                                                                                                                                                           region of chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <EG13>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1917-1948/Domain: ankyrin repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: UNIPROT: P05483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EGF homology can be for ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              homology
                             A;Molecule type: nucleic acid
A;Residues: 1865-1932,'RR',193
A;Experimental source: embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1063-1094/Domain: EGF
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Matches 8; Conserv
Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                        Superfamily: Notch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1025-1056/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                911-942/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                       A; Note: proximal
                                                                                                                                                                                                                                                                                                            A; Gene: notch-1
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notch-1 protein - mouse

notch-1 protein - mouse

N.Alternate names: motch protein

S.Accession: Mus musculus (house mouse)

C.Species: Mus musculus

C.Species: Mus musculus

C.Species: Musculus

C.Species: Musculus

C.Species: Musculus

A.Reference number: A46019; MUID:93194170; PMID:8449489

A.Reference number: A46019
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J. Cell Biol. 121, 631-641, 1993
A;Title: Mouse notch: expression in hair follicles correlates with cell fate determinati
A;Reference number: A46438; MUID:93252998; PMID:8486742
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A; Residues: 1-2531 cnst.
A; Cross-references: UNIPROT:001705; GB:Z11886; GB:S47228; NID:g288502; PIDN:CAA77941.1;
A; Note: sequence extracted from NCBI backbone (NCBIP:127318)
R; Franco del Amo, F.; Smith, D.E.; Swiatek, P.J.; Gendron-Maguire, M.; Greenspan, R.J.;
B; Franco del Amo, F.; Smith, D.E.; Swiatek, P.J.; Gendron-Maguire, M.; Greenspan, R.J.;
A; Pbescription: Expression pattern of Motch, a mouse homolog of Drosophila Notch, suggest
A; Reference number: S25144
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Exp. Cell Res. 204, 364-372, 1993
A:Title: Motch A and Motch B--two mouse Notch homologues coexpressed in a wide variety
A;Reference number: A49175; MUID:93178563; PMID:8440332
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                                                                                                                                                              Riweinmaster, G.; Roberts, V.J.; Lemke, G.
Development 113, 199-205, 1991
A;Tille: A homolog of Drosophila Notch expressed during mammalian development.
A;Reference number: S18188; MUID:92111383; PMID:1764995
A;Accession: S18188
                                                      Species: Rattus norvegicus (Norway rat)
Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 02-Aug-2002; Accession: S18188
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A;Cross-references: EMBL:X68278; NID:g287987; PIDN:CAA48339.1; PID:g287988
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                                                                                                                                                                                                                                                                                                                    A,Accession: S18188
A,Molecule type: mRNA
A,Residues: 1-2531 <WELS
A,Cross-references: EMBL:X57405; NID:G57634; PID:G57635
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology
F;987-1018/Domain: EGF homology <EGF1>
F;1233-1264/Domain: EGF homology <EGF2>
F;1250-1949/Domain: ankyrin repeat homology; ANI>
F;1950-1982/Domain: ankyrin repeat homology; ANI>
F;1960-1982/Domain: ankyrin repeat homology; ANI>
F;2017-2049/Domain: ankyrin repeat homology; ANI>
F;2017-2049/Domain: ankyrin repeat homology; ANI>
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A;Note: sequence extracted from NCBI backbone (NCBIP:126159)
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A;Residues: 1551-2108,'Q',2110-2114,'ALP',2118-2170 <FRA>
A;Cross-references: EMBL:211886
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78;
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Matches 8; Conservative
                    notch protein homolog - rat
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Nucleic, Acids Res. 17, 6463-6471, 1989
A/Itile: Hypervariability of simple sequences as a general source for polymorphic DNA man A/Reference number: S09358; MUID:89385974; PMID:2780284
A/Accession: S09358
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A;Residues: 2565-2551, QQQQ,,2552-2576,'E',2578-2604 <TAU>
A;Residues: 2565-2551, Yedvobnick, B.; Finnerty, V.G.; Artavanis-Teakonas, S.
Cell 40, 55-62, 1985
A;Title: ops a novel family of transcribed repeats shared by the Notch locus and other of
A;Reference number: A05267; MUID:85099329; PMID:2981631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Accession: A24420
A;Molecule type: DNA
A;Residues: 1-2703 «XID>
A;Cross-references: UNIPROT:P07207; GB:K03508; NID:g157991; PIDN:AAA28725.1; PID:g157993
R;Wharton, K.A.; Johansen, K.M.; Xu, T.; Artavanis-Tsakonas, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-48,'I',50-118,'R',120-230,'I',232-256,'N',258-266,'A',268-872,'R',874-958,'
A;Note: the authors translated the codon ATC for residue 49 as Thr, ATT for residue 2044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C,Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 16-Aug-2004 C;Accession: A24420; A24768; S09358; A05267 R;Kidd, S.; Kelley, M.R.; Young, M.W. Woll, Young, M.W. Woll, Sold, S.; Kelley, M.S.; Young, M.W. Askerence number: A24420; MUID:87064624; PMID:3097517
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F;2050-2082/Domain: ankyrin repeat homology <AN4>
F;2050-2115/Domain: ankyrin repeat homology <AN5>
F;2083-2115/Domain: ankyrin repeat homology <AN5>
F;2538-2568/Region: glutamine-rich
F;2538-2568/Domain: neurogenic repetitive element #status predicted <OPA>
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A;Introns: 53/3; 84/3; 171/3; 240/3; 283/3; 2333/3; 2436/3; 2588/3
C;Superfamily: Notch protein; ankyrin repeat homology, EGF homology
C;Superfamily: Notch protein; tandem repeat; transmembrane protein
E;27-43/Domain: transmembrane #status predicted <TMM1>
F;27-43/Domain: EGF homology <EGR1>
F;530-561/Domain: EGF homology <EGF1>
F;568-599/Domain: EGF homology <EGF>
                                                                                                                              Length 2471;
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                                                                                                                                                                                                                        Indels
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1950-1982/Domain: ankyrin repeat homology <ANI>
1983-2015/Domain: ankyrin repeat homology <ANI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              notch protein - fruit fly (Drosophila melanogaster)
N;Alternate names: neurogenic repetitive locus protein
C;Species: Drosophila melanogaster
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                                                                                                                              Query Match 55.0%; Score 66; DB 2; Best Local Similarity 25.8%; Pred. No. 96; Matches 8; Conservative 14; Mismatches
    F;1976-2008/Domain: ankyrin repeat homology <AN4>F;2009-2041/Domain: ankyrin repeat homology <AN5>
                                                                                                                                                                                                                                                                                                                                                           324 CVCVNGWSGDDCSENIDDCAFASCTPGSTCI 354
                                                                                                                                                                                                                                                                                                         1 CXIXN----QXCXQXLDDCCSXXCNXXNXCV 27
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;Residues: 2504-2576,'E',2578-2611 <WHA2>
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                RESULT 12

A49175

Motch B protein - mouse (fragment)

NyAlternate names: Notch homolog
C;Species: Mus musculus (house mouse)
C;Date: 21-Jan-1994 #sequence revision 05-Jan-1996 #text_change 16-Aug-2004
C;Accession: A49175; PH1570; $\overline{3}32113$

R;Lardelli, M.; Lendahl, U.

Exp. Cell Res. 204, 364-372, 1993
A;Fitle: Motch A and Motch B--two mouse Notch homologues coexpressed in a wide variety of A;Reference number: A49175; MUID:93178563; PMID:8440332
A;Accession: A49175
A;Accession: A49175
A;Accession: A49175
A;Accession: A49175
A;Accession: A49175
A;Accession: A19175
A;Accession: A49175
A;Acc
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C;Comment: This protein has many EGF repeats and lin-12/Notch repeats.
C;Comment: This protein is one of the neurogenic proteins controlling the decision betwe
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cell-fate determining gene Notch2 protein - rat
cell-fate determining gene Notch2 protein - rat
cell-fate determining gene Notch2 protein - rat
c.species: Rattus norvegicus (Norway rat)
c.space: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 16-Aug-2004
c.spacession: A49128
R;Weinnaster, G.; Roberts, V.J.; Lemke, G.
Bevelopment 116, 931-941, 1992
A;Title: Notch2: a second mammalian Notch gene.
A;Reference number: A49128; MUID:93202015; PMID:1295745
                                                      Gaps
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A,Residues: 1-2471 <WEI>
A,Cross-references: UNIPROT: Q9QW30
A,Experimental source: Schwann cell
A,Note: sequence extracted from NCBI backbone (NCBIP:127811)
C,Superfamily: Notch protein; ankyrin repeat homology; EGF homology
F;264-295/Domain: EGF homology <EGR1>
F;799-830/Domain: EGF homology <EGR1>
F;877-908/Domain: EGF homology <EGR2>
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A,Status: preliminary; not compared with conceptual translation
                                                 5; Indels
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                                        14; Mismatches
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Pred. No.
    Pred. No.
                                                                                                                                  56
                                                                                                                                                                                    CKSPGTPCSRGMRDCCTSCLSYSNKC 26
                                                                                                                                  1 CXIXNQXCXQXLDDCCSXXCNXXNXC
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F;1067-1098/Domain: EGF homology <EGX3>
F;1153-1184/Domain: EGF homology <EGF3>
F;1191-1222/Domain: EGF homology <EGX4>
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F;674-705/Domain: EGF homology «EGK2»
F;712-743/Domain: EGF homology «EGF3»
F;836-867/Domain: EGF homology «EGF3»
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Best Local Similarity 26.9%;
Matches 7; "Conservative 1
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Matches
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A; Map position: 17
A; Map position: 17
A; Introns: 22/1; 49/2; 148/1; 264/1; 305/1; 384/1; 436/1; 501/1; 539/1; 577/1; 618/1; 671
A; Introns: 22/1; 49/2; 148/1; 264/1; 305/1; 384/1; 436/1; 501/1; 539/1; 577/1; 618/1; 671
C; Superfamily: notch protein; ankyrin repeat homology; EGF homology
C; Keywords: receptor; signal transduction
E; 514-545/Domain: EGF homology <EGF>
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A;Residues: 1-2318 <LAR>
A;Cross_references: UNIPROT:Q61982; EMBL:X74760; NID:g483580; PIDN:CAA52776.1; PID:g48356
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Mech. Dev. 46, 123-136, 1994
A;Title: The novel Notch homologue mouse Notch 3 lacks specific epidermal growth factor-1. A;Reference number: 845306; MUID:95001556; PMID:7918097
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A;Cross-references: UNIPROT:Q9UM47; EMBL:U97669; NID:g2668591; PIDN:AAB91371.1; PID:g2668
R;Joutel, A.; Corpechot, C.; Ducros, A.; Vahedi, K.; Chabrist, H.; Mouton, P.; Alamowitch
          A, Description: Sequence of the mouse major histocompatibility locus class III region.
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A;Residues: 1-1964 <ROW>
A;Cross-references: UNIPROT:P31695; EMBL:AF030001; NID:g2564945; PID:g2564947
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C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C;Accession: 878549; S71825
C;Accession: A: Tournier-Lasserve, E.
SiJoutel, A: Tournier-Lasserve, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S45306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1964;
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1e+02;
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                                                                                                              4;Status: preliminary; translated from GB/EMBL/DDBJ
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F)1872-1904/Domain: ankyrin repeat homology
F)1906-1934/Domain: ankyrin repeat homology
F)1939-1971/Domain: ankyrin repeat homology
F)1972-2004/Domain: ankyrin repeat homology
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Best Local Similarity 30.0
Matches 9; Conservative
                                                   ;Reference number: Z16543
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A;Accession: S78549
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les 7; Conserv
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                                                                               Accession: T09059
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Matches
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                                                                                                                                                                                                                                                                               hypothetical protein F40E10.4 - Caenorhabditis elegans (fragment)
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: T22025
B;Smye, R.
Submitted to the EMBL Data Library, February 1996
A;Reference number: Z19503
A;Accession: T22025
A;Actus: preliminary; translated from GB/EMBL/DDBJ
A;Accession: T22025
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: T2025
A;Actus: DNA
A;Experiments Lype: DNA
A;Experimental source: clone F40E10
C;Genetics: A;Genetics: A;Genetics:
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notch4 - mouse '
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T09059
R;Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; Scaubmitted to the EMBL Data Library, October 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C,Accession: D89711
R; amonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Reference number: A75000; MUID: 99069613; PMID: 9851916
A;Note: see websites genome, wustl.edu/gsc/C_elegans/ and www sanger.ac.uk/Projects/C_elegans/ A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Accession: D89711
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                                                                                                                                                                                                                                                                     ypothetical protein F40E10.4 - Caenorhabditis elegans (fragment)
.Species: Caenorhabditis elegans
.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
.Accession: T22025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein F40E10.4 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
          Gaps
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          Indels
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      12; Mismatches
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13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54.2%; Score 65; 26.9%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                          822 TGQKCETNIDDCVTNPCGNGGTCI 845
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                                                             4 XNOXCXQXLDDCCSXXCNXXNXCV 27
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Best Local Similarity 26.99
Matches 7; Conservative
   7; Conservative
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Best Local Similarity 26.5.
Best Local 5; Conservative
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A:Molecule type: DNA
A:Residues: 1-601 <STO>
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A;Map position: X
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Matches
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4 XNQXCXQXLDDCCSXXCNXXNXCV 27
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                          A; Reference number: Z20112
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A; Residues: 1-3623 <MOE>
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Matches 6; Conserv
                                                                                                                                                                                                                                                     A;Gene: CESP:W02C12.1
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A;Cross-references: EMBL:U97669
C;Gene: notch3
A;Rap position: 19p13.1
x, M.M.; Weissenbach, J.; Bach, J.F.; Bousser, M.G.; Tournier-Lasserve, E.
Nature 383, 707-710, 1996
A;Title: Notch3 mutations in CADASIL, a hereditary adult-onset condition causing stroke
A;Reference number: S71825; MUID:97032728; PMID:8878478
A;Accession: S71825
A;Accession: S71825
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 67-113;138-194;268-333,'G',335-346;536-613;716-765;1240-1279:1815-1888 ATMIN
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1731070
notch homolog - sea urchin (Lytechinus variegatus)
C;Species: Lytechinus variegatus (variegatus)
C;Species: Lytechinus variegatus (variegated urchin)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 31-Jan-2000
C;Date: 22-Oct 1999 #sequence_revision 22-Oct-1999 #text_change 31-Jan-2000
R;Accespion: T31070
Bevelopment 124, 3363-3374, 1997
A;Title: Identification and localization of a sea urchin Notch homologue: insights into A;Accession: T31070
                                                                                                                                                                                                                                                                                                                                                                                        causing a type of stroke and homology
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A;Molecule type: mRNA
A;Residues: 1-2531 <SHE.
A;Cross-references: EMBL:AF000634; NID:92570350; PID:92570351; PIDN:AABB2088.1
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T2533
R;Murray, J; Wohldmann, P.
aubmitted to the EMBL Data Library, December 1996
A;Description: The sequence of C. elegans cosmid W02C12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
                                                                                                                                                                                                                                                                                                                                                                                        A, Description: may be involved in pathogenesis of CADASIL, C, Superfamily: notch protein; ankyrin repeat homology; EGF
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hypothetical protein W02C12.1 - Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;1871-1993/Domain: ankyrin repeat homology
F;1906-1931/Domain: ankyrin repeat homology
F;1938-1970/Domain: ankyrin repeat homology
F;1971-2003/Domain: ankyrin repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F,1838-1870/Domain: ankyrin repeat homology
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661 NCEEDIDDCESRPCHNGGTCV 681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;123-155/Domain: BGF homology <BGX1>
F;162-194/Domain: BGF homology <BGF1>
F;240-271/Domain: BGF homology <BGX2>
F;318-349/Domain: BGF homology <BGR>
F;473-504/Domain: BGF homology <BGR>
F;958-959/Domain: BGF homology <BGR3>
F;928-959/Domain: BGF homology <BGR3>
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30.0%;
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Best Local Similarity 30.0*
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F;123-155/Domain: EGF
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A;Molecule type: DNA
A;Residues: 1-1372 <MURA.
A;Cross-references: UNIRROT:P91526; EMBL:U80815; PIDN:AAB37995.1; GSPDB:GN00022; CESP:W0;
A;Experimental source: strain Bristol N2; clone W02C12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R.Hori, S.; Sairoh, T.; Matsumoto, M.; Makabe, K.W.; Nishida, H.
Dev. Genes Evol. 207, 311-380, 1997
A;Title: Notch homologue from Halocynthia roretzi is preferentially expressed in the cent A;Reference number: Z20775
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Square CUBILIN
Square CUBILIN
Superfamily: intrinsic factor-B12 receptor cubilin; EGF homology
Superfamily: intrinsic factor-B12 receptor cubilin; EGF homology
(1.20/Domain: signal sequence #status predicted <SIG>)
(21-20/Domain: signal sequence #status predicted <SIG>)
(21-3623/Product: intrinsic factor-B12 receptor CUBILIN #status predicted <MAT>)
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;Meestrup, S.K.; Kozyraki, R.; Kristiansen, M.; Kaysen, J.H.; Rasmussen, H.H.; Brault, Biol. Chem. 273, 5235-5242, 1998
;Hitle: The intrinsic factor-vitamin B12 receptor and target of teratogenic antibodies;Reference number: 216459; MUID:98148073; PMID:9478979
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C;Accession: T30201
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C;Superfamily: notch protein; ankyrin repeat homology; EGF homology
                                                                                                                                                                                                                                                                                                                                                                     Length 1372;
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53.3%; Score 64; DB 2; Length 2352;
Best Local Similarity 26.9%; Pred. No. 1.4e+02;
Matches 7; Conservative 13; Mismatches 6; Indels
                                                                                                                                                                                                                                                      A;Map position: 4
A;Introns: 29/1; 66/1; 774/2; 823/2; 1046/1; 1108/2; 1298/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Notch homolog protein - sea squirt (Halocynthia roretzi)
C;Species: Halocynthia roretzi
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99;
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A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                 53.3%; Score 64; 25.0%; Pred. No.
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95 TGENCDQNIDECAASPCQNDAKCI 118
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A;Residues: 1-1687 <SEL>
A;Cross-references: UNIPROT:Q61204; EMBL:US7368; NID:g1336627; PID:g1336628; PIDN:AAB0133
A;Experimental source: strain C57BL/6J; clone DBI-1; whole embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cjacession: A43620
RjOlivera, B.M.; Gray, W.R.; Zeikus, R.; McIntosh, J.M.; Varga, J.; Rivier, J.; de Santos!
Science 230, 1338-1343, 1985
A;Title: Peptide neurotoxins from fish-hunting cone snails.
A;Reference number: A43620; MUID:86070213; PMID:4071055
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C,Species: Mus musculus (house mouse)
C;Decies: Mus musculus (house mouse)
C;Dete: 02-3u1-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Dete: 02-3u1-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I48324
R;Bettenhausen, B.; de Angelis, M.H.; Simon, D.; Guenet, J.L.; Gossler, A.
Development 121, 2407-2418, 1995
A;Accession: I48324
A;Title: Translent and restricted expression during mouse embryogenesis of Dll1, a murint A;Reference number: I48324
A;Title: Translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-722 <RES>
A;Cross-references: UNIPROT:Q61483; EMBL:X80903; NID:g80655; PIDN:CAA56865.1; PID:g80655;
                                                                                                                                                                                                                                 C'Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C'Accession: T310176
R'Sell, C'; Hoff III, H.B.
submitted to the EMBL Data Library, May 1996
A; Bescription: Cloning of a novel mRNA regulated by the insulin like growth factor type
A; Reference number: 220762
A; Accession: T30176
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C, Superfamily: omega-conotoxin
C; Keyberfamily: omega-conotoxin
F; 1-16, 8-19, 15-26, Disulfide bonds: #status predicted
F; 4, 7/Modified site: 4-hydroxyproline (Pro) #status experimental
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N;Alternate names: shaker peptide GVIIA
C;Species: Conus geographus (geography cone)
C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52.5%; Score 63; DB 2; Length 168
26.9%; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Length 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 51.7%; Score 62; DB Local Similarity 26.9%; Pred. No. 11; Pred. 7; Conservative 13; Mismatches
                205 GFTGDNCETDIDECASAPCRNGGACV 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : : : | : : : | | | | : : : | | | 480 GFEGSTCERNIDDCPNHKCQNGGVCV 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |: : :|:::: |||::: ::|:|
CKSPGTPCSRGMRDCCTSCLLYSNKC 26
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                                                                                                                                                                      EGF repeat transmembrane protein - mouse C;Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 26.3%
Best Local 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: A43620
A;Molecule type: protein
A;Residues: 1-29 <OLI>
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Matches
                                                                                                               RESULT 26
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                                                                                                                                                                                                                                                                                                         metallothionein - common bobwhite (fragment)

C.Species: Colinus virginianus (common bobwhite)
C.Species: Colinus virginianus (common bobwhite)
C.Species: Colinus virginianus (common bobwhite)
C.Saccession: S33379; 818174
R.Shartzer, K.L.; Kade, K.; Sobieski, R.J.; Andrews, G.K.
J. Mol. Evol. 36, 255-262, 1993
A;Title: Evolution of avian metallothionein: DNA sequence analyses of the turkey metallothionein: S33378; MUD:93247066; PMID:8483164
A;Reference number: S33378; MUD:93247066; PMID:8483164
A;Recession: S33379
A;Residues: preliminary
A;Molecule type: mRNA
A;Residues: 1-43 -85HA>
A;Residues: J-43 -85HA>
A;Coss-references: UNIPROT:P27087; EMBL:X62512; NID:g62751; PIDN:CAA44371.1; PID:g62752
C;Superfamily: metallothionein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A46836

A46836

A46836

A46836

Ibbropellin C precursor - sea urchin (Strongylocentrotus purpuratus)

N.Alternate names: EGF repeat-containing protein; epidermal growth factor-related protein C,Species: Strongylocentrotus purpuratus (Fuzple urchin)

C,Accession: A48836

R,Bisgrove, B.W.; Raff, R.A.

Boy. Biol. 157, 526-538, 1993

A,Title: The SpEGF III gene encodes a member of the fibropellins: EGF repeat-containing A,Reference number: A48836

A,Status: preliminary

A,Status: preliminary

A,Status: preliminary
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fide bonds: #status predicted
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                                                                           Gaps
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A, Cross-references: UNIPROT: P49013; GB: L07045; NID: g310659; PID: g310660
A, Cross-references: UNIPROT: P49013; GB: L07045; NID: g310659; PID: g310660
A, Note: sequence extracted from NCBI backbone (NCBIN:137724, NCBIP:132725)
F; 1-18/Domain: signal sequence #status predicted <BIS>
F; 19-570/Product: fibropallin C #status predicted <FIB>
F; 19-54/Domain: EGF homology <BGI>
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         Length 3623;
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                                                                           Indels
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   53.3%; Score 64; DB 2; I
29.2%; Pred. No. 1.9e+02;
tive 13; Mismatches 4;
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F;176-211/Domain: BGF homology cEG3>
F;214-249/Domain: BGF homology cEG3>
F;222-287/Domain: BGF homology cEG3>
F;290-325/Domain: BGF homology cEG5>
F;320-355/Domain: BGF homology cEG5>
F;360-315/Domain: BGF homology cEG6>
F;364-401/Domain: BGF homology cEG8>
F;404-39/Domain: BGF homology cEG8>
F;42-570/Region: avidin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 33.3%; Score 63; DB Similarity 33.3%; Pred. No. 12; 9; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CXIXNOXCXOXLDDCCSXXCNXXNXCV 27
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CKCKNCRCRSCRKSCCSCCPAGCNNCV 3.2
                                                                                                                                                                   125 SGONCTENINDCSSNPCLNGGTCI 448
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                                                                                                                            4 XNQXCXQXLDDCCSXXCNXXNXCV 27
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Best Local Similarity 29.2%
Matches 7; Conservative
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les 7; Conservat
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Best Local Similarity
Matches 9; Conserv
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Best Local Si
Matches 7;
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F;23-34,28-43,45-54,62-88,180-191,185-200,202-211,218-229,223-238,240-249,256-267,261-27
57,451-466,468-477,484-495/Disulfide bonds: #Btatus predicted
F;489-504,506-515,52-533,527-542,544-553,560-571,565-580,582-591,598-609,603-618,620-62
08,810-819,826-837,831-846,848-857,864-875,869-884,886-895,902-913,907-922,924-933/Disul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: A32038
R;Skinner, W.S.; Adams, M.E.; Quistad, G.B.; Kataoka, H.; Cesarin, B.J.; Enderlin, F.E.; J. Biol. Chem. 264, 2150-2155, 1989
A;Title: Purification and characterization of two classes of neurotoxins from the funnel A;Reference number: A32038; MUID:89123282; PMID:2914898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Comment: mu-agatoxins cause paralysis in insects by activating neuronal sodium channel C;Superfamily: curratoxin
C;Superfamily: curratoxin
C;Superfamily: curratoxin
F;Z-16,9-22,17-32,34-30/Disulfide bonds: #status predicted
F;3-16,9-22,17-32, amidated carboxyl end (Asn) #status experimental
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A;Title: A new Conus peptide ligand for Ca channel subtypes.
A;Reference number: A58537; MUID:94150815; PMID:8107968
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C:Date: 31-Jul-1989 #sequence_revision 22-Jul-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Conus magus (magus cone)
C;Date: 27-Mar-1997 #sequence_revision 11-Apr-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                            51.7%; Score 62; DB 2; Length 106.26.9%; Pred. No. 1.38+02; Aismarches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50.8%; Score 61; DB 2; Length 29; 28.0%; Pred. No. 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mu-agatoxin I - funnel-weaving spider (Agelenopsis aperta)
                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 26.9%; Pred. No. 1.3e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51.2%; Score 61.5; E
26.7%; Pred. No. 15;
tive 12; Mismatches
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                                                                                                               / <EG19>
/ <EG20>
/ <EG21>
                                                               <EG17>
                                                                                           <EG18>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Accession: A32038
A,Molecule type: protein
A,Residues: 1-36 kSk:
A,Cross-references: UNIPROT:P11057
F;674-705/Domain: BGF homology <E
F;712-743/Domain: BGF homology <E
F;780-781/Domain: BGF homology <E
F;826-857/Domain: BGF homology <E
F;864-895/Domain: BGF homology <E
F;902-933/Domain: BGF homology <E
F;902-933/Domain: BGF homology <E
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nes 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fibropellin Ia - sea urchin (Strongylocentrotus purpuratus)
NyAlternate names: epidermal growth factor homolog precursor
NyAlternate names: epidermal growth factor homolog precursor
NyContains: alternatively spliced fibropellin Ib (EGFI)
C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Date: 13-May-1992 #sequence revision 17-Sep-1997 #text_change 09-Jul-2004
C;Accession: A40136; B40136; G40136; A29316; A43131
R;Delgadillo-Reynoso, M.G.; Rollo, D.R.; Hursh, D.A.; Raff, R.A.
J. Mol. Evol. 29, 314-327, 1989
A;Title: Structural analysis of the uEGF gene in the sea urchin Strongylocentrotus purpu
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AskBB J. 3, 1760-1764, 1989

A; Title: 1989

A; Title: 1989

A; Reference number: A43131; MUID:89196806; PMID:2784773

A; Contents: annotation

C; Comment: EGF homology repeats 10-17 are spliced out in the short form (fibropellin Ib)

F;1-19/Domain: aignal sequence #status predicted <SIG>
F;20-1064/Product: fibropellin I #status predicted <FIB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 'K',747-821,898-978 < DE3>
R; Hursh, D.A.; Andrews, M.E.; Raff, R.A.
Science 237, 1487-1490, 1987
A; Title: A sea urchin gene encodes a polypeptide homologous to epidermal growth factor.
A; Reference number: A29316; MUID:87319677; PMID:3498216
A; Accession: A29316
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A;Residues: 'S',280-481,786-1064 <HUR>
A;Cross-references: GB:M17421; NID:g161474; PIDN:AAA30050.1; PID:g552260
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A;Accession: B40136
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                                                                                                                                                                                                   2; Length 722;
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A;Accession: C40136
                                                                                                                                                                                    DB 3
                                                                                                                                                                                                                                                      12; Mismatches
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C;Genetics:
A;Gene: Dll
C;Superfamily: delta-4 protein; EGF homology
F;31-362/Domain: EGF homology <EGF2>
F;446-477/Domain: EGF homology <EGF>
F;484-515/Domain: EGF homology <EGF>
                                                                                                                                                                                                   51.7%; Score 62; 28.0%; Pred. No.
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433 GFSGRYCEDNVDDCASSPCANGGIC 457
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F;180-211/Domain. EGF homology
F;218-249/Domain. EGF homology
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Best Local Similarity
Matches 7; Conserva
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A,Molecule type: mRNA
A,Residues: 1-114 <DEL>
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R;Thomas, U.; Speicher, S.A.; Knust, E.
Development 111, 749-761, 1991
A;Title: The Drosophila gene Serrate encodes an EGF-like transmembrane protein with a com
A;Reference number: S16148; MUID:91347903; PMID:1840519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-1351, 'T',1353-1408 <THO2>
A; Cross-references: EMBL:X56811; NID:95563; PID:98564
R; Fleming, R.J.; Scottgale, T.N.; Diederich, R.J.; Artavanis-Tsakonas, S.
Genes Dev. 4, 2188-2201, 1990
A; Title: The gene Serrate encodes a putative EGF-like transmembrane protein essential for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;1222-1246/Domain: transmembrane #status predicted <TM1>
F;1247-1408/Domain: intracellular #status predicted <INT>
F;152,196,247,331,412,452,558,739,965,977,1004,1030,1150/Binding site: carbohydrate (Asn)
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C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Apr. 1991 #sequence_revision 30-Apr. 1991 #text_change 02-Aug-2002
C;Accession: B36665
R;Rothberg, J.M.; Jacobs, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S.
Genes Dev. 4, 2169-2187, 1990
A;Title: slit: an extracellular protein necessary for development of midline glia and con A;Reference number: A36665; MUID:91099665; PMID:2176636
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F;85-140/Product: gene serrate protein #status predicted <MAT>
F;85-140/Product: gene serrate protein #status predicted <MAT>
F;85-121/Domain: extracellular #status predicted <EXT>
F;283-316/Domain: EGF homology <EG03>
F;319-348/Domain: EGF homology <EG03>
F;355-388/Domain: EGF homology &EG03>
F;355-388/Domain: EGF homology &EG05>
F;535-608/Domain: EGF homology &EG05>
F;652-68/Domain: EGF homology <EG05>
F;652-68/Domain: EGF homology <EG06>
F;651-645/Domain: EGF homology <EG09>
F;650-320/Domain: EGF homology <EG09>
F;630-300/Domain: EGF homology <EG09>
F;630-300/Domain: EGF homology <EG09>
F;817-796/Domain: EGF homology &EG11>
F;81-818/Domain: EGF homology <EG12>
F;81-818/Domain: EGF homology <EG13>
F;81-818/Domain: EGF hom
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A;Residues: 1-15,20-26,'A',28-1408 <FLE>
A;Cross_references: GB:M35759; NID:g158605; PID:g158606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Thomas, U. submitted to the EMBL Data Library, November 1990 A;Reference number: $16878
                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-1408 <THO1>
A;Cross-references: UNIPROT:P18168; EMBL:X56811
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1-84/Domain: signal sequence #status predicted
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Cross-references: FlyBase:FBgn0004197
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Best Local Similarity 23.1%
Matches 6; Conservative
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A;Molecule type: mRNA
A;Residues: 1-1469 <ROT>
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C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: J3.69p-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: 150719
Nature 375, 737-790, 1995
A;Title: Expression of a Delta homologue in prospective neurons in the chick.
A;Reference number: 150719, MUID:95319507; PMID:7596411
A;Reference number: 150719, MUID:95319507; PMID:7596411
A;Reterence number: 150719
A;Reterence number: 15071
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RiHolmes, G.P.: Negus, K.; Burridge, L.; Raman, S.; Algar, E.; Yamada, T.; Little, M.H.
RiHolmes, G.P.: Negus, K.; Burridge, L.; Raman, S.; Algar, E.; Yamada, T.; Little, M.H.
Mech. Dev. 79, 57-72, 1998
A;Title: Distinct but overlapping expression patterns of two vertebrate slit homologs im
A;Reference number: Z22177; MUID:99279238; PMID:10349621
A;Accession: T42626
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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A;Residues: 71-1025 <HOL>
A;Cross-references: UNIPROT:09R1B9; EMBL:AF074960; NID:g4151258; PID:g4151259; PIDN:AAD0 C;Gene: Slit:2
A;Gene: Slit:2
C;Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein r
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C;Species: Drosophila melanogaster
C;Date: 31-Dec-1991 #sequence Prevision 02-Aug-1994 #text_change 09-Jul-2004
C;Accession: S16148; S16878; Ā36666
                                                     Gaps
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                                                     Indels
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                                         13; Mismatches
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                                                                                                                                                    1 CXIXNQXCXQXLDDCCSXXCNXXNX 25
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                                         7; Conservative
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Best Local Similarity
                                   Matches
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S16148
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A;Accession: T22274
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Kesses: 1-354 <MIL>
A;Cross-references: UNIPROT:Q9XV21; EMBL:Z81540; PIDN:CAB04398.1; GSPDB:GN00023; CESP:F4
A;Experimental source: clone F46B3
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neurogenic protein Delta precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Spate: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 02-Aug-2002
C;Accession: A31246
R;Kopczynski, C.C.; Alton, A.K.; Fechtel, K.; Kooh, P.J.; Muskavitch, M.A.T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein F46B3.9 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T22274
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                   A,Map position: 5
A;Introns: 23/1; 55/1; 82/1; 112/1; 142/1; 170/1; 193/1; 223/1; 299/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ilarity 26.9%; Score 61; DB 2; ilarity 26.9%; Pred. No. 2e+02; Conservative 12; Mismatches
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Best Local Similarity 28.6
Matches 8; Conservative
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Best Local Similarity
Matches 7; Conserv
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A36665
Balit protein 1 precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 02-Aug-2002
C;Accession: A36665, A31640; Si3523
R;Rothberg, J.M.; Jacobb, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S.
Genes Dev. 4, 2169-2187, 1990
A;Title: slit: an extracellular protein necessary for development of midline glia and cc
A;Reference number: A36665; MUD:91099665; FMID:2176636
A;Reference number: A36665, MUD:91099665; FMID:2176636
A;Residues: preliminary
A;Molecule Type: mRNA
A;Residues: 1-1480 - ROT>
A;Cross-references: GB:X53959; NID:g8614; PIDN:CAA37910.1; PID:g8615
R;Rothberg, JM.; Hartley, D.A.; Walther, Z.; Artavanis-Tsakonas, S.
Call 55, 104-1059, 1988
A;Title: slit: An EGF-homologous locus of D. melanogaster involved in the development of A;Reference number: A31640; MUD:89077533; PMID:3144436.
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                                                                                                                        homology; leucine-rich alpha-2-glycoprotein
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                                                                            A Cores - Flyabase: Flyabase: Psymono3425
C; Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-; Fi 66-91/Domain: proteoglycan amino-terminal homology spatis.
F; 66-91/Domain: proteoglycan amino-terminal homology spatis.
F; 101-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology sLRR; F; 172-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology sLRR; F; 173-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology sLRR; F; 173-196/Domain: proteoglycan carboxyl-terminal homology sPAH2.
F; 288-272/Domain: proteoglycan carboxyl-terminal homology sPAH2.
F; 288-313/Domain: proteoglycan amino-terminal homology sPAH2.
F; 373-346/Domain: leucine-rich alpha-2-glycoprotein repeat homology sLRR F; 371-394/Domain: leucine-rich alpha-2-glycoprotein repeat homology sLRR F; 371-394/Domain: leucine-rich alpha-2-glycoprotein repeat homology sLRR F; 371-394/Domain: leucine-rich alpha-2-glycoprotein repeat homology sLRR F; 515-637/Domain: leucine-rich alpha-2-glycoprotein repeat homology sLRR F; 515-537/Domain: leucine-rich alpha-2-glycoprotein repeat homology sLRR F; 512-537/Domain: leucine-rich alpha-2-glycoprotein repeat homology sLRL F; 512-537/Domain: leucine-rich alpha-2-glycoprotein repeat homology sLRL F; 516-643/Domain: leucine-rich alpha-2-glycoprotein repeat homology sLRL F; 551-65/Domain: proteoglycan amino-terminal homology sLRL F; 551-65/Domain: proteoglycan amino-terminal homology sLRL F; 551-65/Domain: proteoglycan amino-terminal homology sLRL F; 708-73/Domain: proteoglycan amino-terminal homology sLRL F; 551-65/Domain: proteoglycan amino-terminal homology sLRL F; 551-65/Domain: proteoglycan amino-terminal homology sLRL F; 570-69/Domain: proteoglycan amino-terminal homology sLRL F; 708-73/Domain: leucine-rich alpha-2-glycoprotein repeat homology sLRL F; 708-73/Domain: proteoglycan amino-terminal homology sLRL F; 708-73/Domain: proteoglycan amino-terminal homology sLRL F; 708-73/Domain: leucine-rich alpha-2-glycoprotein repeat homology sLRL F; 708-73/Domain: proteoglycan pr
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A;Molecule type: DNA
A;Residues: 881-1182,'G',1185-1404,'GT',1463-1464,'YHA' <RO2>
A;Crose.references: GB:M23543; NID:g340939; PID:g514357
C;Genetics:
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Pred. No. 2
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26.9%;
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Best Local Similarity 26.26.
Local Similarity 7. Conservative
A;Cross-references: GB:X53959
C;Genetics:
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EMBO J. 6, 761-766, 1987
A,Title: EGF homologous sequences encoded in the genome of Drosophila melanogaster, and t
A,Reference number: A91081; MUID:87218537; PMID:3107986
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R;Yochem, J.; Greenwald, I.
Cell S8, 553-563, 1989
A;Title: glp-1 and lin-12, genes implicated in distinct cell-cell interactions in Caenort
A;Reference number: A32901; MUID:89336787; PMID:2758466
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R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology|
A;Fitle: Genome sequence of the nematode C. elegans: a platform for investigating biology|
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_elegans/ A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
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A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1295 < vyCc>
A;Cross-references: UNIPROT: Pl3508; GB:WZ5580; NID:g156316; PIDN: AAA28058.1; PID:g156317
G;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology
C;Keywords: transmembrane protein
F;121-151/Domain: EGF homology «EGF.>
F;275-307/Domain: EGF homology «EGT.>
F;373-405/Domain: EGF homology «EGF.>
F;411-442/Domain: EGF homology «EGF.>
F;450-442/Domain: EGF homology «EGF.>
F;650-400,/Domain: EGF homology «EGF.>
F;650-400,/Domain: EGF homology «EGF.>
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Ajcross-references: FlyBase:FBgn0000463
GjSuperfamily: neurogenic protein delta; EGF homology
CjSuperfamily: neurogenic protein
CjSuperdamily: aignal sequence #status predicted <SIG>
Fi1-18/Domain: signal sequence #status predicted <SIG>
Fi19-88/Product: neurogenic repetitive locus delta protein #status predicted <MAT>
Fi457-488/Domain: EGF homology <EGFI>
Fi533-564/Domain: EGF homology <EGFI>
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C;Species: Caenorhabditis elegans
C;Date: 20-Dec.1989 #sequence_revision 04-Sep-1992 #text_change 09-Jul-2004
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C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
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A;Residues: 422-436,'ET',439-458,'A',460-489,'T',491-621 <KNU>
A;Cross-references: GB:X05140; NID:97851; PIDN:CAA28786.1; PID:9929563
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50.0%; Score 60; DB 2; 1
Best Local Similarity 23.1%; Pred. No. 1.7e+02;
Matches 6; Conservative 12; Mismatches 8
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25.8%; Pred. No. 2.2e+02;
ive 13; Mismatches 6,
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Best Local Similarity 25.8
Matches 8; Conservative
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A,Molecule type: mRNA
A,Residues: 1-880 «VME>
A,Cross-references: UNIPROT:P10041; EMBL:X06289; NID:g7852; PID:g7853
R,Knust, E.; Dietrich, U.; Tepass, U.; Bremer, K.A.; Weigel, D.; Vaessin, H.; Campos-Ort
Genes Dev. 2, 1723-1735, 1988
A;Title: Delta, a Drosophila neurogenic gene, is transcriptionally complex and encodes A;Reference number: A31246; MUD:89196890; PMID:3149249
A;Rocession: A31246; MUD:89196890; PMID:3149249
A;Rocession: A31246
A;Molecule type: mRNA
A;Residues: 1-832 <KOP>
A;Coss-references: GB:Y00222
C;Genetics: A3246
C;Genetics: CG:Superfamily: neurogenic protein delta; EGF homology <CGI)
A;Cross-references: FlyBase:FBgn0000463
C;Superfamily: neurogenic protein delta; EGF homology <CGI)
F;295-328/Domain: EGF homology <CGI)
F;533-564/Domain: EGF homology <CGF>
F;533-564/Domain: EGF homology <CGF>
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C.Species: Drosophila melanogaster
C.Species: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C.Accesion: S19087
R.Muskavitch, M.A.T.
Submitted to the EMBL Data Library, June 1991
A.Reference number: S19087
A.Reference number: S19087
A.Status: preliminary
A.Status: preliminary
A.Nolecule type: mRNA
A.Residues: 1-833 <MUS.
A.Cross-references: UNIPROT:P10041; EMBL:Y00222
C.Genetics:
A.Gene: Flybase:D1
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C;Superfamily: neurogenic protein delta; EGF homology
F;335-371/Domain: EGF homology «EGX1»
F;378-415/Domain: EGF homology «EGX1»
F;457-488/Domain: EGF homology «EGF»
F;533-564/Domain: EGF homology «EGF»
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Matches 6; Conserv
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Matches 6; Conserv
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Best Local Similarity
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A; Residues: 1-43 <SHA>
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                                       A Molecule Fype: DNA
A; Residues: 1-1722 <STO>
A; Cross-references: UNIPROT:Q19350; GB:chr_X; PIDN:AAC69012.1; PID:g1125776; GSPDB:GN000
C; Genetics:
A; Gene: F11C7.4
A; Map position: X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A. Title: A new conus peptide ligand for mammalian presynaptic Ca2+ channels.

A. Reference number: JH0699; MUID:92337922; PMID:1352986

A. Accession: JH0701

A. A. Accession: JH0701

A. Residues nucleic acid sequence not shown

A. Molecule type: mRNA

A. Residues: 1-25 cHIL.

A. Cross-references: UNIPROT:PD5485

R. Olivera, B.M.; Cruz, L.J.; de Santos, V.; LeCheminant, G.W.; Griffin, D.; Zeikus, R.;

B. Joinemastry 26, 2086-2090, 1987

A. Title: Neuronal calcium channel antagonists. Discrimination between calcium channel su

A. Reference number: A34115; MUID:87299637; PMID:2441741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: omega-conotoxin
C;Stywords: acetylcholine release inhibition; amidated carboxyl end; calcium channel inh
F;1-16,8-20,15-25/Disulfide bonds: #status predicted
F;25/Modified site: amidated carboxyl end (Cys) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               omega-conotoxin MVIIB - cone shell (Conus magus)
C;Species: Conus magus (magus cone)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: JH0701; B34115
R;Hillyard, D.R.; Monje, V.D.; Mintz, I.M.; Bean, B.P.; Nadasdi, L.; Ramachandran, J.; Neuron 9, 69-77, 1992
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$33382

metallothionein - ring-necked pheasant (fragment)

C;Species: Phasianus colchicus (ring-necked pheasant)

C;Species: Phasianus colchicus (ring-necked pheasant)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Aug-1999

C;Accession: $3338, $3181

J, Mol. Evol. 36, 255-262, 1993

A;Ritle: Bvolution of avian metallothionein: DNA sequence analyses of the tu

A;Reference number: $33378; MUID:93247066; PMID:8483164
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                                                                                                                                                                                                                                                                7; Indels
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                                                                                                                                                                                                                 50.0%; Score 60; DB 2; I 26.7%; Pred. No. 2.7e+02;
                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                           1391 CNCDNNWRGAHCQHQMDTCLDFPCNNDGVC 1420
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                                                                                                                                                                                                                                                                                                                1 CXIXNQ----XCXQXLDDCCSXXCNXXNXC 26
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Pred. No.
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                                                                                                                                                                                        Query Match
Best Local Similarity (
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A;Molecule type: protein
A;Residues: 1-25 <OLI>
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A;Molecule type: mRNA
A;Residues: 1-43 <SHA>
                        A;Status: preliminary
A; Accession: E89753
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metallothionein - common bobwhite (fragment)
C;Species: Colinus virginianus (common bobwhite)
C;Species: Colinus virginianus (common bobwhite)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: 833378; S18173
R;Shartzer, K.L.; Kage, K.; Sobieski, R.J.; Andrews, G.K.
A;Artzer, K.L.; Kage, K.; Sobieski, R.J.; Andrews, G.K.
A;Title: Evolution of avian metallothionein: DNA sequence analyses of the turkey metallo A;Reference number: 833378; MUID:93247066; PMID:8488164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Ahrens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohrmann, G.F. Virology 229, 381-399, 1997
A;Title: The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis A;Reference number: Z17011; MUD:97271300; PMID:9126251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:P27086; EMBL:X62511; NID:g62749; PIDN:CAA44370.1; PID:g62750
C;Superfamily: metallothionein
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C;Species: Autographa californica nuclear polyhedrosis virus, AcMNPV
A;Note: dsDNA virus
C;Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 09-Jul-2004
C;Accession: C72850; A44003
R;Ayres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D.
Virology 202, 586-605, 1994
A;Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus.
A;Reference number: A72850; MuID:94303173; PMID:8030224
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C;Species: Orgyia pseudotsugata nuclear polyhedrosis virus, OpMNPV
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 11-May-2000
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A;Molecule type: DNA
A;Residues: 1-53 <AHR>
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Local Similarity 32.1%; Pred. No. 32;
les 9; Conservative 13; Mismatches /
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25 CAETGAVCVHS-DECCSGACSPVFNYCL 51
1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                   |::|:|:|:|:|CKCKNCRCRSCRKSCCSCCPAGGNNC 31
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A;Residues: 1-53 <AYR>
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A; Accession: JQ0030
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Best Local S
Matches 8
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A;Cross-references: UNIPROT:P41416; GB:L22358; NID:g510708; PIDN:AAA66633.1; FLU:gopyvid Virol. 66, 653-651, 1992
J. Virol. 66, 653-651, 1992
J. Virol. 66, 653-651, 1992
A;Title: Characterization of a baculovirus gene encoding a small conotoxinlike polypepti A;Reference number: A44003
A;Reference number: A44003
A;Accession: A44003
A;Accession: A44003
A;Accession: A44003
A;Residues: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-53 <ELD>
A;Cross-references: GB:L22858; NID:g510708; PIDN:AAA66633.1; PID:g559072
C;Genetics:
A;Gene: Ac-ctx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conditional like protein - Lymantria dispar nuclear polyhedrosis virus
C;Species: Lymantria dispar nuclear polyhedrosis virus, LdMNPV
C;Date: 29-0ct-1999 #sequence_revision 29-0ct-1999 #text_change 09-Jul-2004
C;Accession: T30499
R;Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; Rohr
A;Ticles: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantria of A;Reference number: Z20836; MUD:99124785; PMID:9887315
A;Accession: T30499
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-53 <KUZ>
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A;Residues: 1-63 <WEI>
A;Residues: 1-63 <WEI>
A;Cross-references: EMBL:X06749; NID:g63617; PIDN:CAA29924.1; PID:g63618
A;Note: part of this sequence, including the amino end of the mature protein, was confir
B;Fernando, L.P.; Andrews, G.K.
Gene 81, 177-183, 1989
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metallothionein - chicken
c;Species: Gallus gallus (chicken)
R;Recassion: A34958; Solf (chicken)
A,Title: Structure and expression of chicken metallothionein.
A,Reference number: A34958; MulD:89141100; EMID:2645390
A,Rocession: A34958
A,Status: preliminary; not compared with conceptual translation
A,Rolecule rype: mRNA
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A;Cross-references: UNIPROT:P09576
K;Wei, D.; Andrews, G.K.
Nucleic, Acids Res. 16, 537-553, 1988
A;Title: Molecular cloning of chicken metallothionein. Deduction of the A;Reference number: S01750; MUID:88124253; PMID:3340548
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49.2%; Score 59, DB 2; Length 53;
Best Local Similarity 32.1%; Pred. No. 32;
Matches 9; Conservative 13; Mismatches 4; Indels
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Pred. No. 32;
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Best Local Similarity 32.1%
Matches 9; Conservative
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C; Comment: Metallothioneins are a class of cysteine-rich, heavy-metal-binding proteins pr
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Cispecies: Meleagris gallopavo (common turkey)
Cispecies: Meleagris gallopavo (common turkey)
Cidete: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
CiAccesion: 833381; 833380; 818180
Rishartzer, K.L.; Kage, K.; Sobieski, R.J.; Andrews, G.K.
J. Mol. Bvol. 36, 255-262, 1993
A;Title: Bvolution of avian metallothionein: DNA sequence analyses of the turkey metallot
A;Reference number: 833378; MUID:93247066; PMID:8483164
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metallothionein - duck

C;Species: Anas platyrhynchos (domestic duck)

C;Date: 22-Jun-1990 #sequence revision 22-Jun-1990 #text_change 09-Jul-2004

C;Accession: A34620; B34620; B3154; JC5095

R;Lin, L.Y.; Huang, P.C.

B;Diohem. Biophys. Res. Commun. 186, 182-187, 1990

A;Title: Complete homology in metallothionein from two genera of ducks and their hybrids.

A;Reference number: A34620; MUID:90226357; PMID:2327997

A;Accession: A34620

A;Actatus: preliminary

A;Molecule type: protein
                                                                                  A.Molecule type: DNA
A.Residues: 1-63 <FE2>
R.MoCormick, C.C.; Fullmer, C.S.; Garvey, J.S.
Proc. Natl. Acad. Sci. U.S.A. 85, 309-313, 1988
A.Title: Amino acid sequence and comparative antigenicity of chicken metallothionein.
A.Reference number: A28113; MUID:88124831; PMID:2448773
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A.Title: Cloning and expression of an avian metallothionein-encoding gene. A.Reference number: JQ0030; MUID:90034180; PMID:2806910
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A;Accession: S33381
A;Accession: S33381
A;Accession: S33881
A;Residues: 1-63.cSHA>
A;Cross-references: UNIPROT:P09576; EMBL:X62513
A;Accession: S33380
A;Molecule type: mRNA
A;Residues: 15-57 cSH2>
A;Kesidues: 15-57 cSH2>
A;Cross-references: EMBL:X62514; NID:g64090; PIDN:CAA44372.1; PID:g64091
C;Genetics:
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C;Superfamily: metallothionein
F;1-63/Product: metallothionein #status experimental <MAT>
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Local Similarity 30.8%; Pred. No. 36,
es 8; Conservative 10; Mismatches
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49.2%; Score 59; DB
Best Local Similarity 30.8%; Pred. No. 36;
Matches 8; Conservative 10; Mismatches
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C;Superfamily: metallothionein
                                                                                                                                                                                                                                                                                                                         A,Molecule type: protein
A,Residues: 1-63 <MCC>
A,Experimental source: liver
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C;Accession: S28764
R;Rauch, U.; Karthikeyan, L.; Maurel, P.; Margolis, R.U.; Margolis, R.K.
Biol. Chem. 267, 19536-19547, 1992
A;Title: Cloning and primary structure of neurocan, a developmentally regulated, aggregat A;Reference number: S28764; MUID:92406907; PMID:1326557
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A; Residues: 1-1257 < RAU>
A; Rolecule type: mRNA
A; Residues: 1-1257 < RAU>
A; Cross-references : UNIPROT: P55067; EMBL: M97161; NID: 9205649; PIDN: AAC37679.1; PID: 920564
A; Cross-references: UNIPROT: P55067; EMBL: M97161; NID: 9205649; PIDN: AAC37679.1; PID: 920564
C; Superfamily: aggrecan; C-type lectin homology; Complement factor H repeat homology; EGI
C; Keywords: chondroitin sulfate proteoglycan; glycoprotein
F; 1-22/Domain: signal sequence #status predicted *AAT3-
F; 176-253/Domain: link protein repeat homology *LNK1>
F; 176-253/Domain: link protein repeat homology *LNK2>
F; 176-253/Domain: call attachment (R-G-D) motif
F; 953-984/Domain: EGF homology *CRP>
F; 1029-1149/Domain: C-type lectin homology *LNK3>
F; 1029-1149/Domain: C
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Siberan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft, Submitted to the Protein Sequence Database, March 1999
A;Reference number: Z15261
A;Accession: T04215
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F;121,339,737,167,1164/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;722,410/Binding site: chondroltin sulfate (Ser) (covalent) #status predicted
F;944/Binding site: chondroltin sulfate (Ser) (covalent) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein T5C23.110 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
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C;Date: 22-Nov-1993 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
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A;Residues: 1-419 <BEV>
A;Cross-references: UNIPROT:Q9T0D5; EMBL:AL049500
A;Experimental source: cultivar Columbia; BAC clone T5C23
C;Genetics:
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49.2%; Score 59; DB 2; Le
Best Local Similarity 28.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 12; Mismatches 6;
                                                                                      20 CKCKNCRCRSCRKSCCSCCPAGCNNC 45
                          1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
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A,Introns: 200/2; 241/2; 285/3
A,Note: T5C23.110
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A;Residues: 1-63 <LIN>
A;Cross-references: UNIPROT:P09576
A;Experimental source: Anas platyrhynchos (domestic duck)
A;Accession: B34620
A;Status: preliminary
A;Molecule type: protein
A;Experimental source: Anas platyrhynchos x Cairina moschata (domestic duck x muscovy du A;Experimental source: Anas platyrhynchos y Cairina moschata (domestic duck x muscovy du A;Elin, L.Y; Luu, L.F; Tam, M.F; Huang, P.C.; Vestling, M.; Fenselau, C.
Biochim. Biophys. Acta 1041, 31-35, 1990
A;Title: Primary sequence of duck metallothionein.
A;Reference number: S13154; MUID:91027866; PMID:2223844
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A;Reference number: JC5094; MUID:97075914; PMID:8918237

A;Accession: JC5095

A;Molecule type: mRNA

A;Residues: 1-63 (LEE>

A;Cross-references: GB:U34231; NID:g1000299; PIDN:AAC60048.1; PID:g1000300

A;Experimental source: strain tsai ya duck
C;Comment: This protein has a high metal binding capacity and sulfur content.
C;Genetics:
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C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 09-Jul-2004
C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 09-Jul-2004
C;Accession: C34620, JC5094
R;Lin, L.Y.; Huang, P.C.
Biochem. Biophys. Res. Commun. 168, 182-187, 1990
A;Title: Complete homology in metallothionein from two genera of ducks and the A;Reference number: A34620, MUID:90226357; PMID:2327997
A;Accession: C34620
A;Accession: 
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Gene 176, 85-92, 1996
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R;Lee, Y.J.; Chen, Y.P.; Wang, S.H.; Chow, W.Y.; Lin, L.Y.
Gene 176, 85-92, 1996
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C;Superfamily: metallothionein
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C34620
metallothionein - muscovy duck
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C;Superfamily: metallothionein
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Best Local Similarity 30.8
Matches 8; Conservative
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A,Molecule type: protein
A,Residues: 1-63 <LI3>
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A;Title: Relationships between the gene and protein structure in human complement compone
A;Reference number: I52400; MUID:89118250; PMID:3219351
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Query Match

Best Local Similarity 26.3%; Pred. No. 1.8e+02;
Matches 10; Conservative 12; Mismatches 3;
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A;Status: translated from GB/EMBL/DDBJ
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C;Species: Mus musculus (house mouse)
C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: $52781
R;Rauch, U.; Forsberg, N.; Kulbe, G.; Arnoid-Ammer, I.; Faessler, R.
submitted to the EMBL Data Library, February 1995
A;Reference number: $52781
A;Recession: $52781
A;Recession: $52781
A;Recession: $52781
A;Recession: $52781
A;Recession: $52781
A;Recession: $52781
A;Residues: preliminary
A;Molecule type: mRNA
A;Residues: 1-1268 cRAU>
A;Cross-references: UNIPROT: P55066; EMBL: X84727; NID: g758629; PIDN: CAA59216.1; PID: g7586
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EC
F;176-253/Domain: link protein repeat homology <LNKL>
F;274-355/Domain: link protein repeat homology <LNKL>
F;264-995/Domain: C-type lectin homology <LNKS>
F;1040-1160/Domain: C-type lectin homology <LNKS>
F;1040-1160/Domain: C-type lectin homology <LNKS>
F;1167-1223/Domain: C-type lectin ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein F42C5.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20.8ep-1999 #sequence_revision 20.5ep-1999 #text_change 09-Jul-2004
C;Caccasion: T16342
R;Du, Z.
R;Du, Z,
R;Du, Z.
R
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C;Species: Homo sapiens (man)
C;Date: 27-Nov-1985 #sequence_revision 17-Nov-2000 #text_change 09-Jul-2004
C;Accession: A59363, I52400; A91029; A94019, S68647; A59364; A03208
R;Marzaitti, D.; Eggertsen, G.; Fey, G.H.; Stanley, K.K.
unpublished results, 1988, cited by GenBank
A;Bescription: Relationships between the gene and protein structure in human complement
A;Reference number: A59363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cross-references: UNIPROT:P02748; GB:X02176; NID:929580; PIDN:CAA26117.1; PID:929581; Marazziti, D.; Eggertsen, G.; Fey, G.H.; Stanley, K.K.
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Query Match

49.2%; Score 59; DB 2; Length 1268;
Best Local Similarity 25.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 12; Mismatches 6; Indels
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A;Molecule type: mRNA
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tes 8; Conserv
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A; Molecule type: mRNA
A; Residues: 2-12, 'X', 14-16, 'X', 18-42, 'R', 44-313, 315-416, 'P', 418-559 <DIS>
A; Cross-references: GB: K02766; NID: g1/9725; PIDN: AAA51889.1; PID: g1/9726
R; Lengweiler, S.; Schaller, J.; Rickli, E.E.
FRBS Lett. 380, 8-12, 1996
A; Title: Identification of disulfide bonds in the ninth component (C9) of human complement
A; Reference number: S68647; MUID: 96181657; PMID: 8603752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Molecule type: protein
A,Residues: 34-47;52-59;69-87,'X',89-83,'T',94-98;106-113;118-131;136-145;180-181,'X',18:
R;Witze.Schlomp, K.; Hobart, M.J.; Fernie, B.A.; Orren, A.; Wurzner, R.; Rittner, C.; Kaulmunogenetics 48, 144-147, 1998
A;Title: Heterogeneity in the genetic basis of human complement C9 deficiency.
A,Reference number: A53364; MUID:98298010; PMID:9634479
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A;Residues: 'S',1-313,315-559 <STA>
A;Cross-references: GB:X02176; NID:929580
R;DiScipio, R.G.; Gehring, M.R.; Podack, E.R.; Kan, C.C.; Hugli, T.E.; Fey, G.H.
Proc. Natl. Acad. Sci. U.S.A. 81, 7298-7302, 1984
A;Title: Nucleotide sequence of cDNA and derived amino acid sequence of human complement
A;Reference number: A94019; MUID:85063778; PMID:6095282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.Gene: GDB:C9
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A, Molecule type: DNA
A, Residues: 27-559 < MIT>
A, Cross-references: GB: Y08545; NID: g1834472; PIDN: CAA69849.1; PID: g2258128
A, Experimental source: macronuclear; tissue type blood; cell type lymphocyte
R; Moffsteenge, J.; Blommers, M.; Hess, D.; Furmanek, A.; Miroshnichenko, O.
A; Ettle: The four terminal components of the complement system are C-mannosyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complex: monomer in plasma; 10 to 16 chain multimer in transmembrane form
A Molecule type: DNA
A; Residues: 62-159 < MAR2>
A; Residues: 62-159 < MAR2>
A; Cross-references: 63-102833; NID:g179727; PIDN: AAA51890.1; PID:g179728
B; Stanley, K.K.; Kocher, H.P.; Luzio, J.P.; Jackson, P.; Tschopp, J.
EMBO J. 4, 375-382, 1985
A; Title: The sequence and topology of human complement component C9.
A; Reference number: A91029; MUID:85257464; PMID:4018030
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omega-conotoxin MVIIA [validated] - cone shell (Conus magus)
C.Species: Conus magus (magus cone)
C.Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C.Accession: JH7000; C60133; A34115
R.Hillyard, D.R.: Monje, V.D.; Mintz, I.M.; Bean, B.P.; Nadasdi, L.; Ramachandran, J.; M)
Neuron 9, 69-77, 1992
A;Title: A new conus peptide ligand for mammalian presynaptic Ca2+ channels.
A;Reference number: JH0699; MUID:92337922; PMID:1352986
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A.Status: preliminary
A.Molecule type: nucleic acid
A.Residues: 1-3562 c8H1>
A.Residues: 1-3562 c8H1>
A.Cross-references: UNIPROT: Q90953; GB:D13542; NID: g391643; PIDN: BAA02742.1; PID: g391644
A.Experimental source: stage 22-23 developing limb buds
A.Note: sequence extracted from NCBL backbone (NCBIN: 134456, NCBIP: 134457)
C.Superfamily: chicken chondroitin sulfate proteoglycan PG-M core protein; C-type lectin
F:166-243/Domain: link protein repeat homology cLNK1>
F:264-345/Domain: link protein repeat homology cLNK2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C,Accession: A47171
R,Shinomura, T.; Nishida, Y.; Ito, K.; Kimata, K.
J. Biol. Chem. 268, 14461-14469, 1993
A,Title: cDNA cloning of PG-M, a large chondroitin sulfate proteoglycan expressed during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chondroitin sulfate proteoglycan PG-M core protein - chicken
C;Species: Gallus gallus (chicken)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
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R;Reaume, A.G.; Conlon, R.A.; Zirngibl, R.; Yamaguchi, T.P.; Rossant, J. Dev. Biol. 154, 377-387, 1992
A;Title: Expression analysis of a Notch homologue in the mouse embryo.
A;Reference number: A48825; MUID:93050801; PMID:1426644
                                                                                                                                                    A:Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA A;Residues: 1-861 **REA> A;Experimental source: embryo A;Experimental source: embryo A;Note: sequence extracted from NCBI backbone (NCBIP:119144) C;Superfamily: Notch protein; ankyrin repeat homology; EGF homology *F;26-57/Domain: EGF homology *EGXI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 861;
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F;3258-3237/Domain: EGF homology <EGF2
F;334-3454/Domain: C-type lectin homology <LCH>
F;3461-3517/Domain: complement factor H repeat homology <FHD>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48.3%; Score 58; DB 2; 20.8%; Pred. No. 2.6e+02;
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Best Local Similarity
Matches 5; Conserva
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Best Local Similarity
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                                                                                                                                       A; Accession: A48825
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C;Comment: This protein has many EGF repeats and lin-12/Notch repeats.
C;Comment: This protein is one of the neurogenic proteins controlling the decision betwe C;Cuperfamily: Notch protein; anivyrin repeat homology; EGF homology eBGP>
F;27-58/Domain: EGF homology eBGP>
F;73-104/Domain: EGF homology eBGP>
F;151-185/Domain: EGF homology eBGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A Molecule type: mRNA
KResidues: 1-387 «LAR»
A;Cross-references: UNIPROT:Q01705; EMBL:X68278; NID:g287987; PIDN:CAA48339.1; PID:g2879
A;Experimental source: embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nichternate names: Notch howelog
C;Species: Mus musculus (house mouse)
C;Date: 21-Jan-1994 #sequence revision 05-Jan-1996 #text_change 16-Aug-2004
C;Cocession: B49175; PH1569; $32109
R;Lardelli, M.; Lendahl, U.
Exp. Cell Res. 204, 364.372, 1993
A;Title: Motch A and Motch B--two mouse Notch homologues coexpressed in a wide variety A;Reference number: A49175; MUID:93178563; PMID:8440332
A;Reference number: B49175
A;Status: preliminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:P15787
C;Superfamily: metallothionein
C;Keywords: blocked amino end
F;1/Modified site: blocked amino end (Met) (probably acetylated) #status experimental
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                                                                                                                                                                                                                                                  metallothionein 2 - pigeon

(Species: Columba livia (domestic pigeon)

(Species: Columba livia (domestic pigeon)

(Species: Columba livia (domestic pigeon)

(Species: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004

(Spacession: S08191

R;iin, L.Y.; Lin, W.C.; Huang, P.C.

Biochim. Biophys. Acta 1037, 248-255, 1990

A;ritle: Pigeon metallothonein consists of two species.

A;Reference number: S08190; MUD:90167121; PMID:2407296

A;Molecule type: protein

A;Residues: 1-63 < Lin>
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Notch homolog Motch protein - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 16-Aug-2004
C;Accession: A48825
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Pred. No. 45;
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20.8%; Pred. No. 1.5e+02;
tive 14; Mismatches 5; Indels
                                                                             ::::::|::|::|::|
CVPTEPCEDAEDDCGNDFQCSTGRCIKMRLRCNGDNDC 125
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                                         -SD----
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B49175
Motch A protein - mouse (fragment)
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Matches 10; Conserva
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es 5; Conserv
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Best Local S:
Matches 5
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A;Residues: 1-1531 <NAK>
A;Cross-references: UNIPROT:O88279; EMBL:ABO11530; NID:g3449289; PIDN:BAA32460.1; PID:g34
A;Experimental source: strain Sprague-Dawley; brain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               multiple EGF-like motifs h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 21-Jul-2003
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N;Alternate names: MEGF4 protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Dec.1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
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C,Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
                                                                                                                                                   Gaps
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A;Title: Identification of high-molecular-weight proteins with multiple A;Reference number: 214126; MUID:98360089; PMID:9693030
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                                                                             Length 60;
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Similarity 26.1%; Score 57; DB 2; Length 122
Similarity 26.1%; Pred. No. 4.1e+02;
6; Conservative 12; Mismatches 5; Indels
                                                                                                                                                Indels
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A;Title: Jagged: a mammalian ligand that activates Notchl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Reference number: A56136; MUID:95211842; PMID:7697721
A;Accession: A56136
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Pred. No. 4.8e+02;
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                                                                  47.5%; Score 57; DB 26.9%; Pred. No. 54; tive 12; Mismatches
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F;492-523/Domain: EGF homology <EGF>
F;634-665/Domain: EGF homology <EGF2>
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illarity 30.4%;
Conservative 1
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A,Residues: 1-1220 <LIN>
A,Cross-references: GB:L38483
                                   Query Match
Best Local Similarity
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Best Local Similarity
Matches 6; Conserv
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A; Residues: 1-25 cHIL>
A; Cross-references: UNIPROT: P05484
R; Olivera, B.M.; Gray, W.R.; Zeikus, R.; McIntosh, J.M.; Varga, J.; Rivier, J.; de Santc Science 230, 1338-1343, 1985
A; Title: Peptide neurotoxins from fish-hunting cone snails.
A; Ritle: Peptide neurotoxins from fish-hunting cone snails.
A; Accession: C6013
A; Molecule type: protein
A; Residues: 1-25 coll.>
A; Reference number: A34115; MUID:87299637; PMID:2441741
A; Rontents: annotation anotation by (1) H-NMR, residues 1-25
A; Molesule to the Brookhaven Protein Data Bank, August 1996
A; Contents: annotation; conformation by (1) H-NMR
A; Reference number: A56649; PMID:97070382; PMID:8913308
A; Contents: annotation; conformation by (1) H-NMR
A; Reference number: A56619; MUID:97070382; PMID:8913308
A; Contents: annotation; conformation by (1) H-NMR
B; Rontents: annotation; Conformation by (1) H-NMR
B; Rontents: annotation; Conformation by (1) H-NMR
B; Rontents: annotation; Conformation Data Bank, April 1995
A; Mille: Canada Bank, April 1995
A; Rontents: annotation; Conformation Data Bank, April 1995
A; Rontents: annotation; Conformation Data Bank, April 1995
A; Rontents: Accessing annotation Data Bank, April 1995
A; Rontents: Annotation Data Bank, April 1995
A; Rontents: Annotation Bank, April Bank, 
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A; Contents: annotation; conformation by (1) H-NMR
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Biochim. Biophys. Acta 1089, 407-410, 1991
A;Title: Elucidation of cDNA sequences for metallothioneins from rainbow trout, stone lo A;Reference number: S16996; MUID:91316146; PMID:1859844
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Residues: 1-60 <KI3>
Cross references: UNIPROT:P25127; EMBL:X70042; NID:g62782; PIDN:CAA49636.1; PID:g62783
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metallothionein - northern pike
C;Species: Box lucius (northern pike)
C;Species: Esox lucius (northern pike)
C;Date: 20-Feb-1995 #sequence revision 20-Feb-1995 #text_change 09-Jul-2004
C;Date: 20-Feb-1995 #sequence revision 20-Feb-1995 #text_change 09-Jul-2004
C;Date: 20-Feb-1995 #sequence revision 231723
R;Kille: P.; Ray, J.; Sweeney, G.E.
Biochim: Biophys. Acta 1216, 55-64, 1993
Biochim: Biophys. Acta 1216, 55-64, 1993
A;Title: Analysis of regulatory elements flanking metallothionein genes in Cd-tolerant
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R;Kohno, T.; Kim, J.I.; Kobayashi, K.; Kodera, Y.; Maeda, T.; Sato, K.
Biochemistry 34, 10256-10265, 1995
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C,Keywords: chelation; metal binding; metal-thiolate cluster
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Matches 6; Conservative
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A; Residues: 1-60: < KIL>
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Query Match

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predicted <SIG>
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A;Residues: 1-4,'E',6-60 <KI2>
A;Cross-references: EMBL:X59393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
les 7; Conserv
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Matches 11; Conserv
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Best Local S
Matches 7
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Residues: 1-1810 <JON>
Cross-references: UNIPROT:Q90824; GB:J04519; NID:g211717; PIDN:AAA48745.1; PID:g211718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecule type: mRNA

./Residues: 1-1044,1318-1810 <JO2>

./Cross-references: GB.J04519

./Spring, J.; Beck, K.; Chiquet-Ehrismann, R.

ell 59, 325-334, 1989

./Title: Two contrary functions of tenascin: dissection of the active sites by recombina

./Aference number: A33379; MUID:90030407; PMID:2478295

./Accession: A33379

./Status: preliminary; nucleic acid sequence not shown
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;Residues: 1-204,'G',206-221,'A',223-380,'D',382-386,'H',388-444,'HN',447-450,'V',452-5
;Reserences: GB:M23121; NID:g212746; PIDN:AAA49086.1; PID:g212749
;Accession: B33379
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A;Residues: 1-204,'G',206-221,'A',223-380,'D',382-386,'H',388-444,'HN',447-450,'V',452-5
A;Accession: C33379
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C; Species: Gallus gallus (chicken)
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C; Accession: A32230; B33379; B3379; S01292; A30903
C; Accession: A2230; B32330; B33379; B3379; S01292; A30903
R; Jones, F.S.; Hoffman, S.; Cunningham, B.A.; Edelman, G.M.
Proc. Natl. Acad. Sci. U.S.A. 86, 1905-1909, 1989
Proc. Natl. Acad. Sci. U.S.A. 86, 1905-1909, 1989
A; Jtille: A detailed structural model of cytotactin: protein homologies, alternative RNA
A; Reference number: A32230; MUID:89184536; PMID:2467292
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C;Keywords: alternative splicing; calcium binding; cell adhesion; duplication; extracell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
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A;Cross-references: EMBL:X08030
K;Sulston, J.; Du, Z.; Thomas, K.; Wilson, R.; Hillier, L.; Staden, R.; Halloran, N.; awkins, T.; Ainscough, R.; Waterston, R. submitted to the EMBL Data Library, October 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pearson, C.A.; Pearson, D.; Shibahara, S.; Hofsteenge, J.; Chiquet-Ehrismann, R. BO J. 7, 2977-2982, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:P30652; EMBL:Z11126; NID:g6967; PID:g6973 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19;
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
47.1%; Score 56.5; DB 2; Length 217;
Best Local Similarity 21.4%; Pred. No. 1.4e+02;
Matches 9; Conservative 10; Mismatches 4; Indels 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N,Alternate names: cytotactin; hexabrachion N;Contains: tenascin 190K; tenascin 200K
                                                                                                                                                                                                                                                                                                                                                                A;Introns: 26/3; 68/3; 99/3; 143/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tenascin precursor - chicken
                                                                                                                                                                                         A;Accession: S23244
A;Molecule type: DNA
A;Residues: 1-217 <SUL>
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metallothionein - stone loach
C;Species: Noemachallus barbatulus (stone loach)
C;Dacession: S38335, S17176; S15505
R;Kille, P.; Kay, J.; Sweeney, G.E.
Biochim. Biophys. Acta 1216, 55-64, 1993
A;Fitle: Analysis of regulatory elements flanking metallothionein genes in Cd-tolerant fine A;Reference number: S38334; MUID:94032489; PMID:8218416
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Biochim. Biophys. Acta 1089, 407-410, 1991
A;Title: Elucidation of cDNA sequences for metallothioneins from rainbow trout, stone los
A;Reference number: S16996; MUID:91316146; PMID:1859844
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Mech. Dev. 35, 143-151, 1991
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C;Species: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13;
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                                                                                                                                                                                                                                                                                                                                                    F)1046-1128/Domain: fibronectin type III repeat homology cFN3F> F)1219/Domain: fibronectin type III repeat homology cFN3G> F)1228-1310/Domain: fibronectin type III repeat homology cFN3G> F)1318-1399/Domain: fibronectin type III repeat homology cFN3I> F)1487/Domain: fibronectin type III repeat homology cFN3I> F)445-1575/Domain: fibronectin type III repeat homology cFN3I> F)1495-1575/Domain: fibronectin type III repeat homology cFN3G> F)1590-1798/Domain: fibronectin type III repeat homology cFN3K> F)1590-1798/Domain: fibronectin type III repeat homology cFN3K> F)1590-1798/Domain: fibrinogen beta/gamma homology cFN6C>
                                 723-249/Domain: EGF homology <EGF1>
7316-342/Domain: EGF homology <EGF1>
759-673/Domain: EGF homology <EGF1>
769-673/Domain: EGF homology <EGF1>
769-673/Domain: Eibronectin type III repeat homology <EN3B>
777-859-679/Domain: Eibronectin type III repeat homology <EN3B>
778-867-949/Domain: Eibronectin type III repeat homology <EN3C>
7665-949/Domain: Eibronectin type III repeat homology <EN3D>
777-1037/Domain: Eibronectin type III repeat homology <EN3D>
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C;Superfamily: metallothionein
C;Keywords: chelation; metal binding; metal-thiolate cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F,1734-1747/Domain: calcium binding #status predicted <CAB>
34-1810/Product: tenascin 230K #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  353 GNGRCENGLCVCHEGFVGDDCSQKRCPKTCNNRGRCV 389
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A;Residues: 1-60 <KIL>
A;Cross-references: UNIPROT:P25128; EMBL:X70043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46.7%; Score 56; DB 26.9%; Pred. No. 67;
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A;Cross-references: UNIPROT:018238; EMBL:US8760; NID:g1330384; PID:g1330389; PIDN:AAB00731
A;Experimental squrce: strain Bristol N2; clone C27A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-198 <WIL>
A;Cross-references: UNIPROT:Q22179; EMBL:Z78200; PIDN:CAB01583.1; GSPDB:GN00023; CESP:T0;
A;Experimental source: clone T04H1
                                                                                                                                                                                                                                                                                hypothetical protein C27A2.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T15651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein T04H1.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24476
R;Harris, B
submitted to the EMBL Data Library, August 1996
A;Reference number: Z19896
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A:Introns: 33/1; 75/1; 120/1; 159/1
F:38-74/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F:77-115/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F:121-158/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F:162-197/Domain: LDL receptor ligand-binding repeat homology <LDL3>
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46.7%; Score 56; DB 2; Length 188
Best Local Similarity 23.1%; Pred. No. 1.4e+02;
Matches 6; Conservative 12; Mismatches 8; Indels
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24.2%; Pred. No. 1.5e+02;
Live 13; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, May 1996
A;Description: The sequence of C. elegans cosmid C27A2.
A;Reference number: Z18382
                           ed. No. 1.4e+02;
Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-188 <NHA>
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A;Molecule type: DNA
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93 CCCCRRCCTCCRTCCTRCCTCCRPC 118
                                                                                                                                126 KVEEECCGGAKDDCCGGHEHEHEVC 150
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                                                                                                  2 XIXNQXCXQXLDDCCSXXCNXXNXC
                           Pred.
  24.0%; Pre. 13;
                                                   Conservative
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Best Local Similarity
Matches 8; Conserva
                     Best Local Similarity
Matches 6; Conser
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A; Introns: 19/3; 91/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: CESP:T04H1.6
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A;Title: A cluster of four genes selectively expressed in the male germ line of Drosophila, Reference number: A56565; MUD:92102953; PMID:1684716
A;Rocesaion: 82575
A;Accesaion: 825775
A;Rolecule type: DNA
A;Residues: 1-68 «XUH»
A;Cross-references: UNIPROT:001645; EMBL:X67703; NID:g11072; PIDN:CAA47940.1; PID:g11076
C;Genetics:
A;Acene: Mst84Dd
A;Acene: Mst84Dd
A;Cross-references: FlyBase:FBgn0004175
A;Acene: Mst84Dd
A;Cross-references: FlyBase:FBgn0004175
C;Superfamily: fruit fly testis-specific protein
C;Reywords: spermatogenesis; tandem repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-164 <WIL>
A;Cross-references: UNIPROT:Q22048; EMBL:Z66499; PIDN:CAA91301.1; GSPDB:GN00020; CESP:TC
A;Experimental source: clone T01B7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein UUI01 [imported] - Ureaplasma urealyticum c;Species: Ureaplasma urealyticum c;Species: Ureaplasma urealyticum c;Species: Ureaplasma urealyticum C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000 C;Accession: H82933 R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H. submitted to GenBank, February 2000 A;Reference number: AB2870 A;Reference number: AB2870 A;Accession: H82933
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A;Molecule type: DNA
A;Residues: 1-188 <GLA>
A;Cross-references: GB:AE002110; GB:AF222894; NID:g6899051; PIDN:AAF30507.1; GSPDB:GN001
A;Experimental source: serovar 3; blovar 1
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hypothetical protein TolB7.8 - Caenorhabditis elegans
hypothetical protein TolB7.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 115-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24272
R;Sims, M.
R;Sims, M.
Ewbitted to the EMBL Data Library, October 1995
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Pred. No. 1.38+02;
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                                                                                                                                                                                                                                                                                                                                                                                  2; Length 68;
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A;Accession: T24272
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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23.1%; Pred. No. 1...
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Best Local Similarity 23.11
Matches 6; Conservative
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Matches 6; Conserv
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A;Introns: 20/3; 90/2
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A; Reference number: S54451
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Best Local Similarity
Matches 6; Conserv
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N.Alternate names: delta-like dlk homeotic protein; pref-1
C;Species: Mus musculus (house mouse)
C;Date: 12-Apr-1995 #sequence revision 12-Apr-1995 #text_change 09-Jul-2004
C;Accesion: A54785; A54849; A40746; S21585
R;Smas, C.M.; Green, D.; Sul, H.S.
Biochemistry 33, 9257-9265, 1994
A;Title: Structural characterization and alternate splicing of the gene encoding the pre A;Atters chumber: A54785; MUID:94325292; PMID:7519443
A;Accession: A54785
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
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A; Residues: 1-78'G', 80-249, 'P', 251-319,'CWAPWESSFSTSAKPGCPTCATTCFARRRTSCCSITAARSWRSISS
A; Residues: 1-78'G', 80-249, 'P', 251-319,'CWAPWESSFSTSAKPGCPTCATTCFARRRTSCCSITAARSWRSISS
A; Cross-references: 68:L12721; NID:g309902; PIDN:AAA37175.1; PID:g309093
A; Note: sequence extracted from NCBI backbone (NCBIN:132685, NCBIP:132713)
A; Note: this sequence appears to have been corrected in reference A45484
C; Reywords: alternative splicing; tandem repeat; transmembrane protein
F; 1-385/Product: preadipocyte factor 1; precursor splice form A #status predicted
F; 1-230, 304-385/Product: preadipocyte factor 1 precursor splice form C #status predicted
F; 1-230, 304-385/Product: preadipocyte factor 1 precursor splice form C2 #status predicted
F; 1-230, 304-385/Product: preadipocyte factor 1 precursor splice form C2 #status predicted
F; 1-210, 304-385/Product: preadipocyte factor 1 precursor splice form D #status predicted
homeotic protein dlk - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 15-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S53718
R;Lee, Y.L.; Helman, L.; Hoffman, T.; Laborda, J.
R;Lee, Y.L.; Helman, L.; Hoffman, T.; Laborda, J.
A;Liche, M.C., M.
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A; Residues: 1-78, 'G', 80-343, 'TF', 346-385 < LAB>
A; Residues: 1-78, 'G', 80-343, 'TF', 346-385 < LAB>
A; Croser-references: EMBL: 212171; NID: 950716; PIDN: CAA78162.1; PID: 950717
A; Note: sequence extracted from NCBI backbone (NCBIP: 125744)
A; Note: species designations for this sequence report and for B45484 originally were tra
R; Smas, C.M.; Sul, H.S.
A; 725-734, 1993
A; 716-17, a protein containing EGF-like repeats, inhibits adipocyte differentiati
A; Reference number: A40746; MUID: 93272313; PMID: 8500166
A; Accession: A40746.
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A;Residues: 1-385 <LEE.
A;Cross-references: UNIPROT:Q09163; EMBL:U15980; NID:g562107; PIDN:AAB60495.1; PID:g5621
C;Superfamily: preadipocyte factor 1; EGF homology
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A;Cross-references: UNIPROT:Q09163; GB:S71340
A;Cross-references: UNIPROT:Q09163; GB:S71340
A;Cross-references: UNIPROT:Q09163; GB:S71340
J. Biol. Chem. 268, 3817-3820, 1993
A;Title: dlk, a putative mammalian homeotic gene differentially expressed in small cell
A;Reference number: A45484; MUID:93179372; PMID:8095043
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F:214-246/Domain: EGF homology <EGX1>
F:303-332/Domain: transmembrane #status predicted <TM1>
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19.2%; Pred. No. 2.3e+02;
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Best Local Similarity
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F;1-210,306-385/Product: preadipocyte factor 1 precursor splice form D2 #status predictec F;92-124/Domain: EGF homology <EGF> F;214-246/Domain: EGF homology <EGF1>
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A;Cross-references: UNIPROT:P90850; EMBL:Z81070; PIDN:CAB03007.1; GSPDB:GN00019; CESP:F24
A;Experimental source: clone F26E4
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NiAlternate names: protein YM9583.05c; protein YMR080c; UPF1 protein
C;Species: Saccharomyces cerevisiae
C;Accession: S23408; A44388; S54455
N;Accession: S23408; A44388; S54455
N;Altamura, N; Groudinsky, O; Dujardin, G; Slonimski, P.P.
A;Title: NAM7 nuclear gene encodes a novel member of a family of helicases with a Zn-ligs A;Reference number: S23408
A;Reference number: S23408
A;Reference number: S23408
A;Reference number: S23408
A;Reference number: MALTA
A;Reference number: MAL
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A;Introns: 23/3; 67/1; 108/1; 134/1; 149/2; 179/2; 232/2; 261/2; 306/2; 334/2; 419/2; 466
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21421
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A,Residues: 1-971 <LEE>
A;Cross-roses: GB:M76659; NID:g173141; PIDN:AAA35197.1; PID:g173142
A;Cross-roses; S.; Bowman, S.
S;Gentles, S.; Bowman, S.
submitted to the EMBL Data Library, May 1995
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A;Residudes: 1-971 cGRs.
A;Crosa-references: EMBL:Z49259; NID:g807956; PID:g807962; MIPS:YMR080c
A;Experimental source: strain AB972
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                                                                                                                                                                                                                  Length 385
                                                                                                                                                                                                                                                                                                                                5; Indels
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                                                                                                                                                                                                                  Query Match 46.7%; Score 56; DB 2; 1
Best Local Similarity 19.2%; Pred. No. 2.3e+02;
Matches 5; Conservative 16; Mismatches 5
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70 CSVRTHTCCENRDDDCTVPILGDHLC 95
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4 XNQXCXQXLDDCCSXXCNXXNXCV 27
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1280 DCDTRIDECYRGRCSNNSTCV 1300
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A; Accession: T20968
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Matches 6; Conserv
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         homeotic protein lin-12 precursor - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 16-Aug-2004
C;Accession: 806434; A24769
R;Yochem, J.; Weston, K.; Greenwald, I.
Nature 335, 547-550, 1988
A;Title: The Caenorhabditis elegans lin-12 gene encodes a transmembrane protein with ove
A;Reference number: 806434; MUID:88334747; PMID:3419531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-1429 <YOC>
A;Cross-references: UNIPROT:P14585; EMBL:M12069; NID:g156357; PIDN:AAA70191.1; PID:g1563
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C'Species: Rattus norvegicus (Norway rat)
C'Joate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C'Accession: T13953
R'Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs A;Reference number: Z14126; MUID:98360089; PMID:9693030
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                    A/Gene: SGD.NAM7; UPF1
A/Gross-references: SGD.SO004685; MIPS.YMR080c
A/Map position: 138
C,Keywords: GTP binding; mitochondrion; nucleotide binding; nucleus; P-loop
E;430-437/Region: nucleotide-binding motif A (P-loop)
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A; Residues: 173-712 <GRE>
G; Genetics:
A:Introns: 50/2; 90/1; 109/1; 172/3; 545/1; 589/2; 632/2; 1273/3; 1389/3
G; Superfamily: antyrin: repeat homology; EGF homology
C; Superfamily: antyrin: repeat homology; EGF homology
C; Keywords: glycoprotein: transmembrane protein
F; 254-284/Domain: EGF homology <EGFP>
F; 507-504 (Domain: EGF homology <EGFP>
F; 507-504 (Domain: EGF homology <EGFP>
F; 509-931/Domain: transmembrane #status predicted <TWM>
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Cell 43, 583-590, 1985
A,Reference number: A24769, MUID:86079540, PMID:3000611
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A;Molecule type: mRNA
A;Residues: 1-1523 <NAK>
                                                                                                                                                                                                                                                                                                                                                               65 CGIDSAKCVIKCNSCKKWFCNTKNG 89
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Best Local Similarity
Matches 5; Conserv
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T13953
MEGF5 protein - rat
C, Genetics:
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A;Cross-references: UNIPROT:088280; EMBL:AB011531; NID:g3449291; PIDN:BAA32461.1; PID:g34
C;Genetics:
A;Gene: MEGF5
C;Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein re
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A;Molecule type: DNA
A;Residues: 1-2610 <WIL>
A;Cross-references: UNIPROT:Q19482; EMBL:Z78013; PIDN:CAB01427.1; GSPDB:GN00023; CESP:F1:
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C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 16-Aug-2004
C;Accession: A00767; A60719
R;Maraganore, J.M.; Heinrikson, R.L.
J. Biol. Chem. 261, 4797-4804, 1986
A;Title: The lysine-49 phospholipase A-2 from the venom of Agkistrodon piscivorus piscivc A;Reference number: A00767; MUID:86168190; PMID:3082870
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A;Introns: 169/2; 217/3; 239/3; 284/3; 515/2; 550/3; 738/3; 810/1; 838/3; 890/2; 977/1; 1
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A,Residues: 1-121 CMRN-
A,Cross-references: UNIPROT:P04361
R,van den Bergh, C.J.; Slotboom, A.J.; Verheij, H.M.; de Haas, G.H.
J. Cell. Blochem. 39, 379-399, 1899
A,Fitle: The role of Asp-49 and other conserved amino acids in phospholipases A2 and thei
A,Reference number: A60719; MUID:89255682; PMID:2722967
A,Mocession: A60719
A,Molecule type: protein
A,Residues: 1-8 <VAN>
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A;Reference number: 220187
A;Reference number: 220187
A;Accession: T26278
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-2610 <WIZ>
A;Coss.references: EMBL:278018; PIDN:CAB01449.1; GSPDB:GN00023; CESP:F15B9.7
A;Experimental source: clone W07G4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein F15B9.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20968; T26278
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Local Similarity 29.2%; Pred. No. 5.9e+02;
les 7; Conservative 11; Mismatches 6; Indels
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alpha-amylase inhibitor precursor (clone pUP-44) - barley
                                                  Query Match
Best Local Similarity 36.0%
Matches 9; Conservative
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R; Holland, D.R.; Clancy, L.L.; Muchmore, S.W.; Ryde, T.J.; Einspahr, H.M.; Finzel, B.C.;
J. Biol. Chem. 265, 17649-17656, 1990
A; Title: The crystal structure of a lysine 49 phospholipase A-2 from the venom of the cc
A; Reference number: A33221; WUID:9100322; PMID:3120215
A; Contents: annotation; X-ray crystallography, 2.0 angstroms
C; Comment: This homolog of phospholipase A2 lacks enzymatic activity because a Lys-48 re
C; Superfamily: Phospholipase A2
C; Keywords: venom
F; 26-115, 28-44, 43-95, 49-121, 50-88, 57-81, 75-86/Disulfide bonds: #status experimental
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A;Experimental source: strain 972h-; cosmid c1450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C'Species: Agkistrodon contortrix contortrix (southern copperhead)
C'Date: 15-Reb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C'Accession: S68429; S74296
R'de Araujo, H.S.S.; White, S.P.; Ownby, C.L.
Arch. Biochem. Biophys. 326, 21-30, 1996
A'fitle: CDNA cloning and sequence analysis of a lysine-49 phospholipase A(2) myotoxin A;Reference number: S68429; WUID:96154243; PMID:8579368
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A; Note: the authors confirmed the identity of the purified protein by composition and R; Holland, D.R. "Clancy, L.L.; Muchmore, S.W.; Rydel, T.J.; Einspahr, H.M.; Finzel, B. submitted to the Brookhaven Protein Data Bank, October 1991
A; Reference number: A51920; PDB:1PPA
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C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T40999
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Volckaert, G.
Bubmitted to the EMBL Data Library, March 1999
A;Reference number: 221962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | :::|::| :::| 43 CCFVHKCCYKKLTDCNHKTDRYSYSWKNKAIICEEKNPCL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CXIXNQXCXQXLDDC-----CSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------ CSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 55.5; DB 1;
; Pred. No. 1.2e+02;
15; Mismatches 4;
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Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-571 <LYN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              myotoxin precursor - southern copperhead
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46.2%;
20.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 20.0
Matches 8; Conservative
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A;Residues: 1-137 <DEA>
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A; Introns: 4/3
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N'Alternate names: C3b/C4b inactivator factor I
C;Species: Xenopus laevis (African clawed frog)
C;Date: 20. Feb-1995 #sequence_revision 20. Feb-1995 #text_change 09-Jul-2004
C;Accession: I51601; B15468
R;Kunnath-Muglia, L.M.; Chang, G.H.; Sim, Ř.B.; Day, A.J.; Ezekowitz, R.A.
MOI. Immunol. 30, 1249-1255, 1993
A;Title: Characterization of Xenopus laevis complement factor I structure--conservation c
A;Reference number: I51601; MUID:94019415; PMID:7692240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:Q03711; EMBL:X59958; NID:g64595; PIDN:CAA42582.1; PID:g64596 C;Superfamily: human complement factor I; LDL receptor ligand-binding repeat homology; t:C;Keywords: hydrolase; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: T49515
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, May 2000
A;Reference number: Z25022
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                                                                                                                                                                                                                                                                                                                                              complement C3b/C4b inactivator (EC 3.4.21.-) precursor - African clawed frog
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C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;220-254/Domain: LDL receptor ligand-binding repeat homology <LDL1>F;257-290/Domain: LDL receptor ligand-binding repeat homology <LDL2>F;370-599/Domain: trypsin homology <TRY>
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A;Experimental source: BAC clone B14D6; strain OR74A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Map position: 6
C;Superfamily: Neurospora crassa hypothetical protein B14D6.670
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Best Local Similarity 27.3%; Pred. No. 1.38+02;
Matches 6; Conservative 10; Mismatches 6; Indels
                                                             Indels
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Score 55.5; DB 2;
Pred. No. 3.4e+02;
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A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Molecule type: mRNA
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Best Local Similarity 30.8%; Pred. No. 3.6e
Matches 8; Conservative 11; Mismatches
                                                             11; Mismatches
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                                                                                                                                                                                     86 NLFNKECRYNLDDNVACGSSACNVL 110
                                                                                                                        2 XIXNQXCXQXLDD---CCSXXCNXX 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein B14D6.670 [imported]
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   46.2%;
36.0%;
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cell]

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A Molecule type: mRNA
A; Residues: 1-45, 'HV', 48-383 < LAB2>
A; Cross-references: EMBL: 221272; NID:938478; PIDN:CAA78163.1; PID:938479
A; Note: sequence extracted from NOEI backbone (NCBIP:125735)
B; Jensen, C.H.; Krogh, T.N.; Hojrup, P.; Clausen, P.P.; Skjodt, K.; Larsson, L.I.; Enghill Eur. J. Biochem. 225, 83-92, 1994
A; Title: Protein structure of fetal antigen 1 (FA1). A novel circulating human epidermal·
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A;Gene: GDB: Dikl; dlk; FAl; PG2; Diklin; dlk; dlk; dlag; dlag;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A.Molecule type: protein
A.Residues: 24-107, D'.109-282 «JEN»
R.Hojrup, P.; Jensen, C.H.; Skjodt, K.; Teisner, B.
Protein Sci. 2(Suppl.1), 2558, 1993
A.Title: Primary structure of human fetal antigen 1 (FA1), a putative homeotic glycoprote
A.Reference number: A44549
                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-344,346-383 <LABI>
A;Cross-references: EMBL:U15979; NID:g562105; PIDN:AAA75364.1; PID:g562106
R;Laborda, J.; Sausville, B.A.; Hoffman, T.; Notario, V.
J. Biol. Chem. 268, 3817-3820, 1938
A;Title: dlk, a putative mammalian homeotic gene differentially expressed in small A;Reference number: A45484; MUID:93179372; PMID:8095043
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                                                                                                                              A, Cross-references: EMBL:U15981; NID:g562109; PIDN:AAA75365.1; PID:g562110
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19.2%; Pred. No. 2.9e+02;
ive 16; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 55, Pred. No. 2.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reference number: S48713; MUID:95010145; PMID:7925474
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                                                                                                                                                                                                                          submitted to the EMBL Data Library, October 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     199 GFIDKTCSRPVTNCASSPCQNGGTCL 224
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A;Molecule type: protein
A;Residues: 24-107,'VASM',112-283 <HOJ>
C;Genetics:
                                                                                            1-228,302-383 <LEE2>
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Best Local Similarity 19.2*;
....hes 5; Conservative
                                                                                                                                                                                                                                                                                     A; Reference number: S71068
                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                A; Accession: S71068
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C;Species: Ovis ammon aries (domestic sheep)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Date: 16-Aug-1996 #sequence_revision of genes
C;Date: Dermatol. 103, 310-317, 1994
A;Title: Differential expression of genes encoding a cysteine-rich keratin family in the A;Reference number: 146412; MUID:94358466; PMID:7521375
A;Retus: preliminary; translated from GB/EMBL/DDBJ
A;Retus: preliminary; translated from GB/EMBL/DDBJ
A;Retus: preliminary;
A;Rolecule type: mRNA
A;Retus: preliminary;
A;Rolecule type: mRNA
A;Retus: preliminary;
A;Retus
C;Species: Hordeum vulgare (barley)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession: S0032
Bur. J. Blochem: 172, 129-134, 1988
A;Title: A dimeric inhibitor or insect alpha-amylase from barley. Cloning of the cDNA and RReference number: S00332; MUID:88151978; PMID:3257914
A;Recence number: S00332
A;Retence number: S00332
A;Recence number: S00332
A;Residues: 1-152 < AZA
A;Residues: 1-152 < AZA
A;Residues: 1-152 < AZA
A;Residues: INIPROT:P13691; GB:AJ009801; NID:G3367713; PIDN:CAA08836.1; PID:G336
C;Superfamily: wheat alpha-amylase inhibitor; homodimer
C;Reywords: alpha-amylase inhibitor; homodimer
F;1-30/Domain: signal sequence #status predicted <SIG>F;31-152/Product: alpha-amylase inhibitor #status experimental <AMAT>
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A, Residues: 1-383 <LEE1>
A, Residues: 1-383 <LEE1>
A, Cross-references: UNIPROT: P80370; EMBL: U15979; NID: 9562105; PIDN: AAA75364.1; PID: 95621
A, Note: the authors translated the codon CAG for residue 46 as His and CCT for residue 4
A; Note: the sequence in GenBank entry HSU15979 has a 3 base deletion mutation in the req
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C.Species: Homo sapiens (man)
C.Date: 06-Dec-1996 #sequence_revision 06-Dec-1996 #text change 09-Jul-2004
C.Accession: S53716, 533717, 571068; B45484; S48713; A44549; S31973; S31974
R.Lee, Y.L.; Helman, L.; Hoffman, T.; Laborda, J.
Biochim. Biophys. Acta 1261, 223-232, 1995
A.Title: dlk, pG2 and Pref-1 mRNAs encode similar proteins belonging to the EGF-like A; Reference number: S53716; MUID:95226449; FMID:7711066
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553716
delta-like homeotic protein dlk, long splice form precursor - human
NyAlternate names: fetal antigen 1 (FA1)
NyContains: delta-like homeotic protein dlk, short splice form
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10; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45.8%; Score 55; DB 2; I 29.2%; Pred. No. 1.6e+02; iive 12; Mismatches 5;
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Best Local Similarity 29.2.
Rest Local 7; Conservative
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Matches 6; Conserv
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DB 1; Length 42;

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Query Match
Best Local Similarity 25.8%; Pred. No. 73;
Matches 8; Conservative 11; Mismatches
         C; Keywords: neurotoxin; venom
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                                                                                                                                                              A;Reference number: Z16677; MUID:98241400; PMID:9572993
A;Accession: T09456
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-3623 <KOZ>
A;Cross-references: UNIPROT:060494; EMBL:AF034611; NID:g3929528; PIDN:AAC82612.1; PID:g3
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A Molecule type: protein
A Molecule type: Osher
A Molecule type: 1-42 SHE
A Molecule type: 1-42 SHE
A Molecule tracerences: UNINPROT: P01478
C COmment: In this species, the venom of the male is lethal rather than that of the fema
C COMMENT: Four disulfide bonds are present.
C Superfamily: robustoxin
C Keywords: neurotoxin; venom
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C.Species Atrax robustus
C.Species Atrax robustus
C.Sate: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 09-Jul-2004
C.SAccession: A01738
R.Sheumack, D.D.; Claassens, R.; Whiteley, N.M.; Howden, M.E.H.
FEBS Lett. 181, 154-156, 1985
A.Title: Complete amino acid sequence of a new type of lethal neurotoxin from the venom A.Reference number: A01738; MUID:85127480; PMID:3972101
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T09456
R;Kozyraki, R.; Kristiansen, M.; Silahtaroglu, A.; Hansen, C.; Jacobsen, C.; Tommerup, N
Blood 91, 3593-3600, 1998
A;Title: The human intrinsic factor-vitamin B12 receptor, cubilin: Molecular characteriz
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Cispecies: Atrax versutus
Cispecies: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004
Cispecies: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004
Cispecies: No. 300349
Ristorm, M.R.: Sheumack, D.D.; Tyler, M.I.; Howden, M.E.H.
Biochem, J. 250, 401-405, 1998
A;Title: Amino acid sequence of versutoxin, a lethal neurotoxin from the venom of the A;Reference number: S00343; MUID:88183358; PMID:3355530
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C;Superfamily: intrinsic factor-B12 receptor cubilin; EGF homology
C;Keywords: receptor; vitamin B12 uptake
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-3623/Product: intrinsic factor-B12 receptor #status predicted
F;436-467/Domain: EGF homology <EGF>
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C;Comment: All cysteine residues are linked by disulfide bonds.
C;Superfamily: robustoxin
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Matches 6; Conservative
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Matches 8; Conservative
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A;Residues: 1-42 <BRO>
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Mosiduse 1.198 cLNA
A;Residuse 1.198 cLNA
A;Cross-references: UNIRROT:074728; EMBL:AL031852; PIDN:CAA21242.1; GSPDB:GN00067; SPDB:£
A;Experimental source: strain 972h-; cosmid c1709
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C,Accession: E71414
R,Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirks
R,Bevan, M.; Bancroft, I.; Bent, E.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terryn, N.; Giels
avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.
Nature 391, 485-488, 1998
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A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thali
A;Reference number: A71400; MUID:98121113; PMID:9461215
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                                                                                                                                                                                                                                                                                          protein SPBC1709.03 - fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                                                     C.Species: Schizosaccharomyces pombe
C.Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
Gaps
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A;Introns: 209/3
C;Superfamily: Schizosaccharomyces pombe hypothetical protein SPBC1709.03
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Best Local Similarity 24.3%; Pred. No. 5e+02;
Matches 9; Conservative 14; Mismatches 3; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176 CILCNAEVRKFSKHCRSCDKCV-DCFDHHCRWINNCV 211
                                                                                                                                                                                                                                                                                                                                                                                                                RiLyne, M.; Rajandream, M.A.; Barrell, B.G.; Rieger, M.submitted to the EMBL Data Library, October 1998
A;Reference number: Z21868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CXIXNQXCXQXLDDC----CS-----XXCNXXNXCV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 54.5; DB 2;
Pred. No. 3.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
                                                            1 CXIXNQXCXQXLDDCCSXXC----NXXNXC 26
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3; Indels
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29.0%; Pred. No. 9e+0
tive 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: VSPA6
C;Keywords: surface antigen; tandem repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 29.0°
Matches 9; Conservative
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AGRT
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C,Species: Caenorhabditis elegans
C,Species: Caenorhabditis elegans
C,Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C,Accession: 127822
R;McMurray, A.
R;McMurray, A.
R;McMurray, A.
R;McFactus in EMBL Data Library, April 1996
A;Reference number: 220425
A;Reference number: 220425
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-1208 vMIL>
A;Residues: 1-1208 vMIL>
A;Residues: 1-1208 vMIL>
A;Residues: Conserreferences: UNTRROT: Q23456; EMBL: Z73757; PIDN: CAA94800.1; GSPDB: GN00023; CESP: ZKACCESTIONEL CONSERVERS: CONSERVE
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442125
trophozoite cysteine-rich surface antigen 170 - Giardia lamblia
N.Alternate names: CRP170; cysteine-rich surface antigen CRP170
C;Species: Giardia lamblia
C;Species: Giardia lamblia
C;Species: Giardia lamblia
C;Accession: A42125; B42125; MUID:99186850; PMID:1545800
                                                                                                                   C;Accession: A26838
R;Ceccarelli, A.; McRobbie, S.J.; Jermyn, K.A.; Duffy, K.; Early, A.; Williams, J.G.
Nucleic Acids Res. 15, 7463-7476, 1987
A;Title: Structural and functional characterization of a Dictyostelium gene encoding a I A;Reference number: A26838; MUID:88015608; PMID:3658700
A;Accession: A26838
A;Status: nucleic acid sequence not shown; not compared with conceptual translation A;Molecule type: DNA
A;Residues: 1-1046 <CEC>
A;Essidues: 1-1046 <CEC>
A;Experimental source: strain Ax-2
F;1-18/Domain: signal sequence #status predicted <SIG>F;1-1046/Product: prestalk protein #status predicted <MAT>
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A;Introns: 44/1; 131/3; 167/1; 259/1; 319/1: 355/1; 484/3; 713/3; 765/1; 840/2; 1036/1;
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restalk protein precursor - slime mold (Dictyostelium discoideum)
;Species: Dictyostelium discoideum
;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
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45.4%; Score 54.5; DB 2; Length 1046;
Best Local Similarity 27.0%; Pred. No. 6.3e+02;
Matches 10; Conservative 11; Mismatches 5; Indels 11.
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A;Residues: 1-98 <ADAL>
A;Cross-references: UNIPROT:P15799; GB:M83937; NID:g159124
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45.4%; Score 54.5; DB 2;
Best Local Similarity 39.1%; Pred. No. 6.9e+02;
Matches 9; Conservative 9; Mismatches 4;
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A,Experimental source: trophozoite
A,Note: sequence extracted from NCBI backbone (NCBIN:88421, NCBIP:88427); this ORF is not.
A,Note: the authors report but do not show 19 tandem repeats of the sequence of residues 1A,Note: the authors report but do not show 19 tandem repeats of the sequence of residues A,Notecule type: DNA
A,Residues: 1269-1766 ADM2>
A,Residues: 1269-1766 ADM2>
A,Residues: 1269-1766 ADM2>
A,Residues: Sequence extracted from NCBI backbone (NCBIN:88424, NCBIP:88431); this ORF is not|
A,Note: sequence extracted from NCBI backbone (NCBIN:88424, NCBIP:88431); this ORF is not|
A,Note: sequence extracted from NCBI backbone (NCBIN:88424, NCBIP:88431); this ORF is not|
A,Note: sequence extracted from NCBI backbone (NCBIN:88424, NCBIP:88431); this ORF is not|
A,Note: sequence extracted from NCBI backbone (NCBIN:88424, NCBIP:88431); this ORF is not|
A,Note: number: S00530; MUID:88089405; PMID:3335828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A Molecule type: DNA
A Residues: 1154-1409, A', 1411-1420, K', 1422-1425, R', 1427-1481 <ADA3>
A, Cross-references: EMBL:X06741; NID:g9355; PID:g929603
R; Yang, Y.; Adam, R.D.
Rivang, Y.; Adam, R.D.
A, Title: Albele-specific expression of a variant-specific surface protein (VSP) of Giard)!
A, Reference number: S48056; MUID:94301794; PMID:8029018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-56 < YAN>
A; Cross-references: EBL: L25059
A; Experimental source: trophozoites WBA6
A; Note: the source is designated as Giardia intestinalis
C; Comment: This translation was produced by PIR staff from information provided by the auc; Genetics:
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A.Residues: 1-1779;1799-1959 <RUP>
A.Cross-references: UNIPROT:P25304; GB:M64780; NID:g202798; PIDN:AAA40703.1; PID:g202800
A.Cross-references: UNIPROT:P25304; GB:M64780; NID:g202798; PIDN:AAA40703.1; PID:g202800
A.Role: it is uncertain whether Met-1, Met-18, or Met-24 is the initiator
A.Note: it is uncertain whether Met-1, Met-18, or Met-24 is the initiator
B.Rupp, F.; Oezcelik, T.; Linhal, M.; Peterson, K.; Francke, U.; Scheller, R.
J. Neurosci. 12, 3555-3544, 1992
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Cibate: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
Cibate: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
Cibacession: JH0399; A38856
R;Rupp, F; Payan, D.G.; Magill-Solc, C.; Cowan, D.M.; Scheller, R.H.
Neuron 6, 811-823, 1991
A;Title: Structure and expression of a rat agrin.
A;Reference number: JH0399; MUID:91222570; PMID:1851019
A;Accession: JH0399.
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A,Reference number: A38856; MUID:92407628; PMID:1326608
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R;Saint-Jacques, E.; Seguin, C.
DNA Cell Biol. 12, 329-340, 1993
A;Title: Cloning and nucleotide sequence of a complementary DNA encoding Xenopus laevis n
A;Refees number: I51538; MUID:99263990; PMID:8494609
A;Accession: I51538
A;Status: preliminary; translated from GB/EMBL/DDBJ
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submitted to the EMBL Data Library, October 1995
A;Description: Isolation, charcterization and deduction of primary structure by PCR-ampl)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 1-62 -SA1->
A;Cross-references: UNIPROT:Q05890; GB:M96729; NID:g214585; PIDN:AAB59949.1; PID:g214586
C;Superfamily: metallothionein
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A;Recension: T11547
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-67 <SCU>A;Cross-references: UNIROT:026497; EMBL:266530; NID:g1045269; PID:g1045270
C;Superfamily: metallothionein
C;Superfamily: metallothionein
                                                                                                                                                                                                                                                                                                  metallothionein - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
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:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
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                                                           1065 CIKQSQVCDGKMQCLDGLDEEHCNEEEKCL 1094
    1 CXIXNQXC---XQXLDDCCSXXCNXXNXCV 27
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Job time : 29.5 secs
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Best Local Similarity 26.9%
Matches 7; Conservative
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A; Introns: 29/1; 78/1; 124/1; 216/1; 256/1; 1222/3; 2036/3; 2127/2; 2478/3; 2522/3; 2589
F; 44-77/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F; 81-124/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F; 825-964/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F; 825-964/Domain: LDL receptor ligand-binding repeat homology <LDL5>
F; 925-964/Domain: LDL receptor ligand-binding repeat homology <LDL6>
F; 965-1005/Domain: LDL receptor ligand-binding repeat homology <LDL6>
F; 1013-1047/Domain: LDL receptor ligand-binding repeat homology <LDL6>
F; 103-1132/Domain: LDL receptor ligand-binding repeat homology <LDL6>
F; 1041-1175/Domain: LDL receptor ligand-binding repeat homology <LDL9>
F; 1041-1175/Domain: LDL receptor ligand-binding repeat homology <LDL9>
F; 1041-1175/Domain: LDL receptor ligand-binding repeat homology <LDL9>
F; 1180-1216/Domain: LDL receptor ligand-binding repeat homology <LDL9>
F; 1180-1216/Domain: LDL receptor ligand-binding repeat homology <LDL9>
F; 1228-1265/Domain: LDL9-1265/Domain: LDL9-1265/Domain: LDL9-1265/Domain: LDL9-1265/Domain: LDL9-1265/Domain: LDL9-1265/Domain: LDL9-1265/Domain: LDL9-
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F;1713-1747/Domain: EGF homology <EG4>
F;1807-1959/Domain: EGF homology <EG4>
F;1807-1959/Domain: laminin G repeat homology <LG3>
F;1807-116;105-137,171-191,180-212,244-263,552-284,316-335,324-356,389-408,397-429,454-473
-1476,1483-1494,1488-1504,1506-1515/Disulfide bonds: #status predicted
F;145,672,827,957/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-2643 <DUZ>
A;Cross-references: UNIPROT:001552; EMBL:U97017; PIDN:AAB52363.1; GSPDB:GN0019; CESP:F4
A;Experimental source: strain Bristol N2; clone F47B3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ä
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Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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20.0%; Pred. No. 9.6e+02;
Live 14; Mismatches 5; Indels 13
F;1-1143,1153-1959/Product: agrin, form 2 #status predicted <AG2>
                                                                                 F;88-137/Domain: Kazal proteinase inhibitor homology <RPI1>
F;183-212/Domain: Kazal proteinase inhibitor homology <RPI2>
F;236-284/Domain: Kazal proteinase inhibitor homology <RPI3>
F;307-356/Domain: Kazal proteinase inhibitor homology <RPI3>
F;307-356/Domain: Kazal proteinase inhibitor homology <RPI3>
F;381-429/Domain: Kazal proteinase inhibitor homology <RPI5>
F;446-494/Domain: Kazal proteinase inhibitor homology <RPI5>
F;51-559/Domain: Kazal proteinase inhibitor homology <RPI7>
F;51-559/Domain: Kazal proteinase inhibitor homology <RPI7>
F;540-542/Region: motor neuron attachment (L.R-E) motif
F;688-739/Domain: laminin-type EGF-like homology <LE2>
F;142-786/Domain: laminin-type EGF-like homology <LE2>
F;141-864/Domain: Razal proteinase inhibitor homology <KPI9>
F;141-864/Domain: Razal proteinase inhibitor homology <KPI9>
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116 CELQRAQCNQQRIRLLRQGPCGSRDPCANVTCSFGSTCV 155
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P;1084-1086/Region: metor neuron attachment (L-R-E) motif
F;1147-1215/Region: serine/threonine-rich
F;124-1257/Domain: EGF homology <EG1>
F;1287-1442/Domain: laminin G repeat homology <LG1>
F;1444-1476/Domain: EGF homology <EG2>
F;1483-1515/Domain: EGF homology <EG3>
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submitted to the EMBL Data Library, April 1997
A;Description: The sequence of C. elegans cosmid F47B3.
A;Reference number: 220579
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local Similarity 30.0
Matches 9; Conservative
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n 5.1.6 Compugen Ltd. Search time 117 Seconds (without alignments)	Million cell updates/sec	by chance to have a he result being printed,	Q71kt2 conus purpu P5663 conus purpu P5663 conus purpu P5881 conus purpu P5881 conus catus P58919 conus catus P21783 xenopus lae P37300 conus magus Q616uS phytophthor Q646uS phytophthor Q646uS phytophthor Q646uS phytophthor Q6489 rattus norr P46531 homo sapien Q91bg4 xenopus lae P10040 drosophila Q91cg7 drosophila Q91cg7 drosophila Q91cg1 mus musculu Q7tg52 mus musculu Q7tg50 homo sapien Q91072 xenopus lae Q6150 homo sapien Q91902 xenopus lae Q61g50 homo sapien Q91349 fugu rubrip Q3516 mus musculu Q37tg1 mus musculu Q7tg20 homo sapien Q91342 homo sapien Q91343 rattus norv Q84w30 rattus norv Q84w30 rattus norv
GenCore version 5 Copyright (c) 1993 - 2005 C OM protein - protein search, using sw model Run on: April 18, 2005, 20:00:51; Sea	US-10-627-685A-1 e: 1 CXIXNQXCXQXLDDCCSXXCNXXNX table: BLOSUM62DX Gapop 10.0 , Gapext 0.5 d: 1612378 seqs, 512079187 res umber of hits satisfying chosen para	Length: 2000000000 3: Minimum Match 0* Maximum Match 100* Listing first 100 summaries UniProt_03:* 1: uniprot_trembl:* 2: uniprot_trembl:* is the number of results predisater than or equal to the score prived by analysis of the total strived by analysis of the total sumwaries * COMMARIES *	No. Score Match Length DB ID 2 120 100.0 67 2 071KT2 3 77 64.2 72 1 CXM7_CONPU 73 66.8 26.1 CXOC_CONST 69 57.5 1820 2 06LEMB 68 56.7 74 2 06LEMB 9 68 56.7 74 2 06LEMB 11 68 56.7 74 2 06LEMB 12 67 55.8 2139 1 CKB_DROME 14 67 55.8 2139 1 CKB_DROME 15 67 55.8 2139 1 CKB_DROME 16 67 55.8 2139 1 CKB_DROME 17 67 55.8 2139 1 CKB_DROME 18 67 55.8 2139 1 CKB_DROME 19 67 55.8 2216 2 091EG4 11 67 55.8 2216 2 091EG4 12 67 55.8 2216 2 091EG4 13 67 55.8 2216 2 091EG4 14 67 55.8 2216 2 091EG4 15 67 55.8 2216 2 091G51 16 67 55.8 2216 2 091G51 20 67 55.8 2531 1 NTCL_MOUSE 21 67 55.8 2531 1 NTCL_MOUSE 22 66 55.0 13149 23 66 55.0 13149 24 66 55.0 13149 25 66 55.0 2471 1 NTCZ_MOUSE 26 65 55.0 2471 1 NTCZ_MOUSE 27 66 55.0 2471 1 NTCZ_MOUSE 28 66 55.0 2471 1 NTCZ_MOUSE 29 66 55.0 2528 2 08XZPO

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Signal, Toxin.
SIGNAL
PROPEP 23
Craik D.J.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Olivera B.M.; "Strategy for rapid immobilization of prey by a fish-hunting marine
                                                            05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Four-loop conotoxin preproprotein (Fragment).
Conus purpurascens (Purple cone).
Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Canogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
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Eukaryota, Metazoa, Mollusca, Gastropoda, Orthogastropoda,
Apogastropoda, Caenogastropoda, Sorbeoconcha, Hypsogastropoda,
Neogastropoda, Conoidea, Conidae, Conus.
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MEDLINE=22068471; PubMed=12074021; DOI=10.1038/381148a0;
Terlau H., Shon K.-J., Grilley M.M., Stocker M., Stuehmer W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ); DB 2; Length 67; 6e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                       Duda T.F. Jr., Palumbi S.R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF480312; AAQOS864.1; -.
HSSP; P56633; 1AV3.
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28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Kappa-conotoxin PVIIA precursor (Fin-popping peptide).
                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0005576; C:extracellular; IEA.
GO: 0008200; F:ion channel inhibitor activity; IEA
GO; GO:0008405; P:pathogenesis; IEA.
InterPro: IPR004214; Conotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 67 four-loop conotoxin.
67 AA; 7712 MW; E7E77CCG1.873E1DB CRC64;
                                                    67 AA.
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                                                      PRT;
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J. Biol. Chem. 273:33-38(1998).
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Matches 17; Conservative
                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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CX7_CONPU
CXX7_CONPU
CXX7_CONPU
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DT 28-FEE-
DT 28-FEE-
DT 28-FEE-
DT 28-FEE-
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        RESULT 1
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"Inhibition of single Shaker K channels by kappa-conotoxin-PVIIA.";
Biophys. J. 82:3003-3011(2002).

Biophys. J. 82:3003-3011(2002).

-I-FUNCTION: Kappa-conotoxins bind and inhibit voltage-sensitive potassium channels. The rat brain voltage-gated potassium channel protein Shaker (Drosophila) is sensitive. The protein Kv1.1 is resistant to this toxin, but the voltage-gated potassium channel protein Shaker (Drosophila) is sensitive. The interaction site between the Shaker channel and this toxin is within the S5-S6 loop of the Shaker channel. In fish, this toxin is induces hyperactivity, followed by continuous contraction and extension of major fins, without immobilization or death.

Injection of this peptide together with the delta-conocoxin pvIA causes the sudden tetanus of prey (STOP) syndrome, which is a single, lethal "fin-pop" in envenomated fish. In mice, induces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MUTAGENESIS OF ARG-47; ILE-48; PRO-49; ASN-50; GLN-51; LYS-52; PHE-54; PHE-54; GLM-55; HIS-56; LEU-57; ASP-58; ASP-59; SER-62; ARG-63; LYS-64; ARG-67; PHE-68; ASN-69 AND LYS-57.0.

MEDLINE-20387368; PubMed-10818087; DOI=10.1074/jbc.C900990199; Jacobsen R.B., Koch E.D., Lange-Malecki B., Stocker M., Verhey.J., Van Magoner R.M., Vyazovkina A., Olivera B.M., Terlau H.; "Single amino acid substitutions in kappa-conotoxin PVIIA disrupt interaction with the shaker K+ channel.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Molecular simulation of the interaction of kappa-conotoxin-PVIIA with the Shaker potassium channel pore.";
Eur. Biophys. J. 30:528-536(2001).
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TISSUE SPECIFICITY: Expressed by the venom duct.
MASS SPECIFICITY: NM=3268.4; METHOD=FAB; RANGE=46-72; NOTE=Ref.1.
SIMILARITY: Belongs to the conotoxin O-superfamily. Kappa-type
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Terlau H., Boccaccio A., Olivera B.M., Conti F.;
"The block of Shaker K+ channels by kappa-conotoxin PVIIA is state
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR, A58997, A58997.

PDB; 1AV3; NMR; @=1-27.

PDB; 1KCP; NMR; @=1-27.

InterPro; IPR04214; Conotoxin.

Pfam; PF02950; Conotoxin, 1.

3D-structure; Direct protein sequencing; Hydroxylation;

Ionic channel inhibitor; Neurotoxin; Potassium channel inhibitor;
                                                                                                                                                                                                                                                   Savarin P., Guenneugues M., Gilquin B., Lamthanh H., Gasparini Zinn-Justin S., Menez A.;
Tinn-Justin S., Menez A.;
Three-dimensional structure of kappa-conotoxin PVIIA, a novel potassium channel-blocking toxin from cone snails.";
Biochemistry 37:5407-5416(1998).
"Solution structure and proposed binding mechanism of a novel potassium channel toxin kappa-conotoxin PVIIA."; Structure 5:1585-1597(1997).
                                                                                                                                                                  STRUCTURE BY NMR.
MEDLINE=98217295; PubMed=9548922; DOI=10.1021/bi9730341;
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calcium channel subtypes.";
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les 9; Conserv
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                                                                                                                                                                                                                                                                                                                                        72 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Venom duct;
MEDLINE=20037955; PubMed=10573284; DOI=10.1016/S0196-9781(99)00116-3;
Lu B.-S., Yu F., Zhao D., Huang P.-T., Huang C.-F.;
"Conopeptides from Conus striatus and Conus textile by cDNA cloning.";
Peptides 20:1139-1144(1999).
                                                                                                                                                                                                                                                                                                               Gaps
                                      R-A,K,Q: 100% reduction of toxicity.
I-A: 3-fold decrease of toxicity.
I-A: 100% reduction of toxicity.
N-A: 100% reduction of toxicity.
Q-A: 13-fold decrease of toxicity.
K-A,M: 100% reduction of toxicity.
F-X: 11-fold decrease of toxicity.
Q-A: 3-fold decrease of toxicity.
H-A: 3-fold decrease of toxicity.
D-A: 100% reduction of toxicity.
D-A: 100% reduction of toxicity.
D-A: 100% reduction of toxicity.
N-A: 3-fold decrease of toxicity.
D-A: 100% reduction of toxicity.
D-A: 100% reduction of toxicity.
N-A: 1.5-fold decrease of toxicity.
S-A: 1.5-fold decrease of toxicity.
R-A: 3-fold decrease of toxicity.
R-A: 1.5-fold decrease of toxicity.
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                                                                                                                                                                                                     117-fold decrease of toxicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Novel alpha- and omega-conotoxins from Conus striatus venom.";
Biochemistry 31:9919-9926 (1992).
                                                                                                                                                                                                                                                                                                                                                                                               P2881; Q9UB25; Created)
01-DEC-1992 (Rel. 24, Created)
16-OCT-2004 (Rel. 46, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Omega-conotoxin SVIB precursor (SNX-183).
Conus striatus (Striated cone).
Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
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                                                                                                                                                                                                                                                                                              100.0%; Score 120; DB 1; Length 72; 63.0%; Pred. No. 6.4e-05; ive 10; Mismatches 0; Indels
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8317 MW; 53BFAF79EE751C16 CRC64;
  Kappa-conotoxin PVIIA,
                                   4-hydroxyproline
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nes 17; Conservative
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 SEQUENCE FROM N.A.
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 TISSUE=Venom;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                                                           Nielean K.J., Thomas L., Lewis R.J., Alewood P.P., Craik D.J.,
"A consensus structure for omega-conotoxins with different
selectivities for voltage-sensitive calcium channel subtypes:
comparison of MVIA, SVIB and SNX-202.";
J. Mol. Biol. 263:297-310(1996).
-!- FUNCTION: Omega-conotoxins act thresynaptic membranes, they bind
and block voltage-sensitive calcium channels (VSCC). This toxin
blocks N-, P-, and Q-type calcium channels.
-!- SUBCELBLUAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the venom duct.
-!- SIMILARITY: Belongs to the conotoxin O-superfamily. Omega-type
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cysteine amide (G-72 provides amide
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3D-structure; Amidation; Calcium channel inhibitor;
Direct protein sequencing; Ionic channel inhibitor; Neurotoxin;
Presynaptic neurotoxin; Signal; Toxin.
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Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
STRUCTURE BY NMR.
MEDLINE=97070382; PubMed=8913308; DOI=10.1006/jmbi.1996.0576;
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1F753546AAD39908 CRC64;
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28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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PDB; 1MVJ; NMR; @=46-72.
InterPro; IPR004214; Conotoxin.
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Conus catus (Cat cone).
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Cytoplasmic (Potential)
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EGF-like 19,
EGF-like 20,
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EGF-like 24,
EGF-like 25,
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EGF-like 35.
EGF-like 35.
EGF-like 36.
Lin/Notch 2.
Lin/Notch 2.
Lin/Notch 3.
ANK 1.
ANK 2.
ANK 3.
ANK 5.
                InterPro; IPR006209; EGF like.
InterPro; IPR010660; NOD.
InterPro; IPR008207; Notch.
InterPro; IPR008000; Notch.
Pfam; PP00023; Ank; 6.
Pfam; PP000816; BGF; 36.
Pfam; PP00066; Notch; 3.
Pfam; PP00066; Notch; 3.
Pfam; PP00066; Notch; 3.
PRINTS; PR01415; ANKYRIN.
PRINTS; PR01415; ANKYRIN.
PRINTS; PR00415; ANKYRIN.
PRINTS; PR00415; NOTCH.
SWART; SM00248; ANK; 6.
SWART; SM00179; EGF CA; 24.
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                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Suropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
J. Biol. Chem. 275:35335-35344(2000).
-!- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind and block voltage-sensitive calcium channels (VSCC) (By similarity). This toxin blocks N-, P-, and Q-type calcium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kintner C.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.

Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.

SUBCELLULAR LOCATION: Type I membrane protein.

SUBCELLULAR LOCATION: Type I membrane protein.

SIMILARITY: Belongs to the NOTCH family.

SIMILARITY: Contains 6 ANK repeats.

SIMILARITY: Contains 36 EGF-like domains.

SIMILARITY: Contains 3 EGF-like domains.
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Amidation: Calcium channel inhibitor; Direct protein sequencing; Ionic channel inhibitor; Neurotoxin; Presynaptic neurotoxin; Toxin. Ionic channel inhibitor; Neurotoxin; Presynaptic neurotoxin; Toxin. DISULFID 8 20 By similarity.

MOD_RES 26 26 Cysteine amide.

SEQUENCE 26 AA; 2790 MW; 56EFC382335C4A8B CRC64;
                                                                                                                -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUB SPECIFICITY: Expressed by the venom duct.
-!- SIMILARITY: Belongs to the conotoxin O-superfamily. Omega-type
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1991 (Rel. 18, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
25-JMN-2005 (Rel. 46, Last annotation update)
Neurogenic locus notch protein homolog precursor (XOTCH protein)
Name=XOTCH;
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MEDLINE=90385285; PubMed=2402639;
Coffman C., Harris W., Kintner C.;
Xotch, the Xenopus homolog of Drosophila notch,";
Science 249:1438-1441(1990).
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Interbro; IPR002110; ANK.
Interpro; IPR0001152; Asx hydroxyl_S.
Interpro; IPR000153; BGF_2.
Interpro; IPR001881; BGF_Ca.
Interpro; IPR001438; BGF_II.
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Matches 8; Conservative
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PROSITE; PSSO297; ANK REP REGION; 1.
PROSITE; PSSO088; ANK REPEAT; 4.
PROSITE; PSSO0022; ASK-HYDROXYL; 23.
PROSITE; PSO0122; EGF 1; 34.
PROSITE; PSO1186; EGF 2; 29.
PROSITE; PSSO126; EGF 2; 29.
PROSITE; PSSO026; EGF 3; 36.
PROSITE; PSSO026; EGF 32.
PSSO026; EGF
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MEDLINE=92337922; PUBMcd=135296; DOI=10.1016/0896-6273(92)90221-X;
MEDLINE=92379222; Mintz in 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Structure-activity relationships of omega-conotoxins MVIIA, MVIIC and 14 loop splice hybrids at N and P/Q-type calcium channels."; J. Mol. Biol. 289:1405-1421(1999).
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MEDLINE-99303703; PubMed-10373375; DOI-10.1006/jmbi.1999.2817;
Nielsen K.J., Adams D., Thomas L., Bond T., Alewood P.F., Craik D.J.,
                                                                                                                                                                                                                                                         Gaps
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J. Mol. Biol. 248:106-124(1995).
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Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
NCBI_TaxID=6492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRUCTURE BY NMR.
MEDLINE=55248539; PubMed=7731037;
Farr-Jones S., Miljanich G.P., Nadasdi L., Ramachandran J.,
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1e+02;
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01-OCT-1994 (Rel. 30, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Omega-conotoxin MVIIc precursor (SNX-230) (Fragment).
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SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: Expressed by the venom duct.
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34.6%;
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                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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Sequence 1236867; DOI=10.1038/nature01035;

R Hall N., Pain A., Berriaman M., Churcher C., Harris B., Harris D.,

A Hall N., Pain A., Berriaman M., Churcher C.,

Buckee C.O., Burrows C., Atkin R., Baker S., Barron A., Brooks K.,

Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,

Chillingworth T., Christodoulou Z., Clark L., Clark R., Corto C.,

A Cronin A., Davies R., Davies P., Dear P., Dearden F., Doggett J.,

Reltwell T., Goble A., Goodhead I., Gwilliam R., Hamin N., Hance Z.,

A Hampray S., Jagels K., James D., Johnson D., Kerhornou A., Knight A.,

Roctfortov B., Keyes S., Larke N., Lawson D., Lennard N., Line A.,

A Maddison M., McLean J., Mooney P., Moule S., Murphy L., Oliver K.,

RA Aumond D., Price C., Quall M.A., Rabbinowitsch B., Rajandream M.A.,

RA Rutter S., Rutherford K.M., Sanders M., Simmonds M., Seeger K.,

RA Sharp S., Smith R., Squares R., Squares S., Stevens K., Taylor K.,

RA Tivey A., Unwin L., Whitehead S., Woodward J., Sulston J.E., Craig A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                     PDB; 1CNN; NMR; A=3-29.
PDB; 1OMN; NMR; @=3-29.
3D-structure; Amidation; Calcium channel inhibitor; Hydroxylation; Ionic_channel inhibitor; Neurotoxin; Presynaptic neurotoxin; Toxin.
-!- SIMILARITY: Belongs to the conotoxin O-superfamily. Omega-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Omega-conotoxin MVIIc.
Essential for calcium channel binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydroxyproline (Probable).
Cysteine amide (G-29 provides amide
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Y->A: High decrease in binding.
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ORFNames=MAL6P1.41, PFF0185c;
ORFNames=Malciparum (isolate 3D7).
Eukaryota Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.5%; Score 69; DB 1; Length 29; 30.8%; Pred. No. 3.5; tive 12; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3071 MW; AC7A68948474728A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1820 AA
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PIR; JH0699; JH0699.
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Best Local Similarity
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BINDING
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Berriman M., Pain A., Hall N., Atkin R., Chillingworth C., Doggett J.,
Ormond D., Sanders M., Hayes R., Hall S., Quail M., Barrell B.G,
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR382398; CAG25208.1;
InterPro; IPR000875; Cecropin.
InterPro; IPR009077; Prot act regA.
PROSITE; PS00268; CECROPIN; UNKNOWN I.
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Newbold C., Barrell B.G; "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.";
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Liu Z., Bos J.I.B., Armstrong M., Whisson S.C., da Cunha L.,
Torto-Alalibo T., Win J., Avrova A.O., Wright F., Birch P.R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                                                                                                                                                                                                                                 h Similarity 32.1%; Score 69; DB 2; Length 1820; Similarity 32.1%; Pred. No. 1.5e+02; 9; Conservative 12; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Liu Z., Bos J.I.B., Armstrong M., Whisson S.C., da Cunha L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phytophthora infestans (Potato late blight fungus).
Eukaryota, stramenopiles, Oomycetes, Pythiales, Pythiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Phytophthora infestans (Potato late blight fungus).
Eukaryota, stramenopiles; Oomycetes; Pythiales; Pythiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56.7%; Score 68; DB 2; Length 74; 29.0%; Pred. No. 10; 2; Indels ive 14; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                1820 AA; 218564 MW; 84F330EE57FA6150 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-007-2004 (TrEMBLrel. 28, Created)
25-007-2004 (TrEMBLrel. 28, Last sequence update)
25-007-2004 (TrEMBLrel. 28, Last annotation update)
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1301 CDIYNEFCDDECCDDECCDDEYC 1328
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25-OCT-2004 (TrEMBLrel. 28, Last seg
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                                                 Nature 419:527-531(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phytoxin-like SCR74.
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es 9; Conserv
                                                                                                SEQUENCE FROM N.A
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Name=NOTCH1; Synonyms=TAN1;
Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                        RESULT 11
NTC1 HUMAN
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                                                                                                                                                                                       1;
                 Kamoun S.;
"Patterns of Diversifying Selection in the Phytotoxin-like scr74 Gene Family of Phytophthora infestans.";
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY723720; AAU21461.1;
SEQUENCE 74 AA; 7802 MW; 57A8231D29AB5F8F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Brown Norway;
PubMed=15060004; DOI=10.1101/gr.1987704;
Putr P., Walter L., Sudbrak R., Klages S., Mueller I., Shiina T., Inoko H., Lehrach H., Guenther E., Reinhardt R., Himmelbauer H.;
"The genomic sequence and comparative analysis of the rat major
                                                                                                                                                                                       9
Torto•Alalibo•T., Win J., Avrova A.O., Wright F., Birch P.R.J.,
                                                                                                                                              56.7%; Score 68; DB 2; Length 74; 29.0%; Pred. No. 10;
                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                          2 XIXNOXCXQ-----XLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                              41 DVVSQCCKAINAEPVAFNDCCSKSCNTGSPC 71
                                                                                                                                                                                                                                                                                                                                                          PRT; 1961 AA
                                                                                                                                                                                     14; Mismatches
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InterPro; IPR000110; As hydroxyl_S.
InterPro; IPR000152; As hydroxyl_S.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR004309; EGF_II.
InterPro; IPR006200; EGF_II.
InterPro; IPR006200; ISGF_II.
InterPro; IPR006800; Notch region.
InterPro; IPR008805; Rieske.
                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                histocompatibility complex."
Genome Res. 14:631-639(2004)
                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00248; ANK; 5.
SMART; SM00181; EGF; 28.
SMART; SM00179; EGF_CA; 21.
SMART; SM00004; NL; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS, PRO1415; ANKYRIN.
PRINTS, PR00010; EGFBLOOD
PRINTS; PR01452; NOTCH.
                                                                                                                                                                  Local Similarity 29.09 ces 9; Conservative
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Pfam; PF00008; EGF; 24.
Pfam; PF07645; EGF_CA; 3.
Pfam; PF00066; Notch; 2.
                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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SEQUENCE FROM N.A.
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AC 06668

DE NOGE-JU

DT 05-JU

DE NAME

RA NAME

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                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
bonds (By similarity). Interacts with DTX1 and DTX2.
SUBCELLULAR LOCATION: Type I membrane protein. Following
proteolytical processing NICD is translocated to the nucleus (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS5008; ANK REPEAT; 4.

PROSITE; PS50018; ANK REPE REGION; 1.

PROSITE; PS50010; ASK HYDROXYL; 20.

PROSITE; PS00102; EGF_1; 34.

PROSITE; PS00186; EGF_2; 26.

PROSITE; PS01187; EGF_A; 13.

Interpretation; EGF-1ike domain; Glycoprotein;

Notch signaling pathway; Phosphorylation; Receptor; Repeat; Signal; SIGNAL

1 18 Potential.
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Extracellular (Potential)

Extracellular (Potential).

Cytoplasmic (Potential).

EGF-like 1.

EGF-like 2.

EGF-like 3.

EGF-like 4.

EGF-like 6.

EGF-like 9, calcium-binding (Potential).

EGF-like 10.

EGF-like 20.

EGF-like 30.

EGF-like 3
      Neurogenic locus notch homolog protein 1.
Notch extracellular truncation (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Poly-Gly.
Poly-Gln.
Poly-Gln.
Poly-Ser.
Cleavage (by furin-like protease)
                         Notch extracellular truncation similarity).
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Query Match 55.8%; Score 67; DB 2; Length 487; Best Local Similarity 28.0%; Pred. No. 72; Matches 7; Conservative 13; Mismatches 5; Indels
                           52498 MW; C69E5B14E36B3D22 CRC64;
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  EGF-like domain.
SEQUENCE 487 AA;
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Submitted (JUW-2002) to the EMBL/GenBank/DDBJ databases.

Bubmitted (JUW-2002) to the EMBL/GenBank/DDBJ databases.

Bubmitted (JUW-2002) AAM49878.1;

Bubmitted (JUW-2004) table.1;

Bubmitted (JUW-2004) table.1;

Bubmitted (JUW-2004) table.2;

Bubmitted (JUW-2004) table.2;

Bubmitted (JUW-2004) table.2;

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Bubmitted (JUM-2004)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                              56.7%; Score 68; DB 1; Length 2556; 30.8%; Pred. No. 2.6e+02; tive 12; Mismatches 6; Indels
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Last annotation update)
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By similarity. By similarity.
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PROSITE; PSO1186; ESF_3; 8.
PROSITE; PSO1187; EGF_CA; 4.
PROSITE; PSO025; LAM_G_DOMAIN; 1.
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PRINTS; PR00010; EGFBLOOD.
SMART; SM00179; EGF CA; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                          Local Similarity 30.8 tes 8; Conservative
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QBMSX5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R GO; GO:000559; F:calcium ion binding; IEA.
GO; GO:000559; F:calcium ion binding; IEA.
GO; GO:0005196; F:calcium ion binding; IEA.
R GO; GO:0007155; P:cell adhesion; IEA.
R InterPro; IPR000152; Asx hydroxyl S.
R InterPro; IPR000965; Con like lec gl.
R InterPro; IPR000184; EGF Z.
R InterPro; IPR00184; EGF Z.
R InterPro; IPR00184; EGF Z.
R InterPro; IPR00184; EGF Z.
R InterPro; IPR001919; Laminin G.
R InterPro; IPR001919; Laminin G.
R InterPro; IPR001919; Laminin G.
R Pfam; PF00200; EGF; 12.
R Pfam; PF001019; EGF ZA; G.
R Pfam; PR001019; EGF ZA; G.
R SMART; SM00129; Laminin G Z; 1.
R SMART; SM00129; EGF ZA; G.
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778 AA; 85516 MW; 462D2C84AE435CF6 CRC64;
                                                          01-007-2000 (TrEMBLrel. 15, Created)
01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Secretary protein containing EGF domain precursor.
Xenopus laevis (African clawed frog).
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778 AA
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PROSITE; PS01187; EGF CA; 6.
PROSITE; PS50025; LAM G DOWAIN; 1.
EGF-like domain; Signal.
SEGNITEL.
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Interaction of Par-6 and Crumbs complexes is essential for

photoreceptor morphogenesis in Drosophila.";

Development 130:4363-4372 (2003).

-I FUNCTION: Plays a central role in cell polarity establishment.

Participates in the assembly, positioning and maintenance of
adherens junctions via its interaction with the SAC complex.

Controls the coalescence of the spots of zonula adherens (ZA) into
a adhesive ring around the cells. It may act as a signal. Involved
in morphogenesis of the photoreceptor rhabdomere, for positioning
attd growth of rhabdomere and AJ during the crucial period of
photoreceptor extension along the proximodistal axis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERACTION WITH PATJ.

MEDLINE=99200394; PubMed=10102271; DOI=10.1016/S0092-8674(00)80593-0;
Bhat M.A., Izaddoost S., Lu Y., Cho K.-O., Choi K.-W., Bellen H.J.;
"Discs Lost, a novel multi-PDZ domain protein, establishes and maintains epithelial polarity.";
Cell 96:833-845(1999).
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=Cregon-R; TISSUE=Embryo;
MEDLINE=90263104; PubMed=2244615; DOI=10.1016/0092-8674(90)90189-L;
Tepass U., Theres C., Knust E.;
"Crumbs encodes an EGF-like protein expressed on apical membranes of prosphila epithelial cells and required for organization of
                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=87218537; PubMed=3107986;
Knust E., Dietrich U., Tepass U., Bremer K.A., Weigel D., Vaessin H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bhat M.A., Izaddoost S., Lu Y., Cho K.-O., Choi K.-W., Bellen H.J.;
Cell 115:765-766(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=11076972; DOI=10.1083/jcb.151.4.891;
Tanentzapf G., Smith C., McGlade J., Tepass U.;
"Apical, lateral, and basal polarization cues contribute to the development of the follicular epithelium during Drosophila
                                                                                                                              Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           iDENTIFICATION IN A SAC COMPLEX WITH PART AND SDT.
MEDLINE=21603015; PubMed=11740560; DOI=10.1038/414638a;
Bachmann A., Schneider M., Theilenberg E., Grawe F., Knust E.;
"Drosophila Stardust is a partner of C:cumbs in the control of epithelial cell polarity.";
Nature 414:638-643(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Campos-Ortega J.A.;
"EGF homologous sequences encoded in the genome of Drosophila melanogaster, and their relation to neurogenic genes.";
EMBO J. 6:761-766(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION, AND INTERACTION WITH PAIJ.
                 01-MAR-1989 (Rel. 10, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                              Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERACTION WITH THE PAR-6 COMPLEX.
                                                                           Crumbs protein precursor (95F). Name=crb;
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1663-1955 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cell Biol. 151:891-904(2000).
                                                                                                                                                                                                                                                                                                                                                     Cell 61:787-799(1990).
                                                                                                                                                                                        NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=12900452;
                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     retina
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ERRATUM
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SUBUNIT: Component of the SAC complex, a complex composed of crb, Patj and sdt. May interact with the par-6 complex, which is

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PRESENCE ASSECTS. ASSECTS.

DR PIR; BASSCTS; ASSECTS.

DR PIR; BASSCTS; ASSECTS.

DR PIR; BASSCTS; ASSECTS.

DR PIR; BASSCTS.

DR PIR; BASSCTS.

DR GO; GO:0016244; Capical plasma membrane; NAS.

DR GO; GO:0016247; C:apical plasma membrane; NAS.

DR GO; GO:0016322; E:establishment and/or maintenance of polarit.

DR GO; GO:0016332; P:establishment and/or maintenance of polarit.

DR GO; GO:0016349; P:establishment and/or maintenance of polarit.

DR GO; GO:0016349; P:establishment and/or maintenance of polarit.

DR GO; GO:0042052; P:morphogenesis of an epithalium; NAS.

DR GO; GO:0042052; P:rhabdomere development; NAS.

DR GO; GO:0045186; P:zonula adherens assembly; IMP.

DR GO; GO:0045186; P:zonula adherens maintenance; IMP.

DR GO; GO:0045218; P:zonula adherens maintenance; IMP.

DR InterPro; IPR000189; EGF_2.

DR InterPro; IPR001891; EGF_2.

DR InterPro; IPR001891; EGF_2.

DR InterPro; IPR001991; EGF_2.

DR InterPro; IPR001991; EGF_2.

DR InterPro; IPR001991; EGF_3.

DR REAM; PR00019; EGF_CA; 11.

DR PROSITE; PS001016; EGF_1.

DR PROSITE; PS010166; EGF_3; 17.

DR PROSITE; PS01016; EGF_1.

DR PROSITE; PS01016; EGF_1.
                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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(Potential).
(Potential).
composed of par-6, baz and aPKC, via its interaction with Patj.
Interacts with other proteins with Patj and sdt via its short
cytoplasmic tail.
-!- SUBCELLULAR LOCATION: Type I membrane protein. Specifically
localized to the apical membrane.
-!- PTM: Phosphorylated in the cytoplasmic domain (Potential).
-!- SIMILARITY: Contains 29 EGF-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Crumbs protein.
Extracellular (Potential).
Potential.
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RR PERCENCE FROM N.A.

Adama M.D. Celniker S.E. Holf R.A., Evans C.A. Gocapue J.D.,

Adama M.D. Celniker S.E., Holf R.A., Evans C.A. Gocapue J.D.,

RA Amanatides P.G. Scherer S.E., 1ip Pw., Hoskins R.A., Galle R.F.,

George R.A., Lewis S.E., Richards S. Ashburner M., Henderson S.N.,

RA Amanatides P.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

Barton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Ffeiffer B.D.,

RA Bandon R.C., Baxter E.G., Helf G., Nelson C.R., Gabor G.L.,

Abril J.F., Agbayani A., Andrews-Pfannkoch C., Baldwin D.,

Ballew R.M., Banu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Benkova D. Botchen M.R., Bouck J., Broketein P., Burotter P.,

Burkin S.C., Busam D.A., Bulter H., Cadpie E., Center A., Chandra I.,

Ra Durbin K.J., Bougley S., Dahlke C., Davengort L.B., Davies P.,

RA Durbin K.J., Evangaliste C.C., Ferraz C., Perriera S., Plaischmann W.,

RA Durbin K.J., Evangaliste C.C., Ferraz C., Perriera S., Plaischmann W.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Houston K.A., Howlenn C.H., Ke Z., Kulp D., Lai Z.,

Alalai M., Kalush F., Karpen G.H., Ke Z., Kulp D., Lai Z.,

Liako P., Lei Y., Levitsky A.A., Li J. J., Marris M., Malson D.L.,

RA Mount S.M., Moy M., Murphy L., Murphy L., Morray D.M., Narry W. Relace M.G.,

Reinert K., Remington K., Saunders R.D., Scheld F., Shen H.,

Shier B., Spradina A.C., Penniko H., Strong R., Sun E.,

Syriskas R., Tector C., Turner E., Wang A., San E.,

Syriskas R., Storic M., Weinsech D., Strong R., Sun E.,

Syriskas R., Storic M., Weinsech W., Stuppk M., Singer M., Singer M., Singer M., Stuppk M., Stupk M., S
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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EGF-11ke 27, calcium-binding (Pr
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EGF-like 22.
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EGF-like 19.
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  Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                        "Annotation of the Drosophila melanogaster euchromatic genome:
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                                                                                                                                                                                                                     Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                     Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases
EMBL; AE003747; AAF56276.1; --
HSSP; P00740; 1EDM.
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ID NTC1 BRARE
AC P46530,
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-NOV-1995 (Rel. 36, Last annotation update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Neurogenic locus notch homolog protein 1 precursor.
                                                                                             systematic review.";
Genome Biol. 3:RESEARCH0083-RESEARCH0383(2002).
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                                                         Lewis S.E.;
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Branchotts, Synonymenotch;

Radyots, Metazas, Cybradas, Craite; Verribres; Buelecerom;

OK Mingersyll, Meopersyll, Teleceri; Ostaribphysi, Cypriniformes;

OK Mingersyll, Metazas, Chaite; Verribphysi, Cypriniformes;

New Lingershold, Composervell, Teleceri; Ostaribphysi, Cypriniformes;

New Lingershold, Composervell, Teleceri; Ostaribphysi, Cypriniformes;

NEW LINGS, Asia Composervell, Teleceri, Ostaribphysi, Cypriniformes;

In Transporter, Teleceri, Teleceri, Ostaribphysi, Cypriniformes;

New Lings, Asia Composervell, Teleceri, Ostaribphysi, Cypriniformes;

In STRIKARTY: Delongs of the Drosophila neuropes and composervell, Ostaribphysi, Cypriniformes;

In STRIKARTY: Delongs of the North Manie, Teleceri, Ostaribphysi, Cypriniformes;

In STRIKARTY: Delongs of the North Manie, Teleceri, Ostaribphysi, Cypriniformes;

In STRIKARTY: Delongs of the North Manie, Teleceri, Ostaribphysi, Cypriniformes;

In STRIKARTY: Delongs of the North Manie, Teleceri, Ostaribphysi, Cypriniformes;

In STRIKARTY: Ostarib Strike, Ostarib, Cypriniformes;

In STRIKARTY: Ostarib, Cypriniforme
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Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55.8%; Score 67; DB 1; 1
30.0%; Pred. No. 3.1e+02;
iive 13; Mismatches 4
                      similarity
                                                                                                                                                                                                                                                                                         similarity,
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     Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Rodentia,
NCBI_TaxID=10090;
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  Query Match
Best Local Similarity
Matches 9; Conserv
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AC 07705
AC 07705
DT 01-0C
DT 01-MB
DE Trans
GN Name=
CS Mamma
OC Mamma
OC Mamma
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RP SEQUE
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Transcription regulation; Transmembrane. Potential.
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                                     Pourcagenic locus notch homolog pr

Extracellular (Potential).

Cytoplasmic (Potential).

Cytoplasmic (Potential).

EGF-like 1.

EGF-like 4.

EGF-like 4.

EGF-like 6.

EGF-like 7.

EGF-like 7.

EGF-like 9.

EGF-like 10.

EGF-like 10.

EGF-like 11.

EGF-like 12.

EGF-like 13.

EGF-like 14.

EGF-like 14.

EGF-like 15.

EGF-like 16.

EGF-like 17.

EGF-like 19.

EGF-like 20.

EGF-like 21.

EGF-like 21.

EGF-like 22.

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EGF-like 24.

EGF-like 24.

EGF-like 25.

EGF-like 25.

EGF-like 27.

EGF-l
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SEQUENCE FROM N.A.

STRAIN=C.B-17; TISSUE=Thymus;

X MEDLINE=27551392; PubMed=1280718; DOI=10.1093/carcin/bgg071;

X TEUJI H., Ishii-Ohba H., Ukai H., Katsube T., Ogiu T.,

T "Radiation-induced deletions in the 5' end region of Notchl lead to the formation of truncated proteins and are involved in the fowellopment of mouse thymic lymphoma.";

The formation of truncated proteins and are involved in the carcinogenesis 24:1257-1268(2003).

BENEL; AB106603; BAC77039.1;

RSSP;"POT207; 10778.

RO; GO:0016621; C:integral to membrane; IEA.

RO; GO:0016221; C:integral to membrane; IEA.

RO; GO:0016529; F:calcium ion binding; IEA.

RO; GO:0005509; F:calcium ion binding; IEA.

RO; GO:000154; P:cell differentiation; IEA.
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                   MEDLINE_22753192; PubMed=12807718; DOI=10.1093/carcin/bgg071; Tsuji H., Ishii-Ohba H., Ukai H., Katsube T., Ogiu T.; Radiation-induced deletions in the 5' end region of Notch1 lead the formation of truncated proteins and are involved in the development of mouse thymic lymphoma."; actinogenesis 24:1257-1268(2003).

EMBL; AB100603; BAC77038.1; -.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Last annotation update)
                                                                                                                                                                                              GO: GO:0016021; Cittlegral to membrane; IEA.
GO: GO:0005509; F:calcium ion binding: IEA.
GO: GO:0004842; F:receptor activity; IEA.
GO: GO:000154; F:receptor activity; IEA.
GO: GO:0010154; F:receptor activity; IEA.
InterPro: IPR000152; Asx hydroxyl_S.
InterPro: IPR000152; Asx hydroxyl_S.
InterPro: IPR000152; Asx hydroxyl_S.
InterPro: IPR000152; Asx hydroxyl_S.
InterPro: IPR000152; BGF_2.
InterPro: IPR000800; Notch_region.
Pfam; PF00008; BGF, IIAe.
InterPro: IPR000800; Notch_region.
Pfam; PF00008; BGF, IIAe.
InterPro: IPR000800; Notch_region.
Pfam; PF00006; Notch, 3.
Pfam; PF00006; Notch, 3.
RMART; SM00179; EGF CA; 4.
RMART; SM00179; EGF CA; 4.
RMART; SM00179; EGF CA; 4.
RMART; SM00179; ANK, 6.
RMART; SM00179; ANK, 6.
RMART; SM0186; ANK REPRATI; 4.
RMART; SM0186; ANK REPRATI; 4.
RMART; SM0186; EGF 2; 27.
RMOSITE; PS00186; EGF 2; 27.
RMOSITE; PS0186; EGF 2; 27.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
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01-0CT-2003 (TrEMBLrel. 25, Last seqn
01-MAR-2004 (TrEMBLrel. 26, Last ann
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STRAIN=C.B-17; TISSUE=Thymus,
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Matches 8; Conservative
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Q7TQ51;
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077051
10 07105
AC 07105
AC 07105
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DT 01-0C
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OC BUKAR
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DR GO; GG
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NTCI MOUSE STANDARD, PRT, 2531 AA.

001705; Q06007; Q61905; Q99JC2; Q9QW58; Q9R0X7;
01.NOV-1995 (Rel. 32, Created)
01.NOV-1995 (Rel. 31, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Meurogenic locus notch homolog protein 1 precursor (Notch 1) (Motch A)
Name=Notch1; Synonyms=Motch;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 731-1899 FROM N.A. (ISOFORM 2), AND DEVELOPMENTAL STAGE. STRAIN=CD-1; TISSUE=Embryo; MEDLINE=93050801; PubMed=1426644; Reaume A.G., CONION R.A., Zirngibl R., Yamaguchi T.P., Rossant J.; "Expression analysis of a Notch homologue in the mouse embryo."; Dev. Biol. 154:377-387(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rianco del Amo F., Smith D.E., Swiatek P.J., Gendron-Maguire M., Steenspan R.J., McMahon A.P., Gridley T.;
"Expression pattern of Motch, a mouse homolog of Drosophila Notch, suggests an important role in early postimplantation mouse development.";

Development 115:737-744(1992).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                      R InterPro; IPR000742; EGF_2.
R InterPro; IPR001881; EGF_Ca.
R InterPro; IPR001881; EGF_Ca.
R InterPro; IPR001891; EGF_Ca.
R InterPro; IPR000800; Notch_region.
Pfam; PR000083; Ank; 6.
R Pfam; PR000084; EGF_CA; 4.
R Pfam; PR000086; Notch; 3.
R SMART; SM00179; EGF_CA; 25.
SMART; SM00179; EGF_CA; 25.
SMART; SM00004; Nuk; 3.
R PROSITE; PS50089; ANK REP_REGION; 1.
R PROSITE; PS50010; ASX HYDROXXL; 22.
R PROSITE; PS50010; ASX HYDROXXL; 22.
R PROSITE; PS50010; ASX HYDROXXL; 22.
R PROSITE; PS010186; EGF_2; 27.
R PROSITE; PS01186; EGF_2; 27.
R PROSITE; PS01186; EGF_2; 21.
W ANK repeat; EGF-like Gomain; Receptor; Transmembrane.
Q SEQUENCE 2526 AA; 270583 MW; 017563FCE9703264 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.8%; Score 67; DB 2; Length 2526; 30.8%; Pred. No. 3.2e+02; ive 12; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 XIXNOXCXQXLDDCCSXXCNXXNXCV 27
IPR000742; EGF 2.
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MEDLINE=93194170; PubMed=8449489;
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MEDLINE=98029496; PubMed=9384671;
Messerle M., Follo M., Nehls M., Eggert H., Boehm T.;
"Dynamic changes in gene expression during in vitro differentiation of
mouse embryonic stem cells."
Cytokines Cell. Mol. Ther. 1:139-143(1995).
                                                                                                                                                                                                                               Lee J.S., Ishimoto A., Yanagawa S.I.; "Murine leukemia provirus-mediated activation of the Notchl gene leads to induction of HES-1 in a mouse T lymphoma cell line, DL-3."; FEBS Lett. 455:276-280(1999).
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SEQUENCE OF 1659-1673 FROM N.A.
MEDLINE-99364499; PubMed=10437788; DOI=10.1016/S0014-5793(99)00901-1;
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INTERACTION WITH DTX1 AND DTX2.
MEDLINE=21123790; PubMed=11226752; DOI=10.1016/S0736-5748(00)00071-X;
Kishi N., Tang Z., Maeda Y., Hirai A., Mo R., Ito M., Suzuki S.,
Nakao K., Kinoshita T., Kadesch T., Hui C.-C., Artavanis-Tsakonas S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse notch: expression in hair follicles correlates with cell fate
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"Murine homologs of deltex define a novel gene family involved in vertebrate Notch signaling and neurogenesis.";
Int. J. Dev. Neuroseci. 19:21-35(201).
-!- FUNCTION: Functions as a receptor for membrane-bound ligands Jaggedl, Jagged2 and Deltal to regulate cell-fate determination. Upon ligand activation through the released notch intracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MUTACENESIS OF 1651-ARG--ARG-1654.
MEDLINE=98318619; PubMed=9653148; DOI=10.1073/pnas.95.14.8108;
Logeat F., Bessia C., Brou C., LeBail O., Jarriault S., Seidah N.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POST-TRANSLATIONAL PROCESSING.
MEDLINE=21374376; PubMed=11459941; DOI=10.1073/pnas.161269998;
Mizutani T., Taniguchi Y., Aoki T.; Hashimoto N., Honjo T.;
"Conservation of the biochemical mechanisms of signal transduction
SEQUENCE OF 1161-1547 FROM N.A. STRAIN-CSTBL/6 X CBA; TISSUB-Embryo; STRAIN-CSTBL/6 X CBA; TISSUB-Embryo; MEDLINE-93178563; PubMed-8440332; DOI=10.1006/excr.1993.1044; Lardelli M., Lendahl U.; Motch A and Motch B-two mouse Notch homologues coexpressed in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1865-2075 FROM N.A., AND DEVELOPMENTAL STAGE IN HAIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The Notch1 receptor is cleaved constitutively by a furin-like
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MEDILINE=11523956; PubMed=11218718; DOI=10.1074/jbc.MI07234200;
Saxena M.T., Schroeter E.H., Mumm J.S., Kopan R.;
"Murine notch homologs (N1-4) undergo presenilin-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1655-1659, CLEAVAGE BY FURIN-LIKE CONVERTASE, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                among mammalian Nocch family members.";
Proc. Natl. Acad. Sci. U.S.A. 98:9026-9031(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=8486742; DOI=10.1083/jcb.121.3.631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biol. Chem. 276:40268-40273(2001).
                                                                                                                                          Cell Res. 204:364-372(1993).
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ecroacan, eye and developing whisker ionizing matrix cells expression starts as different cell types become distinguishable in the developing follicle. Expression persists throughout the growth phase of the follicle and maintenins the same expression profile in the second hair cycle. The cells in the follicle that undergo a phase of high level expression are in transition from mitotic precursors to several discreet, differentiating cell types.

-IP TM: Synthesized in the endoplasmic reticulum as an inactive form which is proteolytically cleaved by a furin-like convertase in the trans-Golgi network before it reaches the plasma membrane to yield an active, ligand-accessible form. Cleavage results in a C-terminal fragment N(TM) and a N-terminal fragment N(EC). Following ligand binding, it is cleaved by TNF-alpha converting enzyme (TACE) to yield a membrane-associated intermediate fragment called notch extracellular truncation (NEXT). This fragment is then cleaved by presentlin dependent gamma-secretase to release a notch-derived peptide containing the intracellular domain (NICD) from the membrane.
                                                                                                                                                                                                                                 Note-No experimental confirmation available;
Note-No experimental confirmation available;
TISSUE SPECIFICITY: Highly expressed in the brain, lung and trymus. Expressed at lower levels in the spienn, bone-marrow, spinal cord, eyes, mammary gland, liver, intestine, skeletal muscle, kidney and heart. In the hair follicle, highly expressed ecclusively in the epithelial compartment.

DEVELOPMENTAL STAGE: First detected in the mesoderm at 7.5 dpc By 8.5 dpc highly expressed in presomitic mesoderm, mesenchyme and endothelial cells, while much lower levels are seen in the neuroepithelium. Between 9.5-10.5 dpc expressed at high levels in the neuroepithelium. At 13.5 dpc expressed at high levels in the cetoderm, eye and developing whisker follicles. Hair follicle
                  terminal fragment N(EC) which are probably linked by disulfide bonds. Interacts with DTX1 and DTX2.
SUBCELLULAR LOCATION: Type I membrane protein. Following proteolytical processing NICD is translocated to the nucleus.
                                                                                                                                                                                                                      VSP 001403, VSP 001404;
    SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-terminal fragment N(EC) which are probably linked by Aimiles
                                                                                                                                          Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                        IsoId=Q01705-2; Sequence=VSP 001402,
                                                                                                                                                                                  IsoId=Q01705-1; Sequence=Displayed;
                                                                                                                                                                  Name=1
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This SWISS-PROT entry is copyright. It is produced through a collaboration -i- SIMILARITY: Belongs to the NOTCH family.
-i- SIMILARITY: Contains 5 ANK repeats.
-i- SIMILARITY: Contains 36 EGF-like domains.
-i- SIMILARITY: Contains 3 Lin/Notch repeats. -!- PTM: Phosphorylated.

between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch). WGI:97363; Notchl.
G0:00058187; C:integral to plasma membrane; IC.
G0:0005185; P:protein binding; IPI.
G0:0007184; P:cell differentiation; IMP.
G0:0007386; P:compartment specification; IMP.
G0:0007386; P:determination of left/right symmetry; IMP.
G0:0007219; P:Notch signaling pathway; IC.
G0:0045944; P:positive regulation of transcription from P. . .; IDA.
G0:0048103; P:somatic stem cell renewal; IDA. AJ238029; CAB40733.1; -. X82562; CAA57909.1; -. EMBL; Z11886; CAA77941.1; -. L02613; AAK14898.1; -. X68278; CAA48339.1; -. PIR; A46019; A46019. PIR; B49175; B49175. HSSP; P46531; 1PB5. EMBL; EMBL; 8888888

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21094508; PubMed=11182080; DOI=10.1016/S0886-6273(01)00179-9;
Tanigaki K., Nogaki F., Takahashi J., Tashiro K., Kurooka H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Notch and Notch3 instructively restrict bFGE-responsive multipotent neural progenitor cells to an astroglial fate."; Neuron 29:45-55(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21331789; PubMed=11438922; DOI=10.1002/cne.1059.abs; Irvin D.K., Zurcher S.D., Nguyen T., Weinmaster G., Kornblum H.I.; "Expression patterns of Notch1, Notch2, and Notch3 suggest multiple functional roles for the Notch-DSL signaling system during brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        development.";
J. Comp. Neurol. 436:167-181(2001).
-!- FUNCTION: Functions as a receptor for membrane-bound ligands
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15-JUL-1999 (Rel. 38, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Neurogenic locus notch homolog protein 1 precursor (Notch 1)
                                                                                                                                                                                                                                                                                                              55.8%; Score 67; DB 1; Length 2531; 30.8%; Pred. No. 3.2e+02; Live 12; Mismatches .6; Indels
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MEDLINE=92111383; PubMed=1764995;
Weinmaster G., Roberts V.J., Lemke G.;
"A homolog of Drosophila Notch expressed during mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Weinmaster G.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
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MEDLINB=93202015; PubMed=1295745;
Medimaster G., Roberts V. J., Lemke G.;
"Notch2: a second mammalian Notch gene.";
Development 116:931-941(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                 248 GFAGQNCEENVDDCPGNNCKNGGACV 273
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                  Asx hydroxyl_s.
EGF_2.
EGF_Ca.
EGF_II.
                                                                                                                                   InterPro, IPR008297; Notch.
InterPro, IPR000800; Notch_region.
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Development 113:199-205(1991).
                                                                                                                                                                      Pfam; PF00023; Ank; 7.
Pfam; PF00008; EGF; 35.
Pfam; PF06816; NOD; 1.
Pfam; PF00066; Notch; 3.
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                      PR000152;
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Upport ligand activates genes of the anhancer of split local decain (NICD) is forms a transcriptional activate complex with a Refeate the implementation of differentiation, proliferation and property of the property of the
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STRAIN=BALB/c; TISSUE=Thymus;
MEDLINE=22119593; PubMed=12123574; DOI=10.1016/S0960-9822(02)00888-6;
FOLTS D.R., Santiago M.C., Berechid B.E., Nye J.S.;
"Glycogen synthase kinase-3beta modulates notch signaling and
                                                                                                                                                                                                                Gaps
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RESP, P46431; 1PB5.

RESP, P46431; 1PB5.

RESP, P46531; 1PB5.

RESP, P46531; 1PB5.

RESP, P46531; 1PB5.

RESP, P6531; 1PB7.

RESP, P6531; 1PB7.

RESP, P6531; 1PB7.

RESP, P6531; P6531;
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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SERQUENCE FROM N.A.
MEDLINE=95044925, PUDMed=7956822;
Nye J.S., Kopan R., Axel R.;
"An activated Notch Suppresses neurogenesis and myogenesis but gliogenesis in mammalian cells.";
Development 120:2421-2430(1994).
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                                                                                                                                                                      Score 67; DB 1; Length 2531;
Pred. No. 3.2e+02;
2; Mismatches 6; Indels
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Schallin K.A., Pauley A.M., Nye J.S.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databaees.
EMBL; AFS08809; AAM28905.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
 By similarity.
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                                                                                                                                                                          55.8%;
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Q8K428;
01-0CT-2002 (TEMBLEEL 22,
01-0CT-2002 (TEMBLEEL 22,
01-MAR-2004 (TEMBLEEL 26,
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Best Local Similarity
Matches 8; Conserv
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Name=Notch1;
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EGF-like 4.
EGF-like 5, calcium-binding (Potential).
EGF-like 6.
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PROSITE; PS00022; EGF_1; 35.
PROSITE; PS00186; EGF_2; 26.
PROSITE; PS50026; EGF_3; 26.
PROSITE; PS01187; EGF_CA; 21.
Activator; ANK repeat; Developmental protein; Differentiation; EGF-1ike domain; Glycoprotein; Notch signaling pathway; Phosphorylation; Receptor; Repeat; Signal; Transcription regulation; Transmembrane.
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EGF-like 2.
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Gaps

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Name=dlc; Synonyms=delC;
Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
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Local Similarity 30.8%; Pred. No. 3.2e+02;
Les 8; Conservative 12; Mismatches 6; Indels
                                          PROSITE; PSS0019, ANK_REPEAT; 4.

PROSITE; PSS0297; ANK_REP_REGION; 1.

PROSITE; PS000100 ASX HYDROXYL; 22.

PROSITE; PS01186; EGF_2; 27.

PROSITE; PS01186; EGF_2; 27.

PROSITE; PS01187; EGF_CA, 21.

ANK repeat; EGF-11ke Gomain; Receptor; Transmembrane.

SEQUENCE 2531 AA; 270832 MW; 97C91F69BABF02BF CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                01-00T-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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SNART; SM00051; DSL; 1.
PROSITE; PRO0010; EGFC CA; 4.
PROSITE; PS00010; ASX HYDROXYL; 2.
PROSITE; PS01186; EGF 1; 8.
PROSITE; PS01186; EGF 2; 8.
PROSITE; PS01187; EGF 3; 6.
PROSITE; PS01187; EGF 3; 6.
PROSITE; PS01187; EGF 3; 6.
               SMART; SM00179; EGF_CA; 25.
SMART; SM00004; NL; 3.
                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                      Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                      RESULT 23
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ID Q
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SC STRAIN=C.B-17; TISSUE=Thymus;

X MEDLINE-21753192; PubMed=12807718; DOI=10.1093/carcin/bgg071;

XA TRUIN H., Ishii-Ohba H., Ukai H., Katsube T., Ogiu T.;

RT Tsuji H., Ishii-Ohba H., Ukai H., Katsube T., Ogiu T.;

RT Granation of truncated proteins and are involved in the core propered of truncated proteins and are involved in the carcinogenesis 24:1257-1268(2003).

RT Carcinogenesis 24:1257-1268(2003).

RE AB100603; BAC77040.1; -.

DR GO, GO:0005509; F:calcium ion binding; IEA.

DR GO, GO:0005509; F:calcium ion binding; IEA.

DR GO; GO:0005509; F:calcium ion binding; IEA.

DR GO; GO:0005509; F:calcium ion binding; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR GO; GO:0005509; F:receptor activity; IEA.

DR InterPro; IPR00012; Aax. hydroxyl_S.

DR InterPro; IPR0001891; BGF_Ca.

DR InterPro; IPR0001891; BGF_Ca.

DR InterPro; IPR0001891; BGF_Ca.

DR InterPro; IPR000800; Notch_region.

DR Pfam; PF00008; BGF; 31.

DR Pfam; PF00008; BGF; 31.

DR Pfam; PF00066; Notch; 3.

DR Pfam; PF00066; Notch; 3.

DR Pfam; PF00066; Notch; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                          Query Match 55.8%; Score 67; DB.2; Length 2531; Best Local Similarity 30.8%; Pred. No. 3.2e+02; Matches 8; Conservative 12; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Transmembrane receptor Notch1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 2531 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           248 GFAGQNCEENVDDCPGNNCKNGGACV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
InterPro; IPR001438; EGF II.
InterPro; IPR006209; EGF_like.
InterPro; IPR008297; Notch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
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RESULT 22
077050
D77050
D77050
D7 01-07050

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Gaps

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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A pietchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Rosak S.A., McEwan P.J., McKernan R.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Haxapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55.0%; Score 66; DB 2; Length 1317; 25.8%; Pred. No. 2.2e+02; tive 14; Mismatches 5; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Contains 28 EGF-like domains.
EMBL; BC071562; AAH71562.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1317 AA; 140756 MW; 1A2674F4AF001646 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO, GO: 0005509; F: calcium ion binding; IEA.
InterPro; IPR00152; Asx hydroxyl_S.
InterPro; IPR00143; Agr_Ca.
InterPro; IPR001438; Agr_Ca.
InterPro; IPR001438; Agr_II.
InterPro; IPR005109; Agr_II.
InterPro; IPR005109; Agr_II.
InterPro; IPR0065109; Agr_II.
Ffam; Pr00008; Agr_II.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00181; EGF; 31.
SMART; SM00179; EGF_CA; 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00010; EGFBLOOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 25.8
les 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGF-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=SP1070;
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SEQÜENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9NGV4
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Matches
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          요
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                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-95319507; PubMed=7596411; DOI=10.1038/375787a0;
Henrique D., Adam J., Myat A., Chitnis A., Lewis J., Ish-Horowicz D.;
"Expression of a Delta homologue in prospective neurons in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDINE=95319503; PubMed=7596407; DOI=10.1038/375761a0;
Chichis A., Henrique D., Lewis J., Ish-Horowicz D., Kintner C.;
Chichis A., Henrique D., Lewis J., Ish-Horowicz D., Kintner C.;
"Primary neurogenies in Xenopus embryos regulated by a homologue of
the Drosophila neurogenic gene Delta.";
Nature 375:761-766(1995).
EMBL; L42229; AAC38017.1; -.
HSSP; P00740; 1EPM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                 Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.0%; Score 66; DB 2; Length 721; 32.0%; Pred. No. 1.3e+02; ive 11; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     721 AA; 79922 MW; 9EBDC85C439DD194 CRC64;
                                                                                                                                                                            Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 32.0%; Pred. wo. ____
Best Local Similarity 11.0%; Pred. wo. ____
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0016020; C:membrane; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0007154; P:cell communication; IEA.
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                                                                                                                                                     Created)
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                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00010; ASX HYDROXYL; 3. PROSITE; PS00022; EGF 1; 8. PROSITE; PS01186; EGF 2; 8. PROSITE; PS01187; EGF 3; 6. PROSITE; PS01187; EGF CA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, C)
05-JUL-2004 (TrEMBLrel. 27, Le
05-JUL-2004 (TrEMBLrel. 27, Le
NOTCH2, Drotein (Fragment).
Name=NOTCH2;
Homo sapiens (Human).
                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF01414; DSL; 1.
Pfam; PF00008; EGF; 6.
PRINTS; PR00010; EGFBLOOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00051; DSL; 1.
SMART; SM00179; EGF_CA; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 375:787-790(1995)
                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                Kenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=8355;
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SEQUENCE 721 P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q61Q50
Q61Q50;
                                                                                                                               091902;
                                                                                                091902
                                                  RESULT 24
Q91902
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061050
DD 061051
DT 06-JUI
DT 05-JUI
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Gaps

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variety of tissues.";
Exp. Cell Res. 204:364-372(1993).
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Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
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                              OR NO DR KW KW CO DR CO 
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Notch 2 (Fragment).
Pugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii, Neopterygii; Taleostei; Buteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Takifugu.
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                          TISSUE=Endoplasmic reticulum;
Serano T.L., Pendleton J.D., Rubin G.M.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF238608; AAR63500.1;
HSSP; P00740; IEDM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1551 AA; 167816 MW; A97EA229E9384F31 CRC64;
                                                                                                                                                                           # Rase; Fegen0011879; SP1070.

# Rase; Fegen0011879; SP1070.

# GO; GO:0005509; F:calcium ion binding: IEA.

# GO; GO:0005198; F:structural molecule activity; IEA.

# GO; GO:0005198; F:structural molecule activity; IEA.

# InterPro; IPR000152; Asx hydroxyl.

# InterPro; IPR0001891; EGF_G.

# InterPro; IPR000418; EGF_G.

# InterPro; IPR0004181; EGF_G.

# InterPro; IPR0004181; EGF_II.

# InterPro; IPR0005030; Grow_fac_recept.

# InterPro; IPR0001481; EGF_II.

# InterPro; IPR0001481; EGF_II.

# InterPro; IPR0001481; EGF_II.

# Pfam; PF00210; EGF_II.

# Pfam; PF00210; Laminin G 2; I.

# Pfam; PF00210; Laminin G 2; I.

# RNARTS; PR00010; EGFELOD.

# RNOSITE; PS001010; EGFELOD.

# RROSITE; PS010187; EGF_Z; I.

# RROSITE; PS010187; EGF_Z; I.

# RROSITE; PS01187; EGF_Z; I.
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Submitted (JUN-1997) to the EMBL/GenBark/DDBJ databases
EMBL, ABO04892; BAA20535.1; -.
HSSP, P07207; 1078.
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GO; GO:0016520; C:membrane; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0050134; P:call differentiation; IEA.
GO; GO:0050793; P:regulation of development; IEA.
InterPro; IPR000110; Asx hydroxyl S.
InterPro; IPR000895; Conā like_lec_gl.
InterPro; IPR0001891; EGF Ca.
InterPro; IPR001489; EGF Ca.
InterPro; IPR001489; EGF Li.
InterPro; IPR001438; EGF—II.
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Matches 8; Conserv
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EGF-like domain.
SEQUENCE 1551 P
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EQUENCE OF 316-1518 FROM N.A.
STRAIN=CS7BL/6 X CBA; TISSUE=Embryo;
MEDLINE=93178563; PubMed=8440332; DOI=10.1006/excr.1993.1044;
Lardelli M., Lendahl U.;
"Motch A and Motch B-two mouse Notch homologues coexpressed in a wide
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035516; Q06008; Q60941;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Neurogenic locus notch homolog protein 2 precursor (Notch 2) (Motch
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STRAIN-CS7BL/6; TISSUE-Thymus;
Hamada Y., Higuchi M., Tsujimoto Y.;
"Complete amino acid sequence and mutliform transcripts encoded by single copy of mouse Notch2 gene.",
Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
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MEDLINE-97075110; Pubmed-8917536; DOI=10.1073/pnas.93.23.13014;
Milner L.A., Bigas A., Kopan R., Brashem-Stein C., Bernstein I.D.,
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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R InterPro; IPR008297; Notch.
R InterPro; IPR00800; Notch.
R Ffam; PF000023; Ank; 6.
Ffam; PF000023; Ank; 6.
Pfam; PF000063; Ank; 6.
R Pfam; PF00066; Notch; 3.
Pfam; PF00066; Notch; 3.
R PRINTS; PR01415; ANKTRIN
R PRINTS; PR01415; ANKTRIN
R PRINTS; PR01415; ANKTRIN
R SWART; SW0019; EGFELOOD.
R SWART; SW0019; EGF CA; 22.
SWART; SW00019; EGF CA; 22.
SWART; SW0019; EGF CA; 22.
R PROSITE; PS50098; ANK REPEAT; 4.
R PROSITE; PS00010; ASX_HYDFOXYL; 22.
R PROSITE; PS01186; EGF 1; 35.
R PROSITE; PS01186; EGF 2; 29.
R PROSITE; PS01187; EGF CA; 20.
R PROSITE; EGF CA; 20.
R PROSITE; PS01187; EGF CA; 20.
R PROSITE; PS01187; EGF CA; 20.
R PROSITE; EGF CA; 20.
R PROSITE; PS01187; EGF CA; 20.
R PROSITE; PS01187; EGF CA; 20.
R PROSITE; PS011
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Hamada Y., Kadokawa Y., Okabe M., Ikawa M., Coleman J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   279 CVCVNGWSGLDCSENIDDCDTAACSPGSTCV 309
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                                                                                            EMBL; D32210; BAA22094.1; -. EMBL; X68279; CAA48340.1; -. EMBL; U31881; AAC52924.1; -.
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SMART; SM00179; EGF_CA; 23.
SMART; SM00004; NL; 3.
                                                                                                                                                            PIR, A49175; A49175.
HSSP; Q9UCV4; INZI.
MGD; MGI:97364; Notch2.
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         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21374376; PubMed=1145941; DOI=10.1073/pnas.16126998; Mizutani T., Taniguchi Y., Aoki T., Hashimoto N., Honjo T.; Conservation of the biochemical mechanisms of signal transduction among mammalian Notch family members."

T. "Conservation of the biochemical mechanisms of signal transduction among mammalian Notch family members."

Proc. Natl. Acad. Sci. U.S.A. 98:9026-9031(2001).

-!- FUNCTION: Functions as a receptor for membrane-bound ligands Jagged1, Jagged2 and Deltal to require cell-fate determination. Upon ligand activate of the chancer of split locus.

C. Mall. Acad. Sci. U.S.A. 98:9026-9031(2001).

C. Mall. Acad. Sci. U.S.A. 98:903.

C. Mall. Acad. Sci. U.S.A. 98:903.

C. Mall. Aca
                                                                                                                                       MEDLINE-95333893; PubMed-7609614; DOI-10.1016/0169-328X(94)00257-F; Higuchi M., Kiyama H., Hayakawa T., Hamada Y., Tsujimoto Y.; "Differential expression of Notch1 and Notch2 in developing and adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isoid=035516-2; Sequence=VSP 001405; Note=No experimental confirmation available; TISSUE SPECIFICITY: Expressed in the brain, liver, kidney, neuroepithelia, somites, optic vesicles and branchial arches, but
TBujimoto Y.;"
"Mutation in ankyrin repeats of the mouse Notch2 gene induces early embryonic lethality.";
Development 126:3415-3424 (1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Type I membrane protein. Following proteolytical processing NICD is translocated to the nucleus. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                           POST-TRANSLATIONAL PROCESSING, AND MUTAGENESIS OF MET-1699. MEDLINE=21523956; PubMed=11518718; DOI=10.1074/jbc.M107234200; Saxena M.T., Schroeter E.H., Mumm J.S., Kopan R.; Murine notch homologs (N1-4) undergo presentlin-dependent proteolysis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                             POST-TRANSLATIONAL PROCESSING, AND MUTAGENESIS OF MET-1699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event=Alternative splicing; Named isoforms=2;
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                                                                                                                      DEVELOPMENTAL STAGE, AND ALTERNATIVE SPLICING
                                                                                                                                                                                                           mouse brain.";
Brain Res. Mol. Brain Res. 29:263-272(1995).
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Notch extracellular truncation.
Notch intracellular domain.
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PROSITE; PS00022; EGF 2; 27.
PROSITE; PS01186; EGF 2; 27.
PROSITE; PS01187; EGF 3; 35.
Activator; Alternative splicing; ANK repeat; Developmental protein; Differentiation; EGF 1, 46 domain; Glycoprotein;
Notch signaling pathway; Phosphorylation; Receptor; Repeat; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Extracellular (Potential).
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InterPro; IPR00110; ANK.
InterPro; IPR00110; ANK.
InterPro; IPR00110; ASK. hydroxyl_S.
InterPro; IPR0010181; EGF_G.
InterPro; IPR0010181; EGF_TI.
InterPro; IPR001080; EGF_TI.
InterPro; IPR001060; NOtch.
InterPro; IPR00800; Notch.
InterPro; IPR00800; Notch.
InterPro; IPR00800; Notch.
Ffam; PF00003; ANK; 6.
Pfam; PF00006; EGF; 34.
Pfam; PF00006; NOtch; 2.
Pfam; PF00006; NOtch; 2.
Pfam; PF00006; NOtch; 2.
Pfam; PF00010; EGF8.
PRNFYS; PR09115; ANKYRIN.
PRNFYS; PR09115; ANKYRIN.
PRNFYS; PR09115; ANGYRIN.
PRNFYS; PR09115; ANGYRIN.
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(Potential)
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                     (Potential).
                                                                                                                                                                                                (Potential)
                                                                                                                                                                                    (Potential)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-T-cell;
Lemasson I., Devaux C., Mesnard J.M.;
"Partial sequence of EGF-like repeat domain of human Notch2 mRNA.";
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                            Q047ZI; Q99734; Q98240;
28-FEB-2003 (Rel. 41, Created)
25-JAN-2005 (Rel. 44, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Neurogenic locus notch homolog protein 2 precursor (Notch 2) (hN2)
Name=NOTCH2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4,
            EGF-like 9, calcium-binding (PO EGF-like 9, calcium-binding) (PO EGF-like 10.

EGF-like 11.

EGF-like 12.

EGF-like 12.

EGF-like 13.

EGF-like 14.

EGF-like 14.

EGF-like 15.

EGF-like 16.

EGF-like 16.

EGF-like 17.

EGF-like 17.

EGF-like 19.

EGF-like 20.

EGF-like 20.
                                                                                                                                                                                                                                       Length 2470;
  calcium-binding (calcium-binding (calcium-binding)
                                                                                                                                                                                                                             Score 66; DB 1; L....
Pred. No. 3.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete human notch 2 (hN2) cDNA sequence.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                   322 CVCVNGWSGDDCSENIDDCAYASCTPGSTCI 352
                                                                                                                                                                                                                                                                                      1 CXIXN----QXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                     PRT; 2471 AA
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                                                                                                                                                                                                                                    55.0%;
25.8%;
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                                                                                                                                                                                                                                                           8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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7753
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Cell 90:281-291(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE=Breast tumor;
                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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NTC2_HUMAN
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Gaps

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development: ";

J. Comp. Neurol. 436:167-181(2001).

-!- FUNCTION: Punctions as a receptor for membrane-bound ligands
Jagged1, Jagged2 and Deltal to regulate cell-fate determination.
Upon ligand activation through the released notch intracellular domain (NICD) it forms a transcriptional activator complex with RBP-J kappa and activates genes of the enhancer of split locus. Affects the implementation of differentiation, proliferation and apoptotic programs. May play an essential role in postimplantation development, probably in some aspect of cell specification and/or cell fragment, probably in some aspect of cell specification and/or cell-subjurial fragment N(EC) which are probably linked by disulfide terminal fragment N(EC) which are probably linked by disulfide proteclytical processing NICD is translocated to the nucleus.

-!- SUBCELLULAR LOCATION: Type I membrane protein. Following proteclytical processing NICD is translocated to the nucleus.

-!- TISSUE SPECIFICITY: Highly expressed in postnatal life, within numerous cells throughout the CNS. It is more highly localized to ventral nervous system colls throughout the CNS. It is more highly localized to be sent and choroid the colls throughout the CNS. It is more highly localized to be sent and collised to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE SPECIFICITY.

MEDLINE=21331789; PubMed=11438922; DOI=10.1002/cne.1059.abs;
Irvin D.K., Zurcher S.D., Nguyen T., Weinmaster G., Kornblum H.I.;
"Expression patterns of Notch1, Notch2, and Notch3 suggest multiple functional roles for the Notch-DSL signaling system during brain development.";
                                                                                                                                                                                                                                                                                              4.
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28-FEB-2003 (Rel. 41, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Neurogenic locus notch homolog protein 2 precursor (Notch 2)
                                                                                                                                                                                                                                               Score 66; DB 1; Length 2471;
Pred. No. 4e+02;
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2
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              EGF-like 35.
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Lin/Notch 2.
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ANK 3.
ANK 4.
ANK 4.
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25.8%;
                                                                                                                                                                                                                                                                      Similarity 25.888; Conservative
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Notch extracellular truncation (By
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Phosphorylation; Receptor; Repeat; Signal; Transcription regulation;
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REPOSITE; PSSCO086; ANK_REPEAT; 4.

REPOSITE; PSSCO025; EGF 2; 29.

REPOSITE; PSSCO025; EGF 3; 35.

REPOSITE; PSSCO026; EGF 3; 35.

REFORM REPOSITE; Developmental protein; Differentiation; DEFINE OF PROJUCE OF PROJ
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                                                                                InterPro; IPR001438; EGF_II.
InterPro; IPR006209; EGF_Iike.
InterPro; IPR006209; EGF_Iike.
InterPro; IPR008297; Notch.
InterPro; IPR000809; Notch_region.
Pfam; PP00023; Ank; 6.
Pfam; PP00008; EGF; 35.
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EGF II.
EGF like.
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Pfam; PF06816; NOD; 1.
Pfam; PF00006; NOCch; 2.
PIRSF; PIRSF002279; Nocch; 1.
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                     EMBL: W03661, AAK13588.1;

BR 518, A93163, AA9181

BR 1818, A49181

BR 605, 00003996, Creal surface; ISS.

BR 607, 6001003996, Creal surface; ISS.

BR 607, 6001003998, Crimtegaral to plasma membrane; ISS.

BR 607, 6001003998, Crimtegaral to plasma membrane; ISS.

BR 607, 600100399, Preal cycla arrest; ISS.

BR 607, 600100399, Preal cycla arrest; ISS.

BR 607, 600100399, Preal growth; ISS.

BR 607, 600100399, Preal growth; ISS.

BR 607, 600100399, Preal cycla arrest; ISS.

BR 607, 600100399, Preal cycla arrest; ISS.

BR 607, 600100399, Preagative regulation of elet/right symmetry; ISS.

BR 607, 600100399, Preagative regulation of cell proliferation; ISS.

BR 607, 600100399, Preagative regulation of cell proliferation; ISS.

BR 607, 600100399, Preagative regulation of cell proliferation; ISS.

BR 607, 600100399, Preagative regulation of cell proliferation; ISS.

BR 607, 600100399, Preagative regulation of RAS protein signal t. .; ISS.

BR 607, 600100399, Preagative regulation of RAS protein signal t. .; ISS.

BR 607, 600100399, Preagative regulation of RAS protein signal t. .; ISS.

BR 708, 600100399, Preagative regulation of RAS protein signal t. .; ISS.

BR 11therPro; IPR001369, EGF 11.

BR 11therPro; IPR001369, EGF 12.

BR 11therPro; IPR001369, EGF 13.

BR 11therPro; IPR001379, EGF 14.

BR
                                                                                                                                                                                                            This SWISSS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its web by non-profit institutions as long as its content is in no way modified and thics statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
Potential. Neurogenic locus notch homolog protein
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2471
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SIGNAL 1
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STRAIN=Berkeley;
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                            RESULT 32
NOTC DROME
                                                                                                                              1,
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                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
                                                                                                                                4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | SMART; SMO0179; EGF_CA; 23. |
| SMART; SMO0179; EGF_CA; 23. |
| SMART; SMO0179; EGF_CA; 23. |
| SMART; SMO0104; NJK; EF. |
| SMART; SMO0107; MR REPEAT; 4. |
| PROSITE; PS500297; ANK_REP REGION; 1. |
| PROSITE; PS500109; ASX_HVREOXYL; 23. |
| PROSITE; PS50026; EGF_1; 32. |
| PROSITE; PS50026; EGF_2; 27. |
| PROSITE; PS01186; EGF_CA; 27. |
| PROSITE; PS01187; EGF_CA; 27. |
| PR
                                                                            Score 66; DB 1; Length 2471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 2528;
                                                                                                                           5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Nakamura K., Kikuchi Y., Susaki K., Chiba C., Saito T.;
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB095016; BAC41349.1; -.
HSSP; P07207; 1078.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GG; GO:0016020; C:membrane; IEA.
GG; GO:0005509; F:calcium ion binding; IEA.
GG; GO:0004872; F:calcium ion binding; IEA.
GG; GO:000164; P:cell differentiation; IEA.
GG; GO:0050793; P:cell differentiation; IEA.
InterPro; IPR002110; ANK.
InterPro; IPR000152; FGF_2.
InterPro; IPR000142; EGF_2.
InterPro; IPR001481; EGF_Ca.
InterPro; IPR001481; EGF_Ii.
InterPro; IPR006209; EGF_Iike.
InterPro; IPR006209; CGF_Iike.
InterPro; IPR000800; Notch.
                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55.0%; Score 66; DB 2; 26.7%; Pred. No. 4e+02; tive 15; Mismatches
                                                                                                      4e+02;
                                                                                                                                                                                                       324 CVCVNGWSGDDCSENIDDCAFASCTPGSTCI 354
                                                                                                                                                                                                                                                                                                                                                          PRT; 2528 AA.
                                                                                                                                                                             CXIXN----QXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cynops pyrrhogaster (Japanese common newt).
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  By similarity.
By similarity.
                                                                                                   ; Pred. No. 4e+(
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                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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Pfam; PF00066; NotCh; 3.
PIRSF; PIRSF002279; Notch; 1.
                                                                      Query Match 55.0%;
Best Local Similarity 25.8%;
Matches 8; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR01415; ANKYRIN.
PRINTS; PR00010; EGFBLOOD.
PRINTS; PR01452; NOTCH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Receptor protein Notch1.
Name=Notch-1;
                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00023; Ank; 6.
Pfam; PF00008; EGF; 32.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=8330;
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DISULFID
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QBAXPO;
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Page 26

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09VM55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 2505-2611 FROM N.A. MEDLINE $85092-8674(85)90308-3; MEDLINE=85099329; PubMed=2981631; DOI=10.1016/0092-8674(85)90308-3; Wharton K.A., Yedvobnick B., Finnerty V.G., Artavanis-Tsakonas S.; "opa: a novel family of transcribed repeats shared by the Notch locus and other developmentally regulated loci in D. melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=87257846; PubMed=3037327;
Kelley M.R., Kidd S., Berg R.L., Young M.W.;
"Restriction of P-element insertions at the Notch locus of Drosophila
malanocaster".
                         GENOME REANNOTATION.

MEDLINE=22426069; PubMed=12537572;

Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.B.,

Smith C.D., Tupy J.L., Whitfield B.J., Bayraktaroglu L., Berman B.F

Bettencourt B.R., Celniker S.B., de Grey A.D.N.J., Drysdale R.A.,

Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99221487; PubMed=10206646; DOI=10.1038/19091;
Struhl G., Greenwald I.;
"Presenilin is required for activity and nuclear access of Notch in
                                                                                                                                                        Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99221488; PubMed=10206647; DOI=10.1038/19096; Ye Y., Lukinova N., Fortini M.E.; "Neurogenic phenotypes and altered Notch processing in Drosophila Presenilin mutants.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Diederich R.J., Matsuno K., Hing H., Artavanis-Tsakonas S.,
"Cytosolic interaction between deltex and Notch ankyrin repeats
implicates deltex in the Notch signaling pathway.";
Development 120:473-481(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERACTION WITH DX.

MEDLINE=95401878; PubMed=7671825;

Matsuno K., Diederich R.J., Go M.J., Blaumueller C.M.,

Artavanis-Tsakonas S.;

"Deltex acts as a positive regulator of Notch signaling through interactions with the Notch ankyrin repeats.";

Development 121:2633-2644(1995)
                                                                                                                                                                                                                                                                                                                                                                                     Glover D.M., "From sequence to chromosome: the tip of the X chromosome of D.
                                                                                                                                                                         systematic review.";
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTERACTION WITH DX, AND MUTANT SU42C.
MEDLINE-94215489; PubMed-8162848;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     melanogaster.";
Mol. Cell. Biol. 7:1545-1548(1987).
   Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 287:2220-2222(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-8 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 398:522-525(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cell 40:55-62(1985).
                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLEAVAGE BY PSN.
                                                                                                                                              Lewis S.E.;
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The following of the molecular genetics of the Notch signalling pathway in Drosophila melanogaster: a review.";

Hereditas 186:89-96 (2002).

Hereditas 186:89-96
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SUBCELLULAR LOCATION: Type I membrane protein. Upon activation and the cell membrane and enters into the nucleus in conjunction with Su(H).
FIN: Upon binding its ligands such as Delta or Serrate, it is cleaved (S2 cleavage) in its extracellular domain, close to the transmembrane domain. S2 cleavage is probably mediated by Kuz. It is then cleaved (S3 cleavage) downstream of its transmembrane domain, releasing it from the cell membrane. S3 cleavage requires
                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21575956; PubMed=11719214; DOI=10.1016/S0960-9822(01)00562-0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Novel Notch alleles reveal a Deltex-dependent pathway repressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
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Heitzler P.,
                                                                                                                                    MEDLINE=21657146; PubMed=11799064; DOI=10.1101/gad.942302; Lieber T., Kidd S., Young M.W.; "kuzbanian-mediated cleavage of Drosophila Notch."; Genes Dev. 16:209-221(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2703;
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29.2%; Pred. No. 4.3e+02;
Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9VM55 PRELIMINARY; PRT; 3396 AA.
Q9VM55;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Belongs to the NOTCH family. SIMILARITY: Contains 6 ANK repeats. SIMILARITY: Contains 36 EGF-like domains. SIMILARITY: Contains 3 Lin/Notch repeats.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22256570; PubMed=12369105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neural fate.";
Curr. Biol. 11:1729-1738(2001).
Nature 398:525-529(1999).
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nes 7; Conservative
                                                                                      CLEAVAGE BY KUZ.
                                                                                                                                                                                                                                                                                                                                                                                     MUTANT MCD5
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Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfied B.J., Baytaktaroglu L., Berman B.P. Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                          Annotation of the Drosophila melanogaster euchromatic genome:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 3396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Concains 2 F5/8 type C domains.
EMBL; AEO03615; AAF52472.1; -.
HSSP; P00740; 1EDM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0007155; P:cell adhesion; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 66; DB 2; I
Pred. No. 5.3e+02;
                                                                                                                                                                                                                                                                                               Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGF_2.
EGF_Ca.
EGF_IA.
EGF_II.
EGF_II.
EGF_II.
EGF_II.
EGF_II.
EGF_II.
EA5E_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000152; Asx_hydroxyl_S.
InterPro; IPR008985; ConA_like_lec_gl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LDL receptor A
Sushi SCR CCP.
TNFR C6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PS00010; ASX HYDROXYL; 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               \frac{\text{type_C}; 2.}{3}.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF02210; Laminin G 2; 1.
Pfam; PF00057; Ldl recept a; 1.
Pfam; PF00084; Sushi; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FBgn0031879; SP1070.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro; IPR001368; TNFR CInterpro; IPR003129; TSP N. PF6m, PF00431; CUB; 12. Pfam; PF00608; EGF; 12. Pfam; PF07645; EGF CA; 1. Pfam; PF07764; FS F8 EV F9 F9 F9m; PF0754; FS F8 EV F9 F9 F9 F9m; F025494; HYR; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00010; EGFBLOOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro; IPR000142; B Interpro; IPR001481; B Interpro; IPR001481; B Interpro; IPR001421; B Interpro; IPR008079; G Interpro; IPR008010; Interpro; IPR008110; H Interpro; IPR008110; I Interpro; IPR008112; L Interpro; IPR008112; L Interpro; IPR000436; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nterPro; IPR000859;
                                                                                                                                                                                                                                                                           systematic review.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00032;
SMART; SM00042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SM00179;
                                                                                                                                                                                                            Lewis S.E.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
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SMART;
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                    SO WERE TO THE STATE OF THE STA
                                                                                                                                                                                                                                                                                                                       REAL MEDLINE=20196606; PubMed=10731132; DOI=10.1126/science.287.5461.2185; Addma M.D., Celniker S.E., Holt R.A., Evans C.A., Gocapus J.D., Celniker S.E., Holt R.A., Evans C.A., Gocapus J.D., Celniker S.E., Hichards S., Ashburner M., Henderson S.N., Surderorge R.A., Lewis S.E., I Richards S., Ashburner M., Henderson S.N., Brandon R.C., Nogers Y.H., Blazel R.G., Champe M., Ffeiffer B.D., Man K.H., Doyle C., Baxter E.G., Helf G., Nelson C.R., Gabor G.L., Abril J.F., Benos P.V., Bernedl M.D., Barakaracglu L., Beasley E.M., Ballew R.M., Benos P.V., Bernedla G., Nelson C.R., Gabor G.L., R. Benos P.V., Bernedla G., Nelson C.R., Gabor G.L., R. Benos D.V., Bernedla B.D., Borcharacglu L., Beasley E.M., Borkova D., Borchan M.R., Bouck J., Brokstein P., Borchara J., Borcher A., Ohandra I.N., Andlews-Pfannkoch C., Budhakov S., Borkova D., Borcher A., Dong Z., Maya A.D., Dew I., Diez Z., Mu., Andler Y.J., Cawley S., Daliker C., Davengort L.B., Davies P., R.A., Bornes M., Dugan-Rocha S., Plukov B.C., Dunn P., Bouch S., Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Gloop F., Gorrell J.H., Gu Z., Guan P., Harris M.L., Harvey D., Hernand T.J., Hernandez J.R., Houck J., Song F., Gorrell J.H., Gu Z., Guan P., Harris M.L., Harvey D., Hennan T.J., Hernandez J.R., Houck J., Juli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kecthum K.A., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kecthum K.A., Jalali M., Kalush F., Morther B., McIntoon T.C., Morted M., Murphy B., Murphy E., Steeler F., Shen H., Massardon M., Strong R., Sunders R.D., Steeler F., Shen H., Wang X., Maya S.Y., Wassarman D.A., Wolley R., Wilsenbach J., Wang X., Wang X.Y., Wassarman D.A., Wolley R., Wolley R., Wooley S., Yao Q.A., Yell S., Pang S., Pollard J., Wang X., Wang X.Y., Wassarman D.A., Welley R., Wallshina M., Zhong M.
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Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=22426065; Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Calniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Laverty T., Muzny D.M., Nelson C. R., Pacrleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C. Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; "Finishing a whole-genome shotgun: Release 3 of the Drosophila melanogaster euchromatic genome sequence.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13)
MEDLINE=22426070; PubMed=12537573;
MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
Taninker J.S., Bergman C.M., Lewis S.E., Rubin G.M.,
                                                                                                Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
CG9138-PA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aster euchromatic genome sequence.";
Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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MEDLINE=22426069; PubMed=12537572;
                                                                            Name=SP1070; ORFNames=CG9138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 287:2185-2195(2000).
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                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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Pancer Z.;

Pancer
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Bukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinoidea; Eucchinoidea; Euchinoidea; Echinoidea; Strongylocentrotus.
NCBL_TaxID=7668;
                                                                                Mestin J., Lardelli M.;
Westin J., Lardelli M.;
Westin J., Lardelli M.;
Worth gene novel Notch genes in zebrafish: implications for vertebrate Notch gene evolution and function.";
Dev. Genes Evol. 207:51-163(1997).
EMBL; Y10354; CAA71380.1;
EMBL; Y10354; CAA71380.1;
ZEIN; ZDD-760; LEDM.
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MEDLINE=20542095; PubMed=11069281; DOI=10.1073/pnas.230096397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54.2%; Score 65; DB 2; Length 752; 33.3%; Pred. No. 1.7e+02; Live 10; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                752 AA; 82103 MW; 30939E16E0327F8A CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MRR-2004 (TrEMBLrel. 26, Last annotation update)
Scavenger receptor cysteine-rich protein variant 1.
                                                                                                                                                                                                                                                                                                                                                        PRT; 1075 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 XNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00010; ASX HYDROXYL; 9. PROSITE; PS00022; EGF_1; 17. PROSITE; PS01186; EGF_2; 15. PROSITE; PS50026; EGF_3; 17. PROSITE; PS01187; EGF_3; 17. EGF_1ike domain; Receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 8; Conserva
                             NCBI_TaxID=7955;
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NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09NC90
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                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cynops pyrrhogaster (Japanese common newt).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
NCBI_TaxID=8330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MR-2004 (TrEMBLrel. 26, Last annotation update)
01-MR-2004 (TrEMBLrel. 26, Last annotation update)
Notch receptor protein (Fragment).
Name=notch2; (Synonyme=notch6;
Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A SEQUENCE FROM N.A.

A Nakamura K., Kikuchi Y., Susaki K., Chiba C., Saito T.;
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AB095017; BAC41350.2;
R HSSP; P007440; IEDM.

GO; GO:0005509; F:Calcium ion binding; IEA.

GO; GO:0005509; F:Calcium ion binding; IEA.

GO; GO:00154; P:Calcium ion binding; IEA.

GO; GO:001550; F:Calcium ion binding; IEA.

R InterPro; IPR001152; Asx_hydroxyl_S.

InterPro; IPR001152; Asx_hydroxyl_S.

InterPro; IPR001152; Asx_hydroxyl_S.

InterPro; IPR001152; Asx_hydroxyl_S.

R InterPro; IPR001438; EGF_II.

R InterPro; IPR001438; EGF_II.

R InterPro; IPR001438; EGF_II.

R InterPro; IPR001619; EGF_II.

R InterPro; IPR00181; EGF_II.

R PRINTS; PR00101; EGFILOD.

R SMART; SM000181; EGF S.

R PROSITE; PS00010; ASX_HYDROXYL; 3.

R PROSITE; PS01186; EGF_Z; 7.

R PROSITE; PS01187; EGF_Z; 7.

R PROSITE; PS01187; EGF_Z; 7.
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              5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54.2%; Score 65; DB 2; Length 726
32.0%; Pred. No. 1.6e+02;
ive 11; Mismatches , 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            726 AA; 79866 MW; 352A40219AE67F41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2003 (TrEMBLrel. 23, Created)
1-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Ligand Delta-1.
                                                                                                                                                                                                                                                                                                                          726 AA
   8; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Conservative 11; Mismatches
                                                                                                          2119 TGKNCQHTIDDCASNPCQHGATCV 2142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          437 GFSGRHCDDNLDDCASYPCANGGTC 461
                                                                     4 XNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 XIXNOXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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EGF-like domain.
SEQUENCE 726 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=Delta-1;
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Matches
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042374
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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"Coordinate regulation of cadherin and integrin function by the chondroitin sulfate proteoglycan neurocan.";
J. Cell Biol. 149:1275-1288(2000).
EMBL; AFIL6855; AAD24546.2;
HSSP; P08661; 1BV4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=20309833; PubMed=10851024; DOI=10.1083/jcb.149.6.1275;
                                                                                 Length 1214;
                                                                                                                                         Indels
                          1214 AA; 133807 MW; A9C09C420CC157C2 CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                              Query Match 54.2%; Score 65; DB 2; Le
Best Local Similarity 26.9%; Pred. No. 2.6e+02;
Matches 7; Conservative 14; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO: 0005509; F:calcium ion binding; IEA.
GO; GO:0005540; F:hyaluronic acid binding; IEA.
GO; GO:0005529; F:sugar binding; IEA.
GO; GO:0007155; P:call adhesion; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1290 AA
                                                                                                                                                                                                                             2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000155; Asx hydroxyl_S.
InterPro; IPR00181; EGF_Ca.
InterPro; IPR00181; EGF_Ca.
InterPro; IPR00181; EGF_Ca.
InterPro; IPR001418; EGF_II.
InterPro; IPR001599; IGF_II.
InterPro; IPR001599; IGF_II.
InterPro; IPR001310; IGF_II.
InterPro; IPR001310; IGF_II.
InterPro; IPR0001316; Sushi_SCR_CCP.
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PROSITE; PSO0010; ASX HYDROXYL; 1.
PROSITE; PSO0615; C_TYPE_LECTIN_1;
PROSITE; PS50041; C_TYPE_LECTIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00059; Lectin_C; 1.
Pfam; PF00084; Sushi; 1.
Pfam; PF00193; X11nk; 2.
PRINTS; PR00010; EGFBLOOD.
PRINTS; PR01265; LINKMODLE.
ProDom; PD000918; Link; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00032; CCP; 1.
SMART; SM00034; CLECT; 1.
SMART; SM00179; EGF_CA; 1.
SMART; SM00409; IG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSS0923; SUSHI; 1
                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neurocan core protein.
Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00008; EGF; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9031;
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EGF-like domain.
SEQUENCE 1290
EGF-like domain
SEQUENCE 1214
                                                                                                                                                                                                                                                                                                                                                                                           Q9W6E1
Q9W6E1
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 33.3%; Pred. No. 2.3e+02;
Matches 8; Conservative 10; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21541033; PubMed=11685570;
Kiyota T., Jono H., Kuriyama S., Hasegawa K., Miyatani S.,
Kinoshita T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116178 MW; 61395AD6FD30BA3D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
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862 TGSSCDTEIDDCSSSPCGDNGVCV 885
                                                                   InterPro) IPR001438 EGF 114.
InterPro) IPR001438 EGF 114.
InterPro) IPR001436; Sush1_SCR_CCP.
Efan; PF00108; EGF; 3.
Ffan; PF00530; SRCR; 7.
Ffan; PF0054; Sush1; 1.
FRINTS; PR00010; EGFBLOOD.
PRINTS; PR00258; SPERACTRCPTR.
SWART; SW00179; EGF CA; 2.
SWART; SW00129; EGF CA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27
                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00010, ASX HYDROXYL; 2. PROSITE; PS000186; EGF 1; 2. PROSITE; PS00186; EGF 2; 3. PROSITE; PS00186; EGF 2; 3. PROSITE; PS00187; EGF CA; 1. PROSITE; PS00420; SRCR 1; 3. PROSITE; PS00420; SRCR 1; 3. PROSITE; PS00420; SRCR 1; 3. PROSITE; PS00923; SUSHI; 1. EGF-like domain; Receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 XNOXCXOXLDDCCSXXCNXXNXCV
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  InterPro; IPR000742;
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NCBI_TaxID=8355;
                                                          InterPro; IPR001438;
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Q90YD2
DR NO 
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NTC4_MOUSE
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NTC4 MOUSE
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Rhabditidae; Peloderinae; Caenorhabditis.
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Query Match 54.2%; Score 65; DB 2; Length 1290; Best Local Similarity 26.9%; Pred. No. 2.8e+02; Matches 7; Conservative 13; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence of the nematode C.elegans: A platform for investigating biology.";
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Smye R.;
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
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G0; G0:0005109; F:calcium ion binding; IEA.

G0; G0:0005199; F:structural molecule activity; IEA.

G0; G0:0005159; P:structural molecule activity; IEA.

G0; G0:000155; P:call adhesion; IEA.

InterPro; IPR000505; Asx hydroxyl S.

InterPro; IPR006507; Cys Knot C.

InterPro; IPR00142; EGF Ca.

InterPro; IPR00143; EGF Ca.

InterPro; IPR001438; EGF Iik.

InterPro; IPR001439; EGF Iik.

InterPro; IPR001439; EGF Iik.
                                                                                                                                                                                                                                             01-NOV-1996 (TrEWBLrel. 01, Created)
01-UNM-2003 (TrEWBLrel. 24, Last sequence update)
25-OCT-2004 (TrEWBLrel. 28, Last annotation update)
Hypothetical protein F40E10.4.
                                                                                                                                                                                                                  . PRT; 1410 AA
                                                                                                1005 GFTGENCEIDIDDCLSSPCQNGGTCI 1030
                                                                            2 XIXNOXCXQXLDDCCSXXCNXXVX 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
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InterPro; 1PR001611; LRR.
InterPro; 1PR000483; LRR Cterm.
InterPro; 1PR003129; LRR_typ.
InterPro; 1PR003129; TSP_N.
Pfam; PF00108; BGF; 7.
Pfam; PF01463; LRRT; 1.
Pfam; PF01462; LRRNT; 4.
Pfam; PF01462; LRRNT; 4.
Pfam; PF01462; LRRNT; 4.
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PRINTS; PR00010; EGFBLOOD.
PRINTS; PR00019; LEURICHRPT.
                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
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Q20204;
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Q20204
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SEQUENCE OF 1436-1600 FROM N.A.
MEDLINE-99252212; PubMed=10233982;
Lee J.-S., Haruna T., Ishimoto A., Honjo T., Yanagawa S.-I.;
"Intracisternal type A particle-mediated activation of the Notch4/int3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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TISSUB-Lung, and Testis;
MEDINE-56281668; bubMed-8681805;
Uyttendaele H., Marazzi G., Wu G., Yan Q., Sassoon D., Kitajewski J.;
"Notchfiltz", a mammary proto-oncogene, is an endothelial cell-
Specific mammalian Notch gene.";
Development 122:2251-2256(1956).
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Rowen L., Mahairas G., Qin S., Ahearn M.E., Dankers C., Lasky S.,

Loretz C., Schmidt S., Tipton S., Traicoff R., Zackrone K., Hood L.,

"Sequence of the mouse major histocompatibility locus class III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The mouse mammary tumor associated gene INT3 is a unique member of the NOTCH gene family (NOTCH4).";
Oncogene 14:1883-1890(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=92194507; PubMed=1312643; Robbins J., Blondel B.J., Gallahan D., Callahan R.; Mouse mammary tumor gene int.3: a member of the notch gene family transforms mammary epithelial cells."; J. Virol. 66:2594-2599(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleogtomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NTC4_MOUSE STANDARD; PRT; 1964 AA.
P31695; O35442; O88314; O88316; Q62389; Q62390; Q9R1W9; Q9R1X0;
O1-JUL-1993 (Rel. 26, Created)
O1-NOV-1997 (Rel. 35, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Neurogenic locus notch homolog protein 4 precursor (Notch 4)
GCONGAINS: Transforming protein Int-3].
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R PROSITE; PS01022; EGF 1; 7.
R PROSITE; PS01086; EGF 2; 5.
R PROSITE; PS01086; EGF 3; 7.
DR PROSITE; PS01087; EGF 3; 7.
DR PROSITE; PS01081, EGF 20, 2.
DR PROSITE; PS01081, Hypothetical protein.
RW EGF-like domain; Hypothetical protein.
RR FGF-like domain; Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND REVISIONS.
MEDLINE-97294599; PubMed-9150355; DOI=10.1038/8j.onc.1201035;
Gallahan D., Callahan R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54.2%; Score 65; DB 2; Length 1410; 26.9%; Pred. No. 3e+02; Live 13; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             region.";
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38 GFEGDYCEKNIDDCVNSKCENGGKCV 963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 XIXNOXCXQXLDDCCSXXCNXXNXCV 27
                                                SWART; SM00282; Dame, SWART; SM00082; IRRCT; 4.
SWART; SM00082; IRRCT; 4.
SWART; SM00013; IRR TYP; 7.
PROSITE; PS00010; ASX HYDROXYL; 2.
PROSITE; PS01225; CTCK_2; 1.
PROSITE; PS00022; EGF Z; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=Notch4; Synonyms=Int-3, Int3;
Mus musculus (Mouse).
SM00041; CT; 1.
SM00179; EGF CA; 3.
SM00282; LamG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 54.2%
Best Local Similarity 26.9%
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
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FUNCTION

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Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001110; ANK.
InterPro; IPR001152; Asx hydroxyl_S.
InterPro; IPR0010152; Asx hydroxyl_S.
InterPro; IPR0010181; EGF_Z.
InterPro; IPR001831; EGF_II.
InterPro; IPR006209; EGF_II.
InterPro; IPR006209; Grow_fac_recept.
InterPro; IPR006209; Notch.
InterPro; IPR008297; Notch.
                                       EMBL, 043091, AAC52031, -...
EMBL, 043001, AAB82004.1; -...
EMBL, AB016771, BAA32281.1; ALT_INIT.
EMBL, AB016772, BAA32283.1; ALT_INIT.
EMBL, AB016773, BAA32285.1; ALT_INIT.
EMBL, AB016774, BAA32285.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIRSF; PIRSF002279; Notch; 1.
PRINTS; PR01415; ANKYRIN.
PRINTS; PR0010; EGFBLOOD.
PRINTS; PR01452; NOTCH.
  M80456; AAB38377.1; -.
U43691; AAC52630.1; -.
U43691; AAC52631.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00248; ANK; 6.
SMART; SM00179; EGF_CA; 11.
SMART; SM00004; NL; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00023; Ank; 6.
Pfam; PF00008; EGF; 27.
Pfam; PF06816; NOD; 1.
Pfam; PF00066; Notch; 2.
                                                                                                                                                                             PIR; A38072; TVMVT3.
PIR; T09059; T09059.
HSSP; P08709; 1BF9.
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                                                                                                                                                                                                                                                                          888888888888888888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDILINE-21314376; PubMed=1145941; DOI=10.1073/pnas.161269998;

Mizutani T., Taniguchi Y., Aoki T., Hashimoto N., Honjo T.;

T. Conservation of the biochemical mechanisms of signal transduction among mammalian Notch family members.";

Proc. Natl. Acad. Sci. U.S.A. 98:9026-9031(2001).

-!- FUNCTION: FUNCTIONS as a receptor for membrane-bound ligands of the proc. Natl. Acad. Sci. U.S.A. 98:9026-9031(2001).

-!- FUNCTION: FUNCTIONS and Deltal to regulate cell-fate determination. Upon 19gand activation through the released notch intracellular companial (NICD) it forms a transcriptional activator complex with RBP-J kappa and activates genes of the enhancer of split locus. Affects the implementation of differentiation, proliferation and apoptotic programs (By similarity). May regulate branching morphogenesis in the developing vascular system.

-!- SUBDNIT: Heterodimer of a C-terminal fragment N(EC) which are probably linked by disulfide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEVELOPMENTAL STAGE: Highly expressed in endothelial cells during embryonic development from 9.0 dpc.

FTM: Synthesized in the endoplasmic reticulum as an inactive form which is proteolytically cleaved by a furin-like convertase in the trans-Golgi network before it reaches the plasma membrane to yield an active, ligand-accessible form. Cleavage results in a C-terminal fragment N(TM) and a N-terminal fragment N(EC). Following ligand binding, it is cleaved by TNF-alpha converting enzyme (TACE) to yield a membrane-associated intermediate fragment called cleaved by presentlin dependent gamma-secretase to release a notch-derived peptide containing the intracellular domain (NICD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTM: Phosphorylated.

DISFASE: Loss of the extracellular domain causes constitutive activation of the Notch protein, which leads to hyperproliferation of glandular epithelial tissues and development of mammary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Type I membrane protein. Following proteolytical processing NICD is translocated to the nucleus. TISSUE SPECIFICITY: Highly expressed in lung, moderately in heart kidney, and at lower levels in the ovary and skeletal muscle. A very low expression is seen in the brain, intestine, liver and
                                                                                                                                                                                                                                              SEQUENCE OF 1463-1964, POST-TRANSLATIONAL PROCESSING, AND MUTAGENESIS
                                                                                                                                  Uyttendaele H., Ho J., Rossant J., Kitajewski J.;
"Vascular patterning defects associated with expression of activated
Notch4 in embryonic endothelium.";
gene in a mouse mammary tumor: generation of truncated Notch4/int3
mRNAs by retroviral splicing events.";
J. Virol. 73:5166-5171(1999).
                                                                                                             MEDLINE=21244657; PubMed=11344305; DOI=10.1073/pnas.091584598;
                                                                                                                                                                                                                                                                                        MEDLINE=21523956; PubMed=11518718; DOI=10.1074/jbc.M107234200;
                                                                                                                                                                                                                                                                                                                  Saxena M.T., Schroeter E.H., Mumm J.S., Kopan R.; "Murine notch homologs (NI-4) undergo presenilin-dependent
                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 98:5643-5648(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- SIMILARITY: Belongs to the NOTCH family.
-i- SIMILARITY: Contains 5 MNK repeats.
-i- SIMILARITY: Contains 29 EGF-like domains.
-i- SIMILARITY: Contains 3 Lin/Notch repeats.
                                                                                                                                                                                                                                                                                                                                                                                   J. Biol. Chem. 276:40268-40273(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                POST-TRANSLATIONAL PROCESSING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from the membrane
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EGF-like 1.

EGF-like 2.

EGF-like 3.

EGF-like 4.

EGF-like 5, calcium-binding (Potential).
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PROSITE; PS5008; ANK REPEAT; 5.
PROSITE; PS50010; ASX HYDROXYL; 11.
PROSITE; PS50029; ACF 1; 28.
PROSITE; PS00126; EGF 2; 21.
PROSITE; PS01187; EGF CA; 9.
Activator; ANK repeat; Developmental protein; Differentiation;
Direct protein sequencing; EGF-like domain; Glycoprotein;
Notch signaling pathway; Phosphorylation; Proto-oncogene; Receptor;
Repeat; Signal; Transcription regulation; Transmembrane.
MSD; FOG/09 1 LDE 2.

GO: GO: 0009986; C:cell surface; ISS.
GO: GO: 0009886; C:cell surface; ISS.
GO: GO: 0005587; C:integral to plasma membrane; ISS.
GO: GO: 0005587; C:integral to plasma membrane; ISS.
GO: GO: 0005515; F:calculum ion binding; ISS.
GO: GO: 000515; F:protein binding; ISS.
GO: GO: 000492; F:receptor activity; ISS.
GO: GO: 0001761; P:branching morphogenesis; IMP.
GO: GO: 0001761; P:cell differentiation; ISS.
GO: GO: 0001761; P:cell differentiation; ISS.
GO: GO: 0001709; P:cell date determination; ISS.
GO: GO: 000097; P:hemopoiesis; ISS.
GO: GO: 000097; P:hemopoiesis; ISS.
GO: GO: 0000719; P:hemopoiesis; ISS.
GO: GO: 0001769; P:hemopoiesis; IMP.
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Potential.
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1464
1964
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112
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us-10-627-685a-1.rup

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EGF-like 8, calcium-binding (Potential).
EGF-like 9, calcium-binding (Potential).
EGF-like 10.
EGF-like 11, calcium-binding (Potential).
EGF-like 11, calcium-binding (Potential).
EGF-like 12, calcium-binding (Potential).
                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                         STRAIN=ICR X Swiss Webster, MEDLINE-9550156; Pubmed=7918097; DOI=10.1016/0925-4773(94)90081-7; Lardelli M., Dalstrand J., Lendahl U.; "The novel Notch homologue mouse Notch 3 lacks specific epidermal growth factor-repeats and is expressed in proliferating
                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                          POST-TRANSLATIONAL PROCESSING, AND MUTAGENESIS OF MET-1664.
MEDLINE=21523956; PubMed=11518718; DOI=10.1074/jbc.M107234200;
Saxena M.T., Schroeter E.H., Mumm J.S., Kopan R.;
"Murine notch homologs (N1-4) undergo presenilin-dependent
                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Neurogenic locus notch homolog protein 3 precursor (Notch 3)
                                                                                           Score 65; DB 1; Length 1964; Pred. No. 4e+02;
                                                                                                                  2; Indels
                                                                                                                                                                                                          PRT; 2318 AA.
                                                                                                               12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biol. Chem. 276:40268-40273(2001).
                                                                                                                                             348 GCEENLDDCAAATCAPGSTCI 368
                                                                                                                                  7 XCXQXLDDCCSXXCNXXNXCV 27
                                                                                           54.2%;
                                                                                                                                                                                                                                                                                                                                                                                                       Mech. Dev. 46:123-136(1994).
                                                                                                             7; Conservative
                                                                                                                                                                                                         STANDARD;
 2271
3309
3350
3350
4427
5508
                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
231
311
311
3352
389
429
510
                                                                                                                                                                                                                                                                                                                                                                                             neuroepithelium.
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-!- SUBCELLULAR LOCATION: Type I membrane protein. Following proteolytical processing NICD is translocated to the nucleus.
-!- TRSUE SPECIFICITY: Proliferating neuroepithelium.
-!- DEVELOPMENTAL STAGE: CNS development.
-!- PTM: Synthesized in the endoplasmic reticulum as an inactive form which is proteolytically cleaved by a furin-like convertase in the trans-Golgi network before it reaches the plasma membrane to yield an active, ligand-accessible form. Cleavage results in a C-

SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-terminal fragment N(EC) which are probably linked by disulfide

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terminal fragment N(TM) and a N-terminal fragment N(EC). Following ligand binding, it is cleaved by TNF-alpha converting enzyme (TACE) to yield a membrane-associated intermediate fragment called notch extracellular truncation (NEXT). This fragment is then cleaved by presentlin dependent gamma-secretase to release a notch-derived poptide containing the intracellular domain (NICD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neurogenic locus notch homolog protein 3.
Notch extracellular truncation.
Extracellular domain.
Potential.
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BGF-like 2.
BGF-like 3.
BGF-like 4, calcium-binding (Potential).
BGF-like 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein; Notch signaling pathway;
Receptor; Repeat; Signal; Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PSS0297; ANK REP_REGION; 1.
PROSITE; PSS0088; ANK REP_REGION; 1.
PROSITE; PS00081; ASK_HYDROXYL; 18.
PROSITE; PS000010; ASK_HYDROXYL; 18.
PROSITE; PS00002; EGF_1; 33.
PROSITE; PS01086; EGF_2; 27.
PROSITE; PS01187; EGF_3; 34.
ACLIVACOY, ANK repeat; Developmental protein; Differentiation; EGF-like domain; Glycoprotein; Notch signaling pathway; Phosphorylation; Repeat; Signal; Transcription requla
                                                                                                                                                                                                                                                                                                                                                                                                           R GO; GO: 0005887; C:integral to plasma membrane; IC.
R GO; GO: 0005887; C:integral to plasma membrane; IC.
GO; GO: 0005215; F:protein binding; IPI.
R GO; GO: 0007215; F:protein binding; IPI.
R InterPro: IPR001515; ANK. hydroxyl S.
InterPro: IPR00152; ANK. hydroxyl S.
InterPro: IPR001841; EGF_Ca.
R InterPro: IPR001881; EGF_Ta.
R InterPro: IPR0018827; Notch.
R InterPro: IPR0018090; Notch.
R Ffam; PF00106; ANK; 6.
R Ffam; PF00106; Notch; 3.
R Ffam; PF00106; Notch; 3.
R Ffam; PR00101; EGFBIO.
R PRINTS; PR00101; GGFBIO.
R PRINTS; PR001415; NOTCH.
                                                                                              from the membrane.
-!- FTM: Phosphorylated.
-! SIMILARITY: Belongs to the NOTCH family.
-!- SIMILARITY: Contains 5 ANK repeats.
-!- SIMILARITY: Contains 34 EGF-like domains.
-!- SIMILARITY: Contains 3 Lin/Notch repeats.
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                                                                                                                                                                                                                                                                                                                                                   EMBL; X74760; CAA52776.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00248; ANK; 6.
SMART; SM00179; EGF CA; 19.
SMART; SM00004; NL; 3.
                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:99460; Notch3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2318
2318
1643
1664
2318
2261
78
119
157
196
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HSSP; P00740; 1EDM.
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suppression.

-!SUBUNIT: Hetercodimer of a C-terminal fragment N(TM) and a N-terminal fragment N(EC) which are probably linked by disulfide bonds (By similarity).

-!SUBCENTIVAR LOCATION: Type I membrane protein. Following proteolytical processing NICD is translocated to the nucleus.

-!TISSUE SPECIFICITY: Expressed in postnatal life, within numerous cells throughout the CNS. It is more highly localized to ventricular germinal zones and, in early postnatal life, within numerous cells throughout the CNS. It is more highly localized to ventricular germinal zones.

-!PTM: Synthesized in the endoplasmic reticulum as an inactive form which is proteolytically cleaved by a furin-like convertage in the trans-Golgi network before it reaches the plasma membrane to yield an active, ligand-accessible form. Cleavage results in a C-terminal fragment N(TM) and a N-terminal fragment N(EC). Following ligand binding, it is cleaved by TNN-alpha converting enzyme trans-converting enzyme trans-converting membrane-associated intermediate fragment called converting enzyme trans-converting membrane-associated intermediate fragment called converting enzyme trans-converting membrane associated intermediate fragment called converting enzyme trans-converting membrane associated intermediate fragment called converting enzyme trans-converting membrane called converting enzyme trans-converting membrane called converting enzyme called called membrane associated intermediate fragment called called called membrane associated intermediate fragment called called called membrane associated intermediate fragment called called membrane associated intermediate fragment called called called membrane associated intermediate fragment called cal
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Tanigaki K.; Nogaki F., Takahashi J., Tashiro K., Kurooka H.,
Honjo T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Honjo T.;
"Notchl and Notch3 instructively restrict bFGF-responsive multipotent
neural progenitor cells to an astroglial fate.";
Neuron 29:45-55(2001).
                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   notch extracellular truncation (NEXT). This fragment is then cleaved by presentlin dependent gamma-secretase to release a
                                                                            4
                                                                                                                                                                                                                                            NTC3 RAT STANDARD; PRT; 2319 AA.
Q9R172;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Neurogenic locus notch homolog protein 3 precursor (Notch 3)
                                       Length 2318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. Hartbunians T., Boulter J., Weinmaster G., Schanen N.C.; Hartbun norvegicus mRNA for Notch 3."; submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                        Pred. No. 4.7e+02;
                                       DB 1;
                                                                                                                                    By similarity.
                                                                          13; Mismatches
                                                                                                             1 CXIXN----QXCXQXLDDCCSXXCNXXNXC 26
                                       Score 65;
                                       54.2%;
                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
                                     Query Match
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By similarity.
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4.7e+02;
                             EGF-like 15, c

EGF-like 16, c

EGF-like 19, c

EGF-like 19, c

EGF-like 21, c

EGF-like 22, c

EGF-like 23, c

EGF-like 24, c

EGF-like 27, c

EGF-like 27, c

EGF-like 27, c

EGF-like 37, c

EGF-like 31, c

EGF-like 33, c

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EGF-like 34, c
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                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@leb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytoplasmic (Potential).

EGF-like 1.

EGF-like 2.

EGF-like 3.

EGF-like 4, calcium-binding (Potential).

EGF-like 6, calcium-binding (Potential).

EGF-like 7.

EGF-like 9, calcium-binding (Potential).

EGF-like 9, calcium-binding (Potential).

EGF-like 10, calcium-binding (Potential).

EGF-like 11, calcium-binding (Potential).

EGF-like 11, calcium-binding (Potential).

EGF-like 12, calcium-binding (Potential).

EGF-like 14, calcium-binding (Potential).
notch-derived peptide containing the intracellular domain (NICD) from the membrane (By similarity).

PTM: Phosphorylated (By similarity).

SIMILARITY: Belongs to the NOTCH family.

SIMILARITY: Contains 5 ANK repeats.

SIMILARITY: Contains 34 EGF-like domains.

SIMILARITY: Contains 3 Lin/Notch repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neurogenic locus notch homolog protein 3. Notch extracellular truncation (By
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EGF Ca.
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Interpro; IPR002110; ANK.
Interpro; IPR000152; Asx hydroxyl S.
Interpro; IPR000142; EGP Z.
Interpro; IPR000142; EGP Z.
Interpro; IPR001439; ANC Z.
Interpro; IPR00143; ANC Z.
Interpro; IPR00143; ANC Z.
INTERPROSE Z.
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HSSP; P00740; 1EDM.
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Jourtel A., Corpechot C., Ducros A., Vahedi K., Chabriat H., Mouton P., Alamowitch S., Domenga V., Cecillion M., Marechal E., Maciazek J., Vayssiere C., Cruaud C., Cabanis E.-A., Ruchoux M.M., Weissenbach J., Bach J.-F., Bousser M.-G., Tournier-Lasserve E., Wotch mutations in CADASIL, a hereditary adult-onset condition causing stroke and dementia.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANT CADASIL 114-GLY--PRO-120 DEL.
MEDLINE=20264473; PubMed=10802807;
Joutel A., Chabriat H., Vahedi K., Domenga V., Vayssiere C.,
Ruchoux M.M., Lucas C., Leys D., Bousser M.-G., Tournier-Lasserve E.;
"Splice site mutation causing a seven amino acid Notch3 in-frame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANTS CADASIL TYR-49; CYS-71; CYS-90; CYS-110; CYS-133; CYS-141; ARG-146; CYS-153; CYS-169; CYS-171; CYS-182; ARG-185; SER-212; GLY-222; TYR-224; CYS-286; CYS-586; CYS-586; CYS-5789; CYS-728; CYS-985; CYS-1006; CYS-1011; CYS-1231 AND ARG-1261, AND VARIANTS ARG-170; LEU-496; GLN-1133; MET-1183 AND ALA-2223. MEDLINE=90049753; PubMed=9388399; DOI=10.1016/S0140-6736(97)08083-5; JOUADEL A., Vahedi K., Corpechot C., Troesch A., Chabriat H., Bach J.-F., Tournier-Lasserve E.;
                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bach J.-F., Tournier-Lasserve E.; "Strong clustering and stereotyped nature of Notch3 mutations in
                                                                                                                                                          Neurogenic locus notch homolog protein 3 precursor (Notch 3)
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Gunel M., Artavanis-Tsakonas S.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=97032728; PubMed=8878478; DOI=10.1038/383707a0;
                                                                                    NTC3_HUMAN STANDARD; PRT; 2321 AA. Q9UM47; Q9UMB3; Q9UPL3; Q9Y6L8; 28-F88-2003 (Rel. 41, Created) SP FFB-2003 (Rel. 41, Last sequence update) 25-JAN-2005 (Rel. 46, Last annotation update)
- |: : : | : : | | | :: | | 312 CVCVNGWTGESCSQNIDDCATAVCFHGATC 331
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                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CADASIL patients.
                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                            Name=NOTCH3;
                                                                        HUMAN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                           MEDLINE=99180765; Pubmed=10079256; Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L., Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Tsakonas S.; "Human ligands of the North receptor."; Am. J. Pachol. 154:785-794(1999).
                                                                        AF058882; AAC14346.1; JOINED.
AF058883; AAC14346.1; JOINED.
AF058884; AAC14346.1; JOINED.
AF058885; AAC14346.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                  AF058900; AAC14346.1; -. AF058881; AAC14346.1; JOINED
deletion in CADASIL.";
Neurology 54:1874-1875(2000).
                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U97669; AAB91371.1; -.
                       IDENTIFICATION OF LIGANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                AF058884; AF058885; AF058886;
                                                                                                                                                                     tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
EMBL;
EMBL;
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EMBL;
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AAC14346.1; JOINED. AAC14346.1; JOINED. AAC14346.1; JOINED. AAC14346.1; JOINED. AAC14346.1; JOINED. AAC14346.1; JOINED.

JOINED.

AAC14346.1; AAC14346.1;

JOINED

AAC14346.1;

AAC14346.1; AAC14346.1;

AF058898;

EMBL;

AF058897; AF058895;

JOINED

AAC14346.1;

AAC14346.1; JOINED

AF058893;

AF058892;

EMBL;

EMBL; EMBL; EMBL; EMBL;

EMBL; EMBL;

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Notch homolog.

Lytechinus variegatus (Sea urchin).

Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;

Evternioidea; Euechinoidea; Echinacea; Temnopleuroida; Toxopneustidae;

NCBI_TaxID=7654;
                                                                                                                                                                                                                                     MEDLINE=97454256; PubMed=9310331;
Sherwood D.R., McClay D.R.;
"Identification and localization of a sea urchin Notch homologue:
insights into vegetal plate regionalization and Notch receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R InterPro; IPR00110; ANK.

RINTERPO; IPR00110; ANK.

InterPro; IPR000121; Asx_hydroxyl_S.

R InterPro; IPR000148; EGF_Ca.

R InterPro; IPR00148; EGF_Ca.

R InterPro; IPR00148; EGF_II.

R InterPro; IPR00188; EGF_II.

R InterPro; IPR00189; EGF_II.

R InterPro; IPR000297; Not_Ch.

R InterPro; IPR000800; Not_Ch.

R Pfam; PF000008; EGF_CA; 4.

R Pfam; PF00006; Not_Ch; 3.

R PRINTS; PR01415; Not_Ch; 1.

R PRINTS; PR01415; Not_Ch; 1.

R PRINTS; PR01415; Not_Ch; 1.

R PRINTS; PR01415; NOT_CH.

R SMART; SM0010; EGFELOOD.

R SMART; SM0010; EGFELOOD.

R SMART; SM0010; EGFELOOD.

R SMART; SM0010; EGFELOOD.

R PROSITE; PS5008; ANK REPEAT; S.

R PROSITE; PS5008; NAK REPEAT; S.

R PROSITE; PS50018; NAK REPEAT; S.

R PROSITE; PS001016; EGF_1; 33.

R PROSITE; PS01186; EGF_1; 33.

R PROSITE; PS01186; EGF_2; 25.

R PROSITE; PS01186; EGF_2; 25.
                                 01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0016020; C:membrane; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0030154; P:cell differentiation; IEA.
GO; GO:0050793; P:regulation of development; IEA.
                                                                                                                                                                                                                                                                                                          regulation.";
Development 124:3363-3374(1997).
EMBL; AF000634; AAB82088.1; -.
PIR; T31070; T31070.
HSSP; P01132; 1EGF.
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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Matches
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EGF-like 11, calcium-binding (Potential)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE: PS50297, ANK REPEAT, 4.

PROSITE: PS50297, ANK REPEAT, 4.

PROSITE: PS500081, ANK REPEAT, 4.

PROSITE: PS00010; ASX_HYDROXYL; 18.

PROSITE: PS000186; EGF_2; 25.

PROSITE: PS50026; EGF_2; 25.

PROSITE: PS00187; EGF_2; 25.

PROSITE: PS00187; EGF_2; 16.

Activator; ANK repeat; Developmental protein; Differentiation; Disease mutation; EGF-like domain; Glycoprotein; Oncch asgnaling pathway; Phosphorylation; Polymorphism; Receptor; Signal; Transcription regulation; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarity).
Notch intracellular domain (By
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 65; DB 1; Leus...-
Pred. No. 4.7e+02;
...-rrhes 4; Indels
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                                                                                                                                                                   Asx hydroxyl S.
ConA like_lec_gl.
EGF Z.
EGF Ca.
EGF II.
EGF II.
EMBL; AF058899; AAC14346.1; JOINED.
EMBL; AC004257; AAC04897.1; --
EMBL; AC004663; AAC15789.1; ALT_INIT.
PIR; S78549; S78549.
HSSP; P00740; 1EDM.
Genew; HGNC:7883; NOTCH3.
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                                                                                                                                       InterPro; 1PR00110; ANK.
InterPro; 1PR00110; ANK.
InterPro; 1PR001012; Asx hydroxyl S.
InterPro; 1PR001052; Asx hydroxyl S.
InterPro; 1PR001081; EGF Z.
InterPro; 1PR001181; EGF Z.
InterPro; 1PR001081; EGF Z.
InterPro; 1PR001080; EGF II.
InterPro; 1PR001080; NOCh.
InterPro; 1PR00809; NOCh.
Pfam; PF00023; Ank; 6.
Pfam; PF00068; EGF; 34.
Pfam; PF00066; NOCh; 1.
Pfam; PF00066; NOCh; 3.
Pfam; PF00066; NOCh; 3.
Pfam; PF00066; NOCh; 3.
PRNNTS; PR01415; NOCCh; PRINTS; PR01415; ANKYRIN.
PRINTS; PR01415; ANKYRIN.
PRINTS; PR01415; ANKYRIN.
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SMART; SM00179; EGF_CA; 19.
SMART; SM00004; NL; 3.
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Best Local Similarity
Matches 9, Conserva
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 26, Last annotation update)
Notch homolog Scalloped wings.
Name-Scl;
Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
y Match 54.2%; Score 65; DB 2; Length 2531; Local Similarity 38.1%; Pred. No. 5.1e+02; nes 8; Conservative 11; Mismatches 2; Indels
                                                                                                  :|::::||| |:::::||
661 NCEEDIDDCESRPCHNGGTCV 681
                                                                          7 XCXQXLDDCCSXXCNXXNXCV 27
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Q2523
ID Q2525.
AC Q2525.
DT 01-NO
DT 01-MA
DE NOMECH
GN NOMECH
GN NOMECH
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Gaps

4 ;

13; Mismatches

9; Conservative

300 CVCVNGWTGESCSQNIDDCATAVCFHGATC 329

1 CXIXN----QXCXQXLDDCCSXXCNXXNXC 26

PRT; 2531 AA

PRELIMINARY;

016004 ID 016004 RESULT 44

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Query Match
Best Local Similarity 33.34
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phytoxin-like SCR74.
       Phytoxin-like SCR74.
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Matches 9; Conserv
                                                                                NCBI_TaxID=4787;
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NCBI_TaxID=4787;
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25-OCT-2004
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Q646W1
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                                                                                                                                                                                                                                                                                                      STRAIN-SS seeking;
MEDLINE=98426367; PubMed=9753770; DOI=10.1016/S0965-1748(98)00032-0;
Chen Z., Newsome T., McKenzie J.A., Batterham P.;
"Molecular characterization of the Notch homologue from the Australian
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
Calliphoridae; Lucilia.
                                                                                                               STRAIN=SS seeking;
MEDLINE=96400928; PubMed=8807304;
Davies A.G., Game A.Y., Chen Z., Williams T.J., Goodall S., Yen J.L.,
McKenzie J.A., Batterham P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                      "Scalloped wings is the Lucilia cuprina Notch homologue and a candidate for the modifier of fitness and asymmetry of diazinon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0016020; C:membrane; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0030154; P:ccall differentiation; IEA.
GO:0050050793; P:regulation of development; IEA.
InterPro; IPR002110; ANK.
                                                                                                                                                                                                                                                                                                                                                                               sheep blowfly, Lucilia cuprina.";
Insect Biochem. Mol. Biol. 28:601-612(1998).
EMBL; U58977; AAC36151.1; -.
HSSP; P07207; lOT8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00248; ANK; 7.

SMART; SM00179; EGF_CA; 24.

SMART; SM00179; EGF_CA; 24.

PROSITE; PS50088; ANK_REPERGION; 1.

PROSITE; PS00101; ASK_HYDROXYL; 22.

PROSITE; PS00101; ASK_HYDROXYL; 22.

PROSITE; PS00108; EGF_1; 34.

PROSITE; PS01186; EGF_2; 28.

PROSITE; PS01186; EGF_2; 28.

PROSITE; PS01187; EGF_2; 21.

ANK REPERGION; CASTANT SEGULATION SEGU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            268 QGKNCEQNIDDCPGHLCQNGGTCI 291
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InterPro; IPR00742; EGF_2.
InterPro; IPR01881; EGF_Ca.
InterPro; IPR00438; EGF_II.
InterPro; IPR006209; EGF_II.
InterPro; IPR006209; Notch.
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                                                                                                                                                                                                                                                   Genetics 143:1321-1337(1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF07645; EGF_CA; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF00008; EGF; 31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PR01452; NOTCH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00023; Ank; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nterPro; IPR000800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
ses .7; Conserv
                                                                                              SEQUENCE FROM N.A
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25-OCT-2004 (
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Q646V4
ID Q646V
AC Q646V
DT 25-OC
DT 25-OC
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"Patterns of Diversifying Selection in the Phytotoxin-like scr74 Gene Family of Phytophthora infestans.";
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AY723713; AAU21454.1;
SEQUENCE 74 AA; 7942 MW; CE020986B607F796 FPCA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ramoun S.;
Patterns of Diversifying Selection in the Phytotoxin-like scr74 Gene Family of Phytophthora infestans.";
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY722711; AAU21452.1; -...
SEQUENCE 74 AA; 7825 MW; 537318AAFF612545 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                            SEQUENCE FROM N.A.
Liu Z., Bos J.I.B., Armstrong M., Whisson S.C., da Cunha L.,
Torto-Alalibo T., Win J., Avrova A.O., Wright F., Birch P.R.J.,
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Liu Z., Bos J.I.B., Armstrong M., Whisson S.C., da Cunha L.,
Torto-Alalibo T., Win J., Avrova A.O., Wright F., Birch P.R.J.,
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Liu Z., Bos J.I.B., Armstrong M., Whisson S.C., da Cunha L.,
Torto-Alalibo T., Win J., Avrova A.O., Wright F., Birch P.R.J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53.8%; Score 64.5; DB 2; Length 74; 33.3%; Pred. No. 23; ive 11; Mismatches 0; Indels
Phytophthora infestans (Potato late blight fungus).
Eukaryota, stramenopiles, Oomycetes, Pythiales, Pythiaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phytophthora infestans (Potato late blight fungus).
Eukaryota, stramenopiles, Oomycetes, Pythiales, Pythiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h Similarity 33.3%; Score 64.5; DB 2; Length 74; Similarity 33.3%; Pred. No. 23; 9; Conservative 11; Mismatches 0; Indels
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Eukaryota, stramenopiles, Oomycetes, Pythiales, Pythiaceae;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Phytoxin-like SCR74.
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45 KCCQAINADPIAFHDCCSKSCNTGSPC 71
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us-10-627-685a-1.rup

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SEQUENCE FROM N.A
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Q9VQA9
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RX FEDILINE_218825; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klusner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

RA Hischul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Tooshiyuki S., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Pahey J., Helton E., Ketteman M., Madan A.M., Gibbs R.A.,

RA Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schwutz J., Myers R.M., Butterfield Y.S.,

RA Jones S.J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
       "Patterns of Diversifying Selection in the Phytotoxin-like scr74 Gene Family of Phytophthora infestens."; Submity of Chycophthora infestens."; Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.

EMBL, AY723705; AAU31446.1; -8EQUENCE 74 AA; 7885 MW; 98D110005D613927 CRC64;
                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                     'Match 53.8%; Score 64.5; DB 2; Length 74; Local Similarity 33.3%; Pred. No. 23; les 9; Conservative 11; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0005509; F:calcium ion binding; IBA. InterPro; IPR000152; Asx hydroxyl_S. InterPro; IPR00042; EGF 2. InterPro; IPR0181; EGF 7. InterPro; IPR0181; EGF II. InterPro; IPR005209; EGF II. InterPro; IPR005209; EGF II.
                                                                                                                                    7 XCXQXLD-----DCCSXXCNXXNXC 26
                                                                                                                                                    :|:|:::|
45 KCCQAINPDPIAFHDCCSKSCNTGSPC 71
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SMART; SM00179; EGF_CA; 12.
PROSITE; PS00010; ASX_HYDROXYL; 9.
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                                                                                                                                                                                                                            PRELIMINARY;
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Pfam; PF07649; EGF_CA; 3.
                                                                                                                                                                                                                                                                                      Hypothetical protein.
Homo sapiens (Human).
                                                                                      Query Match
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Q6P3V5;
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Matches
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RADILINE-2196006; Pubbed=10731132; DOI=10.1126/science.287.5461.2185; RADILINE-2195006; Pubbed=10731132; DOI=10.1126/science.287.5461.2185; RADININE-2195006; Pubbed=10731132; DOI=10.1126/science.287.5461.2185; RADININE-2195006; Pubbed=10731132; DOI=10.1126/science.287.5461.2185; RADININE-2195006; RADININE-S.E., LiD P.W., Hoskins R.A., Galle R.F., Addrews P.E., Lewis B. R., Farandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D., RADININE, Baud M. M. H.J., Andrews-Pfannkoch C., Baldwin D., RADILO R. M., Baud M., Baxendale J., Bayraktazoglu L., Basaley E.M., Ballew R.W., Baud M., Barchale J., Bayraktazoglu L., Basaley E.M., RADILO R.D., Botchan M.R., Bouck J., Broketein P., Brottier P., RADILO R.A., Barchale J., Bayraktazoglu L., Basaley E.M., RADINO R.D., Botchan M.R., Bouck J., Broketein P., Brottier P., RADICKOW D., DOIDER, D., Donn P., RADICH R., Cayley S., Dahlke C., Davenport L.B., Davies P., Dunn P., RADIDIN R., E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RADIOR R., Dougles L., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RADIOR R., Cong F., Gorg N. S., Gelbart W.M., Glasser K., A Harris N.L., Harvey D., Heiman T.J., Herrandez J.R., Harris M., Harvey D., Heiman T.J., Herrandez J.R., Harris M., Harvey D., Heiman T.J., Herrandez J.R., Harris M., Harris M., Maturoh R.A., Mowland T.J., Wei M.H., Ibegwam C., Radila M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Moyl M., Murphy B., Morpher S., Wolferson D.L., Markho G., Malshina N.V., Mobarry C., Morris J., Moshrefi A., Molson K.A., Nixon K., Morskern D.R., Pacleb J.W., Radin R.A., Moyl M., Murphy B., Weirek S., Weire R., Wallshin R.C., Staden-Kamos I., Simpson M., Strong R., Sund P., Harris M., Walshin G., Staden G., Pan G., Zhan M., Zhong R., Williams S.M., WoodageT, Worley K.C., Worley K., Walseren B., Walliams S.M., WoodageT, Worley K.C., Wu Weisenbach J., Nara A., Harris M., Walshin G.W., Zhong W., Zhong W., Zhong W., Zhong W., Zhong W., Zhong G., Zhan M., Zhong W., Zhong S., Zhan M., Zhong K.H., Wesserman D.S., Zhon 
                                                                                                                                                                                                                                                                                                                             Gaps
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ebhydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                        Length 647;
                                                                                                                               domain; Hypothetical protein.
647 AA; 68068 MW; B71E79AA16E50CE8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                             53.3%; Score 64; DB 2; Ler
33.3%; Pred. No. 1.9e+02;
ive 12; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                            351 SCEENLDDCIAATCAPGSTCI 371
                                                                                                                                                                                                                                                                                                                                                                                7 XCXQXLDDCCSXXCNXXNXCV 27
PS00022; EGF 1; 14.
PS01186; EGF 2; 10.
PS50026; EGF 3; 15.
PS01187; EGF CA; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2003 (TrEMBLrel. 25,
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                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 7; Conserv
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PROSITE;
PROSITE;
PROSITE;
PROSITE;
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                   "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Waterston R.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WormBase Consortium;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases
EMBL; U80815; AAB37995.1; --
PIR; T25933; T25933.
  (TrEMBLrel. 03, Created)
(TrEMBLrel. 03, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                      elegans cosmid W02C12.";
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                                      01-WAR-2004 (TrEMBLrel. 26, Last appotentical protein WO2Cl2.1. Name=WO2Cl2.1; ORFNames=WO2Cl2.1; Caenorhabditis elegans.
                                                                                                                                                                                                                                STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Bristol N2;
Murray J., Wohldmann P.;
"The sequence of C. elega
                                                                                                                                                                                                                                                                        WormBase Consortium;
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              Celliker S.E., Wheler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M., "Finishing a whole-genome shotgun: Release 3 of the Drosophila melanogaster euchromatic genome sequence.", Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                                                                                                                                                                                                                Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22426069; PubMed=12537572;
Mairar S., Crobby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Annotation of the Drosophila melanogaster euchromatic genome: a systematic review.";
Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
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                                                                                                                                                                                                                                                                                                                                                     a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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HSSP; P00740; 1EDM.
Flybase, FBgn0031414; CG15388.
InterPro; IPR000152; Asx hydroxyl_S.
InterPro; IPR00182; Asx hydroxyl_S.
InterPro; IPR00181; EGF_Ca.
InterPro; IPR00181; EGF_Ca.
InterPro; IPR00181; EGF_Ca.
InterPro; IPR00189; EGF_II.
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EIKGSNCEENVDECMSNPCONGGLC 28
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MEDLINE=22426065; PubMed=12537568; Celniker S.E., Wheeler D.A., Kronm
                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=22426070; PubMed=12537573;
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PROSITE; PS00010; ASX HYDROXYL;
PROSITE; PS00022; EGF_1; 5.

PROSITE; PS01186; EGF_2; 3.

PROSITE; PS50026; EGF_3; 5.
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PRINTS; PR00010; EGFBLODD.
SMART; SM00179; EGF_CA; 3.
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nes 7; Conservative
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EGF-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.3%; Score 64; DB 2; Length 1372; 25.0%; Pred. No. 3.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PSS0923; SUSHI; 1.
BGF-like domain; Hypothetical protein.
SEQUENCE 1372 AA; 150561 MW; 0537FA79BA0576C5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
GO, GO:0005509; F:calcium ion binding; IEA.
InterPro; IPR000152; Asx hydroxyl S.
InterPro; IPR000152; Asx hydroxyl S.
InterPro; IPR000142; EGF Z.
InterPro; IPR00143; EGF Za.
InterPro; IPR00143; EGF Za.
InterPro; IPR001436; EGF II.
InterPro; IPR00150; EGF III.
InterPro; IPR00170; Pentaxin.
InterPro; IPR001759; Pentaxin.
InterPro; IPR001759; Pentaxin.
InterPro; IPR000436; Sushi_SCR_CCP.
Pfam; PF00008; EGF; 10.
Pfam; PF00008; EGF; 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 XNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                 PRINTS, PROGOTO, EGFBLOOD.
PRODOM, PD002153; Pentaxin; 1.
SWART; SM00129; EGF CA; 4.
PROSITE; PS00010; AST HYDROXYL; 5.
PROSITE; PS00022; EGF 1; 11.
PROSITE; PS01186; EGF 2; 8.
PROSITE; PS050026; EGF 1; 12.
PROSITE; PS01187; EGF 2; 8.
PROSITE; PS01187; EGF 2; 8.
PROSITE; PS01187; EGF 2; 8.
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Best Local Similarity
Matches 6; Conserv
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PRT; 1372

PRELIMINARY;

P91526 P91526; RESULT 51 P91526 ID P9152 AC P9152

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EMBL;
EMBL;
MEDIALIALIUN C. LILGUAGE C. MILEGIAGIS E., Henrique D., Carcangiu M.-L., A Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Tsakonas S.; Thuman ligands of the Norch receptor.";

Am. J. Pathol. 154:785-794(1999).

- I- FUNCTION: Functions as a receptor for membrane-bound ligands of the Norch receptor.";

- I- FUNCTION: Functions as a receptor for membrane-bound ligands of the Jagged1, Jagged2 and Deltal to regulate cell-fate determination. Upon ligand activation through the released norch intracellular domain (NICD) it forms a transcriptional activator complex with RBP-J kappa and activates genes of the enhancer of split locus. Affects the implementation of differentiation, proliferation and appototic programs. May regulate branching morphogenesis in the developing vascular system (By similarity).

- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-terminal fragment N(EC) which are probably linked by disulfide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isoid=099466-3; Sequence-VSP 001407; Isoid=099466-3; Sequence-VSP 001407; ItSSUE SPECIFICITY: Highly expressed in the heart, moderately in the lung and placenta and at low levels in the liver, skeletal muscle, kidney, pancreas, spleen, lymph node, thymus, bone marrow and fetal liver. No expression was seen in adult brain or peripheral blood leukocytes.
                                                                                                                                                                                                                                    MEDLINE-97311416; PubMed-9168133; DOI=10.1016/S0378-1119(96)00857-8; Sugaya K., Sasanuma S.-I., Nohata J., Kimura T., Fukagawa T., Nakamura Y., Ando A., Inoko H., Ikemura T., Mita K.; Gorganization of human NOTCH4 and (CTG)n polymorphism in this human counterpart gene of mouse proto-oncogene Int3.";
                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 1), AND POLYMORPHISM OF POLY-LEU REGION.
                                                                                                                                       Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bonds (By similarity).
SUBCELLULAR LOCATION: Type I membrane protein. Following
Proteclytical processing NICD is translocated to the nucleus.
ALTERNAIUE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                 TISSUE-Bone marrow, and Heart;
MEDLINE=98360091; PubMed=9693032; DOI=10.1006/geno.1998.5330;
Li L., Huang G.M., Banta A.B., Deng Y., Smith T., Dong P.,
Friedman C., Chen L., Trask B.J., Spies T., Rowen L., Hood L.;
"Cloning, characterization, and the complete 56.8-kilobase DNA
sequence of the human NOTCH4 gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event=Alternative splicing, Named asoforms=3, Comment=Experimental confirmation may be lacking for some
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-503 FROM N.A., AND VARIANTS GLN-117 AND GLN-317.
Miyagawa T., Tokunaga K., Hojho H.;
"Human notch4 gene variant.";
                          NTC4_HUMAN STANDARD; PRT; 2003 AA. (99466; 000306; Q99480; Q99480; Q99488; Q9UII9; Q9UIJ0; 28-FEB-2003 (Rel. 41, Last sequence update) 25-JAN-2005 (Rel. 46, Last annotation update) Neurogenic locus notch homolog protein 4 precursor (Notch 4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=2;
IsoId=Q99466-2; Sequence=VSP_0014.06;
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORMS 1, 2 AND 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=Q99466-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IDENTIFICATION OF LIGANDS
                                                                                                                                                                                                                          TISSUE=Placenta;
                                                                                                                                                                                   NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            isoforms;
                                                                                                                           Name=NOTCH4;
  RESULT 52
NTC4_HUMAN
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c. 1- PMTA, Synthesized in the endoplasmic retironum as an inactive form that the trans-cold; network before it recents the plans comparates in the crans-cold; network before it recents the plans comparates in the crans-cold; network before it recents the plans comparates in the crans-cold; network before it recents the plans comparates in the creaming and an extra cold; network before it recents the plans compared in a class of the content of the cont
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SEQUENCE FROM N.A.

Hori S., Saitoh T., Matsumoto M., Makabe K.W., Nishida H.;

Hori S., Saitoh T., Matsumoto M., Makabe K.W., Nishida H.;

Hori S., Saitoh T., Matsumoto M., Makabe K.W., Nishida H.;

In the central nervous system during ascidian embryogenesis.";

Dev. Genes Evol. 207:371-380(1997).

EMBL, AB001127; BAA25571.1;

PIR, T30201; T30201.

HSSP; P07207; 1078.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RELIVES; PRO1422; NOTCH.

REMART; SM00249; ANN; 7.

REMART; SM000179; EGF_CA; 19.

REMART; SM00004; MIL; 3.

REMOSITE; PS50089; ANK REPEAT; 5.

REMOSITE; PS50010; ASX-HYDROXYL; 18.

REMOSITE; PS01186; EGF_2; 22.

REMOSITE; PS01186; EGF_2; 22.

REMOSITE; PS01186; EGF_2; 23.

REMOSITE; PS01186; EGF_2; 24.

REMOSITE; PS01186; EGF_2; 22.

REMOSITE; PS01186; EGF_2; 22.

REMOSITE; PS01187; EGF_CA; 18.

REMOSITE; PS01187; EGF_CA; 18.

REMOSITE; PS01187; EGF_CA; 18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53.3%; Score 64; DB 2; Length 2352; 26.9%; Pred. No. 6e+02; tive 13; Mismatches 6; Indel8
                                Halocynthia roretzi (Sea squirt).
Bukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
Stolidobranchia; Pyuridae; Halocynthia.
NCBI_TaxID=7729;
                                                                                                                                                                                                                      070244 PRELIMINARY; PRT; 3623 AA.
070244;
01-AUG-1998 (TrEMBLrel. 07, Created)
01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Intrinsic factor-B12 receptor precursor. Name=CUBILIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           446 GFTGDDCSQNIDECASTPCMNKATCI 471
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
              HrNotch protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00010
                          Name=HrNotch;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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070244
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                                                                                                                                                                                                                                                                                                                                                                                EGF-like 2.
EGF-like 3.
EGF-like 4.
EGF-like 5, calcium-binding (Potential).
EGF-like 6.
EGF-like 7, calcium-binding (Potential).
EGF-like 8, calcium-binding (Potential).
EGF-like 9, calcium-binding (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EGF-like II, calcium-binding (Potential)
EGF-like 12, calcium-binding (Potential)
EGF-like 13, calcium-binding (Potential)
EGF-like 14, calcium-binding (Potential)
EGF-like 15, calcium-binding (Potential)
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                                                                                                                                                                                                                                               Potential.
Neurogenic locus notch protein homolog
Notch extracellular truncation (By
                                                              PROSITE; PSSO297, ANK REP REGION; 1.
PROSITE; PSSO297, ANK REPEAT; 5.
PROSITE; PSSO0010; ASX_HYDROXYL; 11.
PROSITE; PSO0010; ASX_HYDROXYL; 11.
PROSITE; PSO10186; EGF_2; 21.
PROSITE; PSO1186; EGF_2; 22.
PROSITE; PSO1187; EGF_04; 9.
Activator; Alternative splicing; ANK repeat; Developmental protein; Differentiation; EGF-1; Possible and Activator; Plosphorylation; Polymorphism; Receptor; Repeat; Signal; Transcription regulation; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                               Notch intracellular domain (By
                                                                                                                                                                                                                                                                                                                            Extracellular (Potential)
                                                                                                                                                                                                                                                                                                                                                        Cytoplasmic (Potential).
EGF-like 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
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12; Mismatches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGF-like 19.
EGF-like 20.
EGF-like 20.
EGF-like 21.
EGF-like 22.
EGF-like 23.
EGF-like 24.
EGF-like 25.
                                                                                                                                                                                                                                                                                    similarity).
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Lin/Notch 1.
                                                                                                                                                                                                                                                                                                               similarity)
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                         SMART; SM00248; ANK; 5.
SMART; SM00179; EGF_CA; 11.
SMART; SM00004; NL; 3.
                                                                                                                                                                                                                           Triplet repeat expansion.
SIGNAL 1 23
CHAIN 24 2003
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                                                                                                                                                                                                                                                                                                2003
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1044
1085
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Best Local Similarity
7, Conserva
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1432
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01-AUG-1998
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TRANSMEM
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061240
ID 06124
AC 06124
DT 01-AU
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Page 42

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P49013;
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SEQUENCE
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DOMAIN
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FBP3_STRPU
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Matches
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              Moestrup S.K., Kozyraki R., Kristiansen M., Kaysen J.H., Rasmussen H.H., Brault D., Pontillon F., Goda F.O., Christensen E.I., Hammond T.G., Verroust P.J., Hammond T.G., Verroust P.J., "The intrinsic factor-vitamin Bl2 receptor and target of teratogenic antibodies is a megalin-binding peripheral membrane protein with homology to developmental proteins.";
S. Biol. Chem. 273:8235-5242(1998).
PIR; T08618; T08618.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and quail.",
J. Mol. Bvol. 36:255-262(1993).

-!- FUNCTION: Metallothioneins have a high content of cysteine
residues that bind various heavy metals.
-!- DOWAIN: Class I metallothioneins contain 2 metal-binding domains:
four divalent ions are chelated within cluster A of the alpha
domain and are coordinated via cystein/I thiolate bridges to 11
cysteine ligands. Cluster B, the corresponding region within the
beta domain, can ligate three divalent ions to 9 cysteines.
-!- SIMILARITY: Belongs to the metallothionein superfamily. Family 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Liver,
MEDLINE=93247066; PubMed=8483164;
Shartzer K.L., Kage K., Sobieski R.J., Andrews G.K.;
"Evolution of avian metallothionein: DNA sequence analyses of the turkey metallothionein gene and metallothionein pheasant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Colinus virginianus (Bobwhite Grani) (Common bobwhite).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Odontophoridae; Colinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
0
MEDLINE=98148073; PubMed=9478979; DOI=10.1074/jbc.273.9.5235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53.3%; Score 64; DB 2; Length 3623; 29.2%; Pred. No. 8.9e+02; Live 13; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    20 Fotential.
23 intrinsic factor-B12 receptor.
398984 MW; 39FB792AC6545540 CRC64;
                                                                                                                                 HSSP, POOT40; IIXA.

GO; GO:0005509; F:calcium ion binding; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0004872; F:receptor activity; IEA.

InterPro; IPR000152; ASX_hydroxyl_S.

InterPro; IPR000742; EGF_Ca.

InterPro; IPR001891; EGF_Ca.

InterPro; IPR001891; EGF_Ca.

InterPro; IPR001891; EGF_Ca.

Ffam; PF00081; EGF_Ca.

Ffam; PF00081; EGF_Ca.

R Ffam; PF00081; EGF_Ca.

R SMART; SM00042; CUB: 27.

R SMART; SM00042; CUB: 27.

R SMART; SM00042; CUB: 27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
08-FEB-2003 (Rel. 41, Last annotation update)
Metallothionein B (MTB) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : |:|::::|| |::| ::|:
425 SGQNCTENINDCSSNPCLNGGTCI 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 XNOXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00022; EGF 1; 4.
PROSITE; PS01166; EGF 2; 2.
PROSITE; PS01026; EGF 3; 6.
PROSITE; PS01187; EGF CA; 4.
EGF-like domain; Receptor; Signal.
                                                                                                                                                                                                                                                                                                           400179; EGF CA; 4.
PS00010; ASX HYDROXYL; 3.
PS01180; CUB; 27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 29.27
Best Local 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                    3623
                                                                                                                                                                                                                                                                                                                                                                                                                                              3623 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9014;
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MTB COLVI
P27087;
                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 55
MTB_COLVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Gastrula;
MEDIATE-93273088; PubMed=8500658; DOI=10.1006/dbio.1993.1155;
MEDIATE-9273088; PubMed=8500658; DOI=10.1006/dbio.1993.1155;
Whe SpEGF III gene encodes a member of the fibropellins: EGF repeat-containing proteins that form the apical lamina of the sea urchin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1996 (Rel. 33, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Fibropellin C precursor (Epidermal growth factor-related protein 3)
(EGF III) (Fibropellin III)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dev. Biol. 157:526-538(1993).
-!- FUNCTION: Forms the apical lamina, a component of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1612EB40EE6EB875 CRC64;
                                                                                                                                                                                                                                InterPro; IRR003019; Metallthion.
InterPro; IRR003019; Metallthion.
InterPro; IRR0010006; Metallthion.
InterPro; IRR001212; Somatomedin.B.
Pfam; PR00131; Metallothio; 1.
PRINTS; PR00080; MTVERTEBRATE.
PRINTS; PR000203; MATALLOTHIONEIN VRT; PARTIAL.
Metal.-binding; Metal-thiolate cluster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52.5%; Score 63; DB 1; 33.3%; Pred. No. 20; ive 10; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              570 AA.
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Cluster B.
Cluster B.
Cluster B.
Cluster B.
Cluster A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 CKCKNCRCRSCRKSCCSCCPAGCNNCV 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1996 (Rel. 33, Created)
                                                                                                                                                                          EMBL; X62512; CAA44371.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4429 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                              S33379; S18174.
                                                                                                                                                                                                                  HSSP; P04355; 1MRT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strongylocentrotus.
NCBI_TaxID=7668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43
43 AA;
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Dev. Biol. ;
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE 57BL/6; TISSUE=Brain;

X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Aleschul S.F., Zeeberg B., Buetow K.H., Schaefer C.R., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Ra Bischeron M., Soares M.B., Bonaldo M.F., Carannor T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toonhyuki S., Carninci P., Frange C.,

RA Brownstein M.J., Usdin T.B., Toonhyuki S., Carninci P., Frange C.,

RA Brownstein M.J., Wokin T.B., Toonhyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Wokin P.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Britang M., Madan P.J., Mockernan R.J., Malak J.J., Lu X., Glibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Aones S.J., Max M.J., Smailus D.E., Schnerch A., Schein J.E.,

RA Gones S.J., Max M.J., Smailus D.E., Schnerch A., Schein J.E.,

RA Gones S.J., Max M. Sanishos M. Smailus D.E., Schnerch A., Schein J.E.,

RA Gones S.J., Max M. Smailus Of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                               Gaps
By similarity.
N-linked (GLCNAC. ...) (Potential).
N-linked (GLCNAC. ...) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
1- SIMILARITY: Contains 6 EGF-like domains.
EMBL, BCO52002, AAH22002.1;
HSSP; P00740; 1EDM.
MGD; MGI-1096877; D113.
MGD; MGO:0005615; C:extracellular space; TAS.
MGO; GO:0016021; C:integral to membrane; TAS.
MGO; GO:0017386; P:compartment specification; IMP.
R InterPro; IPR001438; EGF_II.
R InterPro; IPR001438; EGF_II.
R InterPro; IPR006209; EGF_II.
                                                                                                                                                                                                                                                  Query Match 52.5%; Score 63; DB 1; Length 570; Best Local Similarity 26.9%; Pred. No. 2.1e+02; Matches 7; Conservative 12; Mismatches 7; Indels
                                                                                                                                                                                                               BE665E3E1C05E6EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Delta-like 3, isoform 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     585 AA
                                                                                                                                                                                                                                                                                                                                                              205 GFTGDNCETDIDECASAPCRNGGACV 230
                                                                                                                                                                                                                                                                                                                                      2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                               61116 MW;
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STRAIN-C57BL/6; TISSUE-Brain;
    363
398
398
4419
428
330
357
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                                                                                                                                                                  136 1
357 3
570 AA;
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CARBOHYD
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Q80W06
    FT FT FT FT S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Extracellular.
DEVELOPMENTAL STAGE: Low levels in unfertilized eggs and during early cleavage, then rapidly increases in abundance between late morula and mesenchyme blastula stages to maximal levels maintained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Potential)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE, PROGRAM ASK HYDROXYL, 8.
PROSITE; PRO1010, ASK HYDROXYL, 8.
PROSITE; PRO1010; CUB. 1.
PROSITE; PS01020; EGF 1; 8.
PROSITE; PS01066; EGF 2; 7.
PROSITE; PS01087; EGF 2; 8.
BROSITE; PS01187; EGF CA, 6.
Biotin, Calcium-binding; EGF-1ike domain; Glycoprotein; Repeat;
                                                                                                   through subsequent stages.

MISCELLANEOUS: Expressed both maternally and zygotically.
SIMILANTY: Contains 1 avidin domain.
SIMILANITY: Contains 1 CUB domain.
SIMILANITY: Contains 8 EGF-like domains.
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calcium-binding (
calcium-binding (
calcium-binding (
calcium-binding (
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EGF-like 6, calcium-binding
EGF-like 7.
EGF-like 8, calcium-binding
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Fibropellin C.
CGE-like 1.
CGF-like 2, calc
EGF-like 3, calc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR00152; Asx hydroxyl S. InterPro; IPR005469; Avidin. InterPro; IPR005469; Avidin/str. InterPro; IPR000859; CUB. InterPro; IPR0000859; CUB. InterPro; IPR001891; EGF_2. InterPro; IPR001891; EGF_II. InterPro; IPR001891; EGF_II. InterPro; IPR005209; EGF_II. Pfam; PF01382; Avidin; 1. Pfam; PF001008; EGF; 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Avidin
                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L07045; AAA30045.1; -. PIR; A48836; A48836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00709; AVIDIN.
PRINTS; PR00010; EGFBLOOD.
  extracellular matrix.
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SIGNAL
CHAIN
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Rattus norvegicus (Rat)
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515
589
2213
2213
312
312
3391
429
                                                                                                                                                                                      (By similarity).
                                                                          NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                        BEQUENCE FROM N.A.

WA Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,

Buzuki Y., Nagai K., Sugano S., Ishii S., Kawai Hio Y., Saito K.,

A Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,

Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,

Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;

Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

HSSP; PO0740; 1EDM.

RHSSP; PO0740; 1EDM.

RINEFPC; IPR001438; EGF_II.

RINEFPC; IPR006210; EGF_IK.

RINEFPC; IPR006210; EGF_IK.

RINEFPC; IPR0061005; MyD_DNA_binding.

Pfam; PP00008; EGF; S.

RINTES; PR000105; MyD_DNA_binding.

PRINTS; PR00010; EGFELOD.
                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                    Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
0
                                                                                                                    Query Match 52.5%; Score 63; DB 2; Length 585; Best Local Similarity 30.8%; Pred. No. 2.1e+02; Matches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52.5%; Score 63; DB 2; Length 58, 30.8%; Pred. No. 2.1e+02;
                                                                                                  585 AA; 61125 MW; EB276F60899BD4E9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             587 AA; .61144 MW; 2FF5E3EN66789B1B CRC64;
                                                                                                                                                                                                                                                 01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein FLJ90821.
                                                                                                                                                                                                                                   587 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              589 AA
        InterProj IPR001005; Myb_DNa_binding. Pfan, Pr00008; RGF; 5.
PRLNTS; PR00010; EGFBLOOD. SMART; SM00181; EGF; 6.
PROSITE; PS00122; EGF 1; 6.
PROSITE; PS50126; EGF 2; 6.
PROSITE; PS50026; EGF 3; 5.
PROSITE; PS00134; MYB_2; UNKNOWN_1.
EGF-like domain. S85 AA; 61125 MW; EB276F;01
                                                                                                                                                                        380 GFAGPRCEHDLDDCAGRACANGGTCV 405
                                                                                                                                                           2 XIXNOXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   382 GFAGPRCEHDLDDCAGRACANGGTCV 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00022; EGF 1; 6.
PROSITE; PS01186; EGF 2; 6.
PROSITE; PS0026; EGF 3; 6.
PROSITE; PS00334; MYB 2; UNKNOWN 1.
EGF-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    088671;
16-OCT-2001 (Rel. 40, Created)
InterPro; IPR006210; IEGF
                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DLL3 RAT
ID DLL3 RAT
AC 088671;
DT 16-0CT-200
                                                                                                                                                                                                                                Q8NBS4
Q8NBS4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                            RESULT 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

Boulter J., Greenfield A., Weinmaster G.;

Boulter J., Greenfield A., Weinmaster G.;

Boulter J., Greenfield A., Weinmaster G.;

Bountted (AUG-1998) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: Inhibits primary neurogenesis. May be required to divert neurons along a specific differentiation pathway. Play a role in the formation of somite boundaries during segmentation of the
                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     paraxial mesoderm (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
-!- DOMAIN: The DSL domain is required for binding to the Notch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R GG; GC:000512; F:Notch binding; ISS.
R GG; GC:0001701; P:embryonic development (sensu Mammalia); ISS.
R GG; GC:0001701; P:embryonic development (sensu Mammalia); ISS.
R GG; GC:0001701; P:embryonic development (sensu Mammalia); ISS.
R GG; GC:0001701; P:notch signaling pathway; ISS.
R GG; GC:0001501; P:Reletal development; ISS.
R GG; GC:0001501; P:Reletal development; ISS.
R InterPro; IPR000742; EGF_1.
R InterPro; IPR000743; EGF_1.
R InterPro; IPR00010; EGFF[1].
R RINTS; PR00010; EGFF[1].
R RENTY; PR00010; EGFF[2].
R PROSITE; PS00022; EGF_1; 6.
R PROSITE; PS00026; EGF_1
16-OCT-2001 (Rel. 40, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Delta-like protein 3 precursor (brosophila Delta homolog 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytoplasmic (Potential)
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-!- SIMILARITY: Contains 6 EGF-like domains.
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EGF-like 2.
EGF-like 3.
EGF-like 4.
EGF-like 5.
EGF-like 6.
POLY-Ala.
By similarity.
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HSSP; P00740; IEDM.
RGD; 70953; D113.
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TISSUE SPECIFICITY: Predominantly expressed in the neuroectoderm
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EGF-like 2.
EGF-like 3.
EGF-like 4.
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EGF-like 6.
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EMBL, AF068865; AAC40169.1; -.
EMBL, Y11895; CAA72637.1; -.
                                                                                                                                                                                                                                                      EMBL; AB013440; BAA33716.1; -. HSSP; P00740; 1EDM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98324780; PubMed=9662403; DOI=10.1038/961; Kusumi K., Sun E.S., Kerrebrock A.W., Bronson R.T., Chi D.-C., Blotsky M.S., Spencer J.B., Birren B.W., Frankel W.N., Lander E.S.; "The mouse pudgy mutation disrupts Delta homologue Dll3 and initiation of early somite boundaries.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nakayama K., Nakayama N., Tomooka Y., Hayashi Y., Takahashi M.;
"Specific expression of a divergent type of Delta in a set of earliest generated neurons including the prospective subplate neurons.";
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Inhibits primary neurogenesis. May be required to divert neurons along a specific differentiation pathway. Play a role in the formation of somite boundaries during segmentation of the
                                                                                                                                                                                                                                                     DLL3 MOUSE

ID DLL3 MOUSE STANDARD;

AC 0885I6; 035675; Q9QWL2;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 25-JAN-2005 (Rel. 46, Last annotation update)

DD DE Delta-like protein 3 precursor (Drosophila Delta homolog 3) (M-Delta-
                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C57BL/6 X DBA; TISSUE=Embryo;
STRAIN=C57BL/6 X DBA; TISSUE=Embryo;
MEDLINE=97417575; PubMed=9272948;
Dunwoodie S.L., Henrique D.M.P., Harrison S.M., Beddington R.S.P.;
"Mouse D113: a novel divergent Delta gene which may complement the
function of other Delta homologues during early pattern formation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    paraxial mesoderm.
SUBUNIT: Can bind and activate Notch-1 or another Notch receptor
                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Type I membrane protein (Probable).
ALTERNATIVE PRODUCTS:
                                                                                                                                      52.5%; Score 63; DB 1; Length 589; 30.8%; Pred. No. 2.1e+02;
                                                                                                                                                            8; Indels
                                                                                                                 A17B3BF9B95EC17F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Event=Alternative splicing; Named isoforms=2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=O88516-1; Sequence=Displayed;
                                                                                                                                                                                                384 GFAGPRCEHDLDDCAGRACANGGTCV 409
                                                                                                                                                                                   2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
  Development 124:3065-3076(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                61424 MW;
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                                                                                                                                                Local Similarity 30.8
1es 8; Conservative
 3352
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3370
4440
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589 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tube;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mouse embryo.";
 343
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                                                                                                                   -!-DISBASE: A truncating mutation in Dl13 is the cause of the pudgy (pu) phenotype. Pudgy mice exhibit patterning defects at the earliest stages of somitogenesis. Adult pudgy mice present severe vertebral and rib deformities.
-!-SIMILARITY: Contains 1 DSL domain.
-!-SIMILARITY: Contains 6 EGF-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R MGD; MGI:1096877; Dill.

R MGD; MGI:1096877; Dill.

R GO; GO:0001709; P:cell fate determination; NAS.

GO; GO:0001709; P:cell fate determination; NAS.

GO; GO:0001709; P:cell fate determination; NAS.

R GO; GO:000739; P:cell fate development (sensu Mammalia); NAS.

GO; GO:0007219; P:meurogenesis; NAS.

GO; GO:0007219; P:Notch signaling pathway; NAS.

GO; GO:0007219; P:Notch signaling pathway; NAS.

R GO; GO:0007219; P:Notch signaling pathway; NAS.

R InterPro; IPR00042; EGF_1.

R InterPro; IPR006209; EGF_1.

R PRINTS; PR00001; EGF_1.

R PROSITE; PS01086; EGF_1.

R PROSITE; PS01086; EGF_1; 6.

R Alternative splicing; Developmental protein; Differentiation;

R EGF_1ke domain; Notch signaling pathway; Repeat; Signal;
and paraxial mesoderm during embryogenesis.
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Delta-like protein 3.
Extracellular (Potential).
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(in dbSNP:1110627).
        SIMILARITY: Contains 1 DSL domain.
SIMILARITY: Contains 6 EGF-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Potential.
                                                                                                                                                 EMBL; AF241373; AAF62542.1; --
EMBL; AF241367; AAF62542.1; --
EMBL; AF24136; AAF62542.1; JOINED.
EMBL; AF241369; AAF62542.1; JOINED.
EMBL; AF241370; AAF62542.1; JOINED.
EMBL, AF241370; AAF62542.1; JOINED.
EMBL, AF241372; AAF62542.1; JOINED.
EMBL; AF241372; AAF62542.1; JOINED.
EMBL; BC00218; AAH00218.1; --
HSSP; PO0740; 1EDM.
GGROW, HGNC:2209; DLL3.
H-INVDB; HIXOU5121; --
MIM; 602768; --
MIM; 277300; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Signal; Transmembrane.
SIGNAL
1 26
COMAIN 27 618
DOMAIN 27 492
TRANSMEM 493 513
DOMAIN 514 618
DOMAIN 176 215
DOMAIN 216 249
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Attended S.F., Wagner L., Shemmen C.M., Schuler G.D.,

Attended S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Attended S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Brichenko L., Marusina K., Farmer A.A., Rubin G.M., Hsieh F.,

Brichenko L., Marusina K., Farmer A.A., Rubin G.M., Hsieh F.,

R. Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hsieh F.,

R. Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hsieh F.,

R. Diatchenko L., Marusina K., Farmer A.A., Hsieh F.,

R. Diatchenko L., Marusina K., Farmer A.A., Hsieh F.,

Raha S.G., Loquellano N.A., Peters G.J., Malek J.A., Gunaratne P.H.,

Richards S.A., McEwan P.J., McKerman K.J., Malek J.A., Gunaratne P.H.,

Richards S.A., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.M., Butterfield Y.S.M., Gremutz J., Myers R.W.,

Blakesley R.W., Tuchman J.W., Gremutz J., Myers R.W.,

Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of moze than 15,000 full-length human mouse conva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor:
D12BABS: D2Ects in DLL3 are the cause of autosomal recessive spondylocostal dysostosis type 1 (SCDO1) [MIM:277300]. SCDO1 is characterized by multiple hemivertebrae, rib fusions and deletions with a non-progressive kyphoscoliosis.
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND VARIANT SCDO1 ASP-385.
MEDLINE=20206573; PubMed=10742114; DO1=10.1038/74307;
Bulman M.P., Kusumi K., Frayling T.M., McKeown C., Garrett C.,
Lander E.S., Krumlauf R., Hattersley A.T., Ellard S., Turnpenny P.D.;
defects in the human delta homologue, DLL3, cause axial skeletal
Nat. Genet. 24:438-441(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
-!- FUNCTION: Inhibits primary neurogenesis. May be required to divert neurons along a specific differentiation pathway. Play a role in the formation of somite boundaries during segmentation of the
                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            paraxial mesoderm (By similarity). SUBUNIT: Can bind and activate Notch-1 or another Notch receptor
                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                               Length 592;
  DWLIQVLF -> A (in isoform 1)
                                                                           'Match 52.5%; Score 63; DB 1; Length 592
Local Similarity 30.8%; Pred. No. 2.2e+02;
les 8; Conservative 10; Mismatches 8; Indels
             /FTIG=VSP 001376.
E -> K (in Ref. 3).
G -> A (in Ref. 1).
: 1A84F8022E7E7DCC CRC64;
                                                                                                                                                                                                                            618 AA
                                                                                                                                               380 GFAGPRCEHDLDDCAGRACANGGTCV 405
                                                                                                                               2 XIXNOXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                            PRT;
                                                  62069 MW;
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                                       401
                          94
401
592 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                     DLL3 HUMAN
Q9NY<u>J</u>7;
                                                                                                                                                                                                                                                                                                     Name=DLL3;
                        CONFLICT
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00008; EGF; 5.
PRINTS; PR0010; EGFBLOOD.
PROSITE; PS00106; EGF 1; 6.
PROSITE; PS50026; EGF 2; 6.
PROSITE; PS50026; EGF 3; 6.
Developmental protein; Differentiation; Disease mutation; EGF-like domain; Notch signaling pathway; Polymorphism; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0016021; C:integral to membrane; NAS.
GO; GO:0005112; F:Notch binding; NAS.
GO; GO:0001709; P:cell fate determination; ISS.
GO; GO:0001701; P:mbryonic development (sensu Mammalia); ISS.
GO; GO:0007399; P:neurogenesis; ISS.
GO; GO:0007219; P:Notch signaling pathway; ISS.
GO; GO:0001501; P:skeletal development; IMP.
InterPro; IPR00742; EGF_I.
InterPro; IPR00438; EGF_II.
InterPro; IPR006209; EGF_II.
Finan PROMONG ROP.
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Extracellular (Potential)
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EGF-like 2.
EGF-like 3.
EGF-like 4.
EGF-like 5.
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Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Alausmer R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Rachards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Nilalon D.K., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Muting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcerfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Embryo;
MEDIINE=253341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                     Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia; Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                   TISSUE=Embryo;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dev. Dyn. 225:384-391(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences.
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                                                                                           Xenopodinae; Xenopus
NCBI_TaxID=8355;
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Best Local Similarity
Matches 8; Conserv
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EGF-like domain.
SEQUENCE 642 AP
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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                                                                                                              52.5%; Score 63; DB 1; Length 618; 30.8%; Pred. No. 2.2e+02;
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30.8%; Pred. No. 2.38+02;
ive 11; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to the EMBL/GenBank/DDBJ databases.
/FTId=VAR 016776.

G -> D (in SCDO1).

/FTId=VAR 009952.

; 58A9BCOA7DEADIA0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Jen W.C., Wettstein D.A., Chitnis A.B., Kintner C.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ datab
EMBL; U70843; AAB37131.1; -
HSSP; P00740; 1EDW.
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Last annotation update)
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GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0007154; P:call communication; IEA.
InterPro; IPR001774; DSL.
InterPro; IPR001774; DSL.
InterPro; IPR00181; EGF Z.
InterPro; IPR00181; EGF Z.
InterPro; IPR00181; EGF Z.
InterPro; IPR00181; EGF Z.
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                                                                                                                                                                                                                                  382 GFAGPRCEHDLDDCAGRACANGGTCV 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Notch ligand X-Delta-2.
Name=X-Delta-2;
Xenopus laevis (African clawed frog).
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PRINTS; PRO0010; EGFBLOOD.
SWART; SW00051; DSL; 1.

SWART; SW00179; EGF_CA; 3.

PROSITE; PS00010; ASX HYDROXYL; 2.

PROSITE; PS01012; EGF_1; 8.

PROSITE; PS00186; EGF_2; 7.

PROSITE; PS01186; EGF_2; 7.

PROSITE; PS01187; EGF_2; 7.
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                                                                  618 AA; 64617 MW;
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                                                                                                                                    Best Local Similarity 30.89 Matches 8; Conservative
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Pfam; PF00008; EGF; 5.
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NCBI_TaxID=8355;
                     385
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01-JUN-2003 (
01-MAR-2004 (
                                                                  SEQUENCE
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P79941
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Q7ZXT4
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Genetic and genomic tools for Xenopus research: The NIH Xenopus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Klein S., Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC044262; AAH44262.1; -
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0005509; F:calcium ion binding; IEP
GO; GO:0007154; P:cell communication; IEA.
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InterPro; IPR001438; EGF_II.
InterPro; IPR006209; EGF_III.
InterPro; IPR006209; EGF_II.
InterPro; IPR006009; EGF_II.
InterPro; IPR006009; EGF_II.
IPR08178; PR00101; EGF_CA; I.
IPR08178; PR001019; EGF_CA; I.
IPR08178; PR001019; EGF_CA; I.
IPR08178; PR001019; EGF_CA; I.
IPR08178; PR001010; EGF_CA; I.
IPR08178; PR09178; PR09178;
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EGF-like 1.

EGF-like 2.

EGF-like 3.

EGF-like 4.

EGF-like 4.

EGF-like 6, calcium-binding (Potential).

EGF-like 7, calcium-binding (Potential).

EGF-like 8.

EGF-like 9.

EGF-like 10.

EGF-like 11.

EGF-like 11.

EGF-like 12.

EGF-like 13.

EGF-like 14.

EGF-like 15.

EGF-like 14.

EGF-like 15.

EGF-like 16.

EGF-like 16.

EGF-like 17.

EGF-like 18.

EGF-like 19.

EGF-like 10.

EGF-like 
                                                                                                 protein; EGF-like domain; Glycoprotein;
                                                                                                                                           Extracellular (Potential)
Potential.
Cytoplasmic (Potential).
DSL.
                                                                                                                  pathway; Repeat; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             By similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Potential.
By similarity.
**SO1186; EGF_1; 15.
**SO1186; EGF_2; 11.
**PROSITE; PSSO106; EGF_3; 15.
**KW Calcium-binding; Developmental pro.
**KW Notch signaling pathway; Repeat**
FT NON TER
**T DOMÄIN
**I 10°**
TRANSMEM 108**
DOMAIN
**DOMAIN
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DISULFID
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                           MEDLINE=97105852; PubMed=8948600; DOI=10.1006/dbio.1996.0310;
Shawber C., Boulter J., Lindsell C.E., Weinmaster G.;
"Jagged2: a serrate-like gene expressed during rat embryogenesis.";
L. bev. Baol. 180:370-376[1966].

-! FUNCTION: Putative Notch ligand involved in the mediation of Notch signaling. May have a role in neurogenesis in the peripheral nervous system, limb development and in the adult brain.

-! SUBCLIDIAR LOCATION: Type I membrane protein.

-! Buyle And Stage Ell.5 is it is detected in dorsal root ganglia, AER, and surface ectcoderm. At El4.5, found as well in salivary gland, tooth buds and hair follicles.

-! SIMILARITY: Contains 16 EGF-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R EMBL; UTOGOSO, AACS2946.1;

R RGD; 2938; Jag2.

R GO; GO:000813; JCCF.

R GO; GO:000812; F:growth factor activity; ISS.

R GO; GO:000812; F:growth factor activity; ISS.

R GO; GO:0007049; P:cell differentiation; NAS.

R GO; GO:0007049; P:cell differentiation; NAS.

R GO; GO:0007049; P:cell differentiation; NAS.

R GO; GO:0007099; P:cell fate determination; NAS.

R GO; GO:0007099; P:cell fate commitment; ISS.

R GO; GO:0007219; P:limb morphogenesis; NAS.

R GO; GO:0007219; P:limb morphogenesis; NAS.

R GO; GO:0007219; P:regulation of cell migration; ISS.

R GO; GO:0007283; P:regulation of cell migration; ISS.

R GO; GO:000783; P:regulation of cell migration; ISS.

R GO; GO:00048061; P:thymic T-cell differentiation; ISS.

R InterPro; IPR000142; RGF_2.

R InterPro; IPR00143; RGF_1.

R InterPro; IPR00143; RGF_1.

R InterPro; IPR006209; EGF_11:

R InterPro; IPR006409; EGF_11:

R InterPro; IPR00441; PMP_SGCI.
                                                                                                                                                                 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Jagged 2 (Jagged2) (Fragment).
                                                                                                                                         PRT; 1.202 AA
                                    : : : | | | | | : : | | | | 15 GFSGPRCELNIDDCASSPCANGGTCV 440
                2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01414; DSL; 1.
Pfam; PF00008; EGF; 14.
PRINTS; PR00010; EGFBLOOD.
PROSITE; PS00010; ASX_HYDROXYL; 10.
                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                          Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                            TISSUE=Brain;
                                                                                                                                                                                                                                          Name=Jag2;
                                                                                                                                    JAG2 RAT
                                                                                                                                                  P97607
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-i- SIMILARITY: Contains 1 DSL domain.
-i- SIMILARITY: Contains 16 EGF-like domains.
-i- SIMILARITY: Contains 1 VWFC domain.
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                                                                                                                            EMBL, AF020201; AAB71189.1; EMBL, AF020201; AAB61285.1; EMBL, AF029778; AAB84215.1; EMBL, AF029778; AAB84216.1; EMBL, AF111170; AAD15562.1; EMBL; X14330; CAA74706.1; HSSP; P01132; 1GK5.
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Pfam; PF00008; EGF; 14
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Luo B., Aeter J.C., Hasserjian R.P., Kuo F., Sklar J.;
Lisolation and functional analysis of a cDNA for human Jagged2, a gene
encoding a ligand for the Notchl receptor.";
Mol. Cell. Biol. 17:6057-6067(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=Short; Synonyms=HJAG2.del_E6; 1804=697219-2; Sequence=VSP 001395; Isod=697219-2; Sequence=VSP 001395; Isod=697219-2; Sequence=VSP 001395; Isode SPECIFICITY: Expressed in heart, placenta and skeletal muscle and to a lesser extend in pancreas. Very low expression in brain, lung, liver and kidney.

DISBASE: May be associated to Usher syndrome type IA (USHAIA) which describes a congenital sensory deafness associated with retinitis pigmentosa and feeble-mindedness.
                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Fetal brain;
MEDLINE=99180765; PubMed=10079256;
Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L.,
Banks A., Leiman J., Ward D., 18h-Horowitz D., Artavanis-Tsakonas S.;
"Human ligands of the Notch receptor.";
                                                                 Gaps
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                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Bone marrow;
MEDLINE=20130121; PubMed=10662552; DOI=10.1006/geno.1999.6045;
Deng Y., Madan A., Banta A.B., Friedman C., Trask B.J., Hood L.,
                                                                  ö
                                         52.5%; Score 63; DB 1; Length 1202; 23.1%; Pred. No. 4.1e+02; ive 13; Mismatches 7; Indels
791 806 By similarity.
808 817 By similarity.
1202 AA, 129703 MW; 09CB44E5271FF8BE CRC64;
                                                                                                                                                                  JAG2_HUMAN STANDARD; PRT; 1238 AA. Q9Y219; Q9Y6D0; Q9Y6D9; Q9UNK8; Q9Y6P9; Q9Y6Q0; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 25-JAN-2005 (Rel. 46, Last annotation update)
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                                    Query Match
Best Local Similarity 23.1%; Pred. No. ...
Marches 6; Conservative 13; Mismatches
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                                                                                                    582 GFTGTYCHENIDDCMGQPCRNGGTCI 607
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM LONG).
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                                                                                                                                                                                                                        Jagged 2 precursor (Jagged2) (HJ2) Name=JAG2;
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                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PROSITE; PS00010; ASX HYDROXYL; 10.
PROSITE; PS0108; EGF 1; 16.
PROSITE; PS01186; EGF 2; 12.
PROSITE; PS01187; EGF CA; 7.
PROSITE; PS01187; EGF CA; 7.
Alternative splicing; Calcium-binding; Developmental protein; Alternative splicing; Calcium-binding; Developmental protein; SGF-like domain; Glycoprotein; Notch signaling pathway; Repeat; Signal; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIN, 60270; -..

R GO; GO: 0005887; C: integral to plasma membrane; ISS.

R GO; GO: 0005887; C: integral to plasma membrane; ISS.

R GO; GO: 00005012; F: Notch binding; IPI.

R GO; GO: 00007049; P: cell differentiation; IDA.

R GO; GO: 00007049; P: cell differentiation; IDA.

R GO; GO: 0000705; P: cell differentiation; IDA.

R GO; GO: 00007267; P: cell-cell signaling; ISS.

R GO; GO: 00007219; P: plain morphogenesis; ISS.

R GO; GO: 0007219; P: plain morphogenesis; ISS.

R GO; GO: 0007219; P: Precupition of cell migration; IDA.

R GO; GO: 0007219; P: regulation of cell migration; IDA.

R GO; GO: 0004207; P: regulation of cell migration; IDA.

R GO; GO: 0004207; P: regulation of cell migration; IDA.

R GO; GO: 0004207; P: regulation of cell migration; IDA.

R GO; GO: 0004207; P: regulation of cell migration; IDA.

R GO; GO: 0004207; P: regulation of cell migration; IDA.

R GO; GO: 0004207; P: regulation of cell migration; IDA.

R InterPro; IPR001742; EGF Z.

R InterPro; IPR001742; EGF Z.

R InterPro; IPR001841; EGF Z.

R InterPro; IPR001841; EGF Z.

R InterPro; IPR001841; PMP_SGCI.

R InterPro; IPR001404; PMP_SGCI.

R Pfam: PF01414; DSL: 1.
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EGF-like 3.
EGF-like 4.
EGF-like 5, calcium-binding (PEGF-like 6, calcium-binding (PEGF-like 7, calcium-binding (PEGF-like 9.
EGF-like 9.
EGF-like 10 (atypical).
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Extracellular (Potential).
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   calcium-binding (Potential)
calcium-binding (Potential)
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/FIGH VSP (On1395.

RLPRR -> KIPPPA (in Ref. 1).
L -> F (in Ref. 1).
L -> F (in Ref. 1).
L -> SA (in Ref. 1).
L -> SA (in Ref. 1).
K -> E (in Ref. 1).
ANB -> VND (in Ref. 1).
X -> E (in Ref. 2).
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   BGF-like 11, calcium-binding (F
BGF-like 12, calcium-binding (F
BGF-like 13.
BGF-like 14.
BGF-like 16, calcium-binding (P
BGF-like 16, calcium-binding (P
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Pred. No. 4.2e+02;
3; Mismatches 7;
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MEDLINE=97459705; PubMed=9315665;

MEDLINE=97459705; PubMed=9315665;

Luo B., Aster J.C., Hasserlian R.P., Kuo F., Sklar J.;

Luo B., Aster J.C., Hasserlian R.P.

Luo B., Aster J.C., Hasserlian R.P.

Mol. Cell. Biol. 17:607-667(1997).

Mol. Cell. Biol. 17:607-667(1997).

Le FUNCTION: Putative Norch ligand involved in the mediation of Norch signaling. Plays an essential role during limb, craniofacial and chymology plays an essential role during limb, craniofacial and cevelopment of peripheral and central nervous systems.

Lipsub SPECLIFICITY: Found to be highest in fetal thymus, epidermis, foregut dorsal root ganglia and inner ear. In 2-week.

Clamice, abundant in heart, lung, thymus, skeletal muscle, brain and teetis. Expression overlaps partially with Notchl expression.

Cloral root ganglia. At 13 dpc, found in paravertebral vessels and developing thymus and in the muscles of the tongue. By 15 dpc, in many risans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 302-819 FROM N.A.
SEQUENCE OF 302-819 FROM N.A.
TISSUE-Brain;
MEDLINE-98051918; PubMed=9341252;
Lan Y., Jiang R., Shawber C., Weinmaster G., Gridley T.;
"The Jagged2 gene maps to chromosome 12 and is a candidate for the 1gl and sm_mutations."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Brain;
MEDLINE=98145947; PubMed=9486542; DOI=10.1016/S0925-4773(97)00146-9;
Valsecchi C., Ghezzi C., Ballabio A., Rugarli B.I.;
"JAGGED2: a putative Notch ligand expressed in the apical ectodermal ridge and in sites of epithelial-mesenchymal interactions.";
Mech. Dev. 69:203-207(1997).
                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                           7AG2_MOUSE STANDARD; PRT; 1247 AA. 090XE5; 055139; 070219; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 25-JAN-2005 (Rel. 46, Last annotation update) Jagged 2 precursor (Jagged2).
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EMBL; AF038572; AAF16411.1; -. EMBL; AF010137; AAC14010.1; -.
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STRAIN=Swiss Webster / NIH;
                                                                                                                                                                                                                                                   Mus musculus (Mouse).
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Length 1238; Indels

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461 N -> T (in Ref. 2).
478 CQHGGTCKDL -> VSAWGHLQGP (in Ref. 2).
549 G -> V (in Ref. 2).
549 G -> V (in Ref. 2).
549 A -> V (in Ref. 2).
549 A -> V (in Ref. 2).
549 RCAC -> PAR (in Ref. 3).
809 N -> H (in Ref. 2).
812 R -> A (in Ref. 2).
813 + A (in Ref. 2).
814726 MW; 1D80C8626FAFAEEC CRC64;
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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Q61204;
01-1004-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAX-2004 (TrEMBLrel. 26, Last annotation update)
EGF repeat transmembrane protein.
Name=Ddx26;
           By similarity.
By sim
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NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                               Pfam;
                                                                                                                                                                                                                                                                                                                                        Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 69
CXO7_CONGE
                             DR RESERVED BY SECONDARY S
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RC STRAIN=CS7BL/6J; TISSUE=Whole embryo;

RX MEDLINE=98142023; PubMed=9473344; DOI=10.1006/excr.1997.3865;

RA Hoff H.B. III, Treshini M. Li S., Sell C.;

RT response to insulin-like growth factor: 1.";

RL EXD. Cell Res. 238:359-370(1998).

REMEL, U57368; AAB01338:1; -.

REMEL, U57368; AAB01338:1; -.

REMEL, U57368; AAB01338:1; -.

REMEL, U57368; AAB01338:1; -.

ROSP; PORTOS; IPFE.

ROSP; PORTOS; IPFE.

ROSP; PORTOS; IPFE.

ROSP; PORTOS; IPROSPOS; F:calcium ion binding: IEA.

RICEPRO; IPRO00622; BAX hydroxyl_S.

RICEPRO; IPRO00629; EGF_Z.

RICEPRO; IPRO00629; EGF_Z.

RICEPRO; IPRO00629; EGF_Z.

RICEPRO; IPRO00629; EGF_Z.

RICEPRO; IPRO00639; EGF_Ike.

REAM; PROO068; EGF_S.

REAM; PROO068; EGF_S.

REAM; PROO069; EGF_S.

REAM; PROSITE; PSO0002; EGF_Z.

RROSITE; PSO0022; EGF_Z.

RROSITE; PSO0022; EGF_Z.

RROSITE; PSO1187; EGF_Z.

RROSITE PSO1187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AgCP1653 (Fragment).
Name=agCG50053; ORFNames=ENSANGG0000007782;
Anophales gambiae str. PEST.
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TaxID=180454;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-WAR-2004 (TrEMBLrel. 26, Created)
01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52.5%; Score 63; DB 2; I
26.9%; Pred. No. 5.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 3523 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000152; Asx hydroxy, S. InterPro; IPR008985; Cond like_lec_gl. InterPro; IPR008985; CUB. InterPro; IPR00142; EGF_2. InterPro; IPR001881; EGF_C. InterPro; IPR001881; EGF_II. InterPro; IPR001881; EGF_II. InterPro; IPR001899; EGF_II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 26.97
"...heg 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=PEST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q7QCP4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 68
Q7QCP4
              RC
RT
RT
RT
RT
RT
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DR
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DR
DR
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CXO7_CONGE STANDARD; PRT; 29 AA.
P05483;
01-NOV-1988 (Rel. 09, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Omega-conotoxins GVIIA/GVIIB (Shaker peptides GVIIA/GVIIB) (SNX-178).
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Apogastropoda, Caenogastropoda, Sorbeoconcha, Hypsogastropoda,
Neogastropoda, Conoidea, Conidae, Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-86070213; PubMed-4071055; Olivera B.M., Gray W.R., Zeikus R.D., McIntosh J.M., Varga J., Rivier J.E., de Santos V., Cruz L.J.; "Peptide neurotoxins from fish-hunting cone snails.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 3523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3523 3523
3523 AA; 385001 MW; B58BB588B2A484E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52.5%; Score 63; DB 2; I
33.3%; Pred. No. 1.1e+03;
tive 11; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2247 TGKNCQHTVDDCESAPCQNGGTCV 2270
IPR000421; FAS8 C.
IPR009030; Grow_fac_recept.
IPR003410; Hyalin.
                                                      InterPro; IPR002172; LDL receptor A. InterPro; IPR001304; Lectin C. InterPro; IPR000436; Sushi SCR_CCP. Ffam; PP00431; CUB; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 XNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                           PROSITE, PS00010; ASX HYDROXYL, 11.
PROSITE, PS01180; CUB; 3.
PROSITE, PS00021; EGF 11.
PROSITE, PS01082; EGF 2; 13.
PROSITE, PS00026; EGF 2; 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conus geographus (Geography cone)
                                                                                                                                                     Pfam; PF07645; BGF CA; 2.
Pfam; PF00754; F5 F8 type_C; 2.
Pfam; PF00249; HYR; 3.
Pfam; PF00057; Ldl recept a; 1.
Pfam; PF00059; LecTin_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS50068; LDLRA_2;
PS50923; SUSHI; 6
                                                                                                                                                                                                                                                                        PRINTS; PRO0010; EGFBLOOD.
PROSITE; PS00010; ASX HYDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 33.3x
Best Local Similarity
Conservative
                                                                                                                                                                                                                                                         Sushi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=6491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGF-like domain.
                                                                                                                                                                                                                                                       PF00084;
                                       InterPro; 1
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Local Similarity
Les 7; Conserv
                                                                                    HSSP; P05484; 1DW4
                                                                                                                                                                                                                                                                                                                                 73 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phytophthora.
NCBI_TaxID=4787;
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                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                              PEPTIDE
                                                                                                                                                                                                                                                                                                MOD_RES
                                                                                                                                                                                         SIGNAL
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Q646U3;
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                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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10 AC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., SEQUENCE OF 46-72, SYNTHESIS, AND STRUCTURE
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Apogastropoda, Caenogastropoda, Sorbeoconcha, Hypsogastropoda,
Neogastropoda, Conoidea, Conidae, Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda; Neogastropoda; Conoidea; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 62; DB 2; Length 62;
Pred. No. 35;
                                                                                                                       Score 62; DB 1; Length 29;
Pred. No. 18;
                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Duda T.F. Jr., Palumbi S.R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF480316; AAQ05868.1; -.
                                                                    L -> S (in GVIIB).
57307C69583FB1E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                    Four-loop conotoxin preproprotein (Fragment). Conus tulipa (Fish-hunting cone snail) (Tulip cone).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 four-loop conotoxin.
916B1EB16D6A5085 CRC64;
                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
 4-hydroxyproline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Omega-conotoxin CVID precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73 AA.
                                                                                                                                                       13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Mismatches
                                                                                                                                                                                           56
                                                                                                                                                                                                               1 CKSPGTPCSRGMRDCCTSCLLYSNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CXIXNQXCXQXLDDCCSXXCNXXNX 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CXIXNQXCXQXLDDCCSXXCNXXNXC
                                                                                                                                                                                                                                                                                                                                                   Created
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7
16
19
26
21
3290 MW;
                                                                                                                       51.7%;
26.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51.7%;
32.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 AA; 7083 MW;
                                                                                                                                                                                                                                                                                                                                               05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 32.08
Matches 8; Conservative
                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conus catus (Cat cone)
                                                                                                                                   Local Similarity
es 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=6495;
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                                  DISULFID
DISULFID
                                                                    VARIANT
SEQUENCE
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                                                                                                                     Query Match
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CXOD_CONCT
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271KS8
AC Q71KS
AC Q71KS
DT 05-JU
DT 05-JU
DT 05-JU
DE POUT-
OS COURS
OC APOGRA
OC APO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                              Pfam; PF02950; Conotoxin; 1.
Amidation; Calcium channel inhibitor; Direct protein sequencing; Ionic channel inhibitor; Neurotoxin; Presynaptic neurotoxin; Signal;
similarity). This toxin blocks N-type calcium channels.
-!- SUBCELULAR LOCATION: Secreted.
-!- TISSUE SPECIFULTY: Expressed by the venom duct.
-!- SIMILARITY: Belongs to the conotoxin O-superfamily. Omega-type
                                                                                                                                                                                                                                                                                                                                                                                                                  Cysteine amide (G-73 provides amide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Liu Z., Bos J.I.B., Armstrong M., Whisson S.C., da Cunha L.,
Torto-Alalibo T., Win J., Avrova A.O., Wright F., Birch P.R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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Phytophthora infestans (Potato late blight fungus).
Eukaryota, stramenopiles; Oomycetes; Pythiales; Pythiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phytoxin-like SCR74.
Phytophthora infestans (Potato late blight fungus).
Eukaryota, stramenopiles, Oomycetes, Pythiales, Pythiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 62; DB 1; Length 73; Pred. No. 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51.7%; Score 62; DB 2; Length 74;
25.8%; Pred. No. 41;
iive 14; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Patterns of Diversifying Selection in the Phytotoxin-li
Family of Phytophthora infestans.";
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY723724, AAUJ1465.1;
SEQUENCE 74 AA; 7910 MW; C925922881E5EA3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                           group).
C4CEBD30C77DAEC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-OCT-2004 (TrEMBLrel. 28, Last sequence update) 25-OCT-2004. (TrEMBLrel. 28, Last annotation update)
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                                                                                                                                                                                                                                                                                                                  Omega-conotoxin CVID.
By similarity.
By similarity.
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 XIXNQXCXQ-----XLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 KVTSKCCKAINADPIAFHDCCSKSCNTGSPC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                       Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CXIXNQXCXQXLDDCCSXXCNXX 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46 CKSKGAKCSKLMYDCCSGSCSGT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                               InterPro; IPR004214; Conotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51.7%;
30.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               7748 MW;
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nes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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EMBL; AY723703; AAU21444.1; -.
SEQUENCE 74 AA; 7817 MW; 5373030B547B94FF CRC64;
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EMBL, AY723702; AAU21443.1;
EMBL, AY723699; AAU21440.1;
EQUENCE 74 AA, 7851 Mm. no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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les 8; Conserv
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                                                                                                                                        "Patterns of Diversifying Selection in the Phytotoxin-like scr74 Gene Family of Phytophthora infestans.";
Submitted (MGG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY723723; AAU31464.1;
SEQUENCE 74 AA, 7879 WW; FF19FRA1F67DBBAD CALCA
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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EMBL, AY723704; AAUJ2445.1; -. BDD10BA1F26FC5B0 CRC64;
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"Patterns of Diversifying Selection in the Phytotoxin-like scr74 Gene
Family of Phytophthora infestans.";
Submitted (AUG-2004) to the EMBL/GenBark/DDBJ databases.
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                                         SEQUENCE FROM N.A.
Liu Z., Bos J.I.B., Armstrong M., Whisson S.C., da Cunha L.,
Torto-Alalibo T., Win J., Avrova A.O., Wright F., Birch P.R.J.,
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Liu Z., Bos J.I.B., Armstrong M., Whisson S.C., da Cunha L.,
Torto-Alalibo T., Win J., Avrova A.O., Wright F., Birch P.R.J.,
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Liu Z., Bos J.I.B., Armstrong M., Whisson S.C., da Cunha L.,
Tortœ-Alalibó T., Win J., Avrova A.O., Wright F., Birch P.R.J.,
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Phycophthora infestans (Potato late blight fungus).
Eukaryota; stramenopiles; Oomycetes; Fythiales; Pythiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Phytoxin-like SCR74.
Phytophthora infestans (Potato late blight fungus).
Bukaryots, stramenopiles; Oomycetes; Pythiales; Pythiaceae;
                                                                                                                                                                                                                                                                                                          Query Match 51.7%; Score 62; DB 2; Length 74; Best Local Similarity 25.8%; Pred. No. 41; Matches 8; Conservative 14; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 51.7%; Score 62; DB 2; Length 74; Best Local Similarity 25.8%; Pred. No. 41; Matches 8; Conservative 14; Mismatches 3; Indels
                                                                                                                                                                                                                                                              7879 MW; FF19FBA1F67B8A3E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-0CT-2004 (TrEMBLrel. 28, Created)
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 DVVSKCCKAINADPIAFHDCCSKSCNTGSPC 71
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NCBI_TaxID=4787;
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NCBI_TaxID=4787;
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0646W
AC 0646W
AC 0646W
DT 25-0C
DT 25
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0646W3
AC 0646W
DD 25-0C
DT 25-0C
DT 25-0C
DB Phyto
OC Phyto
OC Phyto
OC Phyto
CO Phyto
RA NCH
RA KAMOU
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicocyledons, core eudicots, asterids,
lamiids, Lamiales, Pedaliaceae, Sesamum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Patterns of Diversifying Selection in the Phytotoxin-like scr74 Gene Family of Phytophthora infestens."; Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY723700; AAUZ1441.1; -
                                                            Gaps
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P SEQUENCE FROM N.A.

A Tal S.S.K., Lee T.T.T., Tsai C.C.Y., Yiu T.-J., Tzen J.T.C.;

A Tal S.S.K. Lee T.T.T., Tsai C.C.Y., Yiu T.-J., Tzen J.T.C.;

Tal S.S.K. Lee T.T.T., Tsai C.C.Y., Yiu T.-J., Tzen J.T.C.;

Tal Expersion pattern and deposition of three storage proteins, 11S

Talobulin, 2S albumin and 7S globulin in maturing sesame seeds.";

P Stain Physiol. Biochem. 39:981-992(2001).

R RNBL; AP240005; AAK15088.1; -..

R RNBL; PP0105; 1HSS.

R RNBL; PP005; 1HSS.

R RNBL; PR00465735; F:nutrient reservoir activity; IEA.

InterPro; IPR00460; Glutelin.

DR InterPro; IPR00460; Glutelin.

DR Pfam; PF00234; Tryp_alpha_amyl; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Liu Z., Bos J.I.B., Armstrong M., Whisson S.C., da Cunha L.,
Torto-Alalibo T., Win J., Avrova A.O., Wright F., Birch P.R.J.,
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                                                                                                                                                                                                                                                                                                                                                                                             Phytophthora infestans (Potato late blight fungus).
Eukaryota: stramenopiles; Oomycetes; Pythiales; Pythiaceae;
            Length 74;
                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51.7%; Score 62; DB 2; Length 74; 25.8%; Pred. No. 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7851 MW; D9D10BA1F67B94F1 CRC64;
                                                                                                                                                                                                                                                                                               25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                       3;
Ouery Match 51.7%; Score 62; DB 2; Best Local Similarity 25.8%; Pred. No. 41; Matches 8; Conservative 14; Mismatches
                                                                                                                                                                                                                                                             74 AA.
                                                                                           2 XIXNOXCXQ-----XLDDCCSXXCNXXNXC 26
                                                                                                                             41 DVVSKCCKAINADPIAFHDCCSKSCNTGSPC 71
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ive 14; Mismatches
                                                                                                                                                                                                                                                             PRT;
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or send an email to license@isb-sib.ch)
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                                                                                                                                                                  PROSITE, PS00010; ASX HYDROXYL; PROSITE; PS00022; EGF 1: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40404 MW;
                                                                                                                                                                                                                                                                       ; Transmembrane
                                                                                                                                                Pfam; PF00008; EGF; 5. -
PRINTS; PR00010; EGFBLOOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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3326
3326
3326
1122
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248
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SIGNAL
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ID EFL9 HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 1).

STRAIN=FVB/N; TISSUE-Salivary gland;

MEDLINE=2318825; PubMed=12477932; DoI=10.1073/pnas.242603899;

MEDLINE=2318825; PubMed=12477932; DoI=10.1073/pnas.242603899;

A Straubberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

A Alachul S.F., Zebebrg B., Buetow K.H., Schaefer C.F., Bhata N.R.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,

A plachul S.P., Jordan H., Moore T., Max S.I., Wang J., Heish F.,

B pleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B romatein M.J., Usdin T.B., Tonahlyuki S., Carninci P., Prange C.,

R aha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Richards S., Worley K.C., Hale S., Garcia A.M., Glabbs R.A.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glabbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

R Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,

B. Mandan A., Schein J.E., Jones S.J.M., Marra M.A.;

Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buxopean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                             Q8KIĒ3; Q9QYP3;
25-OCT-2004 (Rel. 45, Created)
25-OCT-2004 (Rel. 45, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Multiple EGF-like-domain protein 9 precursor (Endothelial cell
specific protein S-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fukudome K., Tsuneyoshi N., Kimoto M.;
"Endothelial cell specific protein S-1.";
Submitted (FBB-1998) to the EMBL/GenBank/DDBJ databases.
-! SUBCELLULAR LOCATION: Type I membrane protein (Potential).
                                                                51.7%; Score 62; DB 2; Length 153; 39.1%; Pred. No. 79;
                                                                                            5; Indels
                         SMART; SM00499; AAI; 1.
SEQUENCE 153 AA; 17504 MW; 6A8F9117DAE81568 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note=No experimental confirmation available; SIMILARITY: Contains 6 EGF-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                   382 AA
                                                                                            9; Mismatches
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                                                                                                                                      4 XNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and mouse cDNA sequences.";
PRINTS; PR00211; GLUTELIN PRINTS; PR00496; NAPIN.
                                                                              Local Similarity 39.1 nes 9; Conservative
                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                             Name=Egfl9;
                                                                                                                                                                                                                   EFL9 MOUSE
                                                                 Query Match
                                                                                            Matches
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EGF-like 3.
EGF-like 4.
EGF-like 5, calcium-binding (Potential).
EGF-like 6, calcium-binding (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (in isoform 2).
                                                                                                                                                                                                                                                                                          PROSITE; PS01186; EGF_2; 6.
PROSITE; PS50026; EGF_3; 6.
PROSITE; PS01187; EGF_CA; 2.
Alternative splicing; Calcium; Calcium-binding; EGF-like domain;
                                                                                                                                                                                                                                                                                                                                                                                                                  Multiple EGF-like-domain protein 9. Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QGUYII; Q9BQ54;
25-OCT-2004 (Rel. 45, Last sequence update)
25-OCT-2004 (Rel. 45, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Multiple EGF-like-domain protein 9 precursor (UNQ2903/PRO28633).
Name=EGFL9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F2C82AD649CA0B3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytoplasmic (Potential)
EGF-like 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; I
1.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             By similarity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 32.0%; Pred. no. ...
Marches 8; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FTId=VSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Potential
                                        HSSP; P00750; ITPG.
MGD; MGI:2146838; Egf19.
InterPro; IPR000152; Asx hydroxyl_S.
InterPro; IPR00143; EGF_Z.
InterPro; IPR001438; EGF_II.
InterPro; IPR001438; EGF_II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       203 GFAGRFCTINLDDCASRPCQRGARC 227
EMBL; BC019431; AAH19431.1; -.
EMBL; AB011019; BAA88686.1; ALT_INIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Missing
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Genew; HGNC:21113; EGFL9
                    Name=1;
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PEAM; PF00008; EGF; 5.

PRINTS; PR0010, EGFBLOOD.

SMART; SM0011, EGF; 6.

SMART; SM001179; EGF CA; 4.

PROSITE; PS00100; ASX HYDROXYL; 2.

PROSITE; PS01186; EGF 1; 6.

PROSITE; PS01187; EGF 2; 6.

PROSITE; PS01187; EGF 3; 6.

PROSITE; PS01187; EGF 2; 6.

Alternative splicing; Calcium; Calcium-binding; EGF-like domain;
                     InterPro; IPR001841; Znf_ring
                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane,
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3383
3306
3327
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383
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172
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wes 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                               Repeat; Signal;
SIGNAL
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DOMAIN
TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhar N.K., A Hopkins R.F., Jordan H., Moore T., Mang J., Hsieh F., Batchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Scheetz T.E., RA Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C., RA Bosak S.A., McEwan P.J., McKernan K.J., Mahek J.A., Gunarate P.H., Rha Bosak S.A., McEwan P.J., McKernan K.J., Mahek J.A., Gunarate P.H., Rhilalon D.K., Mazny D.M., Sodergren E.J., Lu X., Gibbs R.A., Altialon D.K., Mazny D.M., Sodergren E.J., Lu X., Gibbs R.A., Altialon D.K., Mazny D.M., Sodergren E.J., Lu X., Gibbs R.A., Altialon D.K., Mazny D.M., Sodergren E.J., Lu X., Gibbs R.A., Altialon D.K., Mazny D.M., Sodergren E.J., Lu X., Gibbs R.A., Altialon D.K., Mazny D.M., Sodergren E.J., Lu X., Gibbs R.A., Altialon D.K., Mazny D.M., Sodergren E.J., Lu X., Gibbs R.A., Altialon D.K., Mazny D.M., Sodergren E.J., Lu X., Gibbs R.A., Alterlada Y.S.N., Kozrywinski M.I., Schautz J., Myers R.M., Touchman J.W., Green E.D., Dickson M.C., A Butterfield Y.S.N., Krzywinski M.I., Schautz J., Marra M.A., Tonch A., Schant J.B., Jones S.J.M., Marra M.A., Tonch A., Schain J.E., Jones S.J.M., Marra M.A., Tonch A., Schain J.E., Jones S.J.M., Marra M.A., Tonch A., Schail M.I., Schautz J., Shalska U., S
                                                                                                                     MEDLINE-22887296; PubMed=12975309; DOI=10.1101/gr.1293003;

MEDLINE-22887296; PubMed=12975309; DOI=10.1101/gr.1293003;

A Clark H.F., Gurney A.L., Abaya B., Baker K., Baldwin D., Brush J.,

Chow B., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,

Baton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,

Huang A., Kim H.S., Klinowski L., Jul Y., Johnson S., Lee J.,

Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,

Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagtes A.,

Vandlen R., Watanabe C., Waleand D., Woods K., Xie M.-H., Yansura D.,

A vandlen R., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,

Godowski P., Gray A., Zhang M., Zhang Z., Goddard A., Wood W.I.,

"The secreted protein discovery initiative (SPDI), a large-scale

for the city of the control of the 
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isold=Q6UY11-2; Sequence=VSP 011767;
Note=Splicing acceptor site not canonical. No experimental confirmation available;
-!- SIMILARITY: Contains 6 EGF-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUB=Eye;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 2).
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EMBL; BC000230; AAH00230.1; -.
EMBL; BC006425; AAH06425.1; -.
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EGF-like 3.

EGF-like 4.

EGF-like 5, calcium-binding (Potential).

EGF-like 6, calcium-binding (Potential).

Multiple EGF-like-domain Extracellular (Potential) Potential.

Cytoplasmic (Potential). EGF-like 1.

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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta; Pterygota,
Neoptera, Endopterrygota, Diptera, Nematocera, Culicoidea, Anopheles.
NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                             By similarity.
N-linked (GlcNAc. . .) (Potential).
Missing (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                         51.7%; Score 62; DB 1; Length 383; 32.0%; Pred. No. 1.8e+02; Live 11; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anopheles Genome Sequencing Consortium,
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
                                                                                                                                                                                                                                                                                                                                                                                        701AC6B043863EA7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O.-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
ENSANGP00000014402 (Fragment).
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                638 AA
                                                                                                                                                                                                                                                                                                                                                                        Id=VSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               203 GFAGRFCTINLDDCASRPCQRGARC 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 XIXNQXCXQXLDDCCSXXCNXXNXC 26
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                                                                                                                                                                                                                                                                                                                                                                                      383 AA; 40547 MW;
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DOMAIN
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EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Podocoryne carnea.
Bukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
Hydractiniidae; Podocoryne.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                        Length 638;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bauer P., Plickert G.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF397902; AAK92130.1; -.
HSSP; P00140; 1EDM.
                                                                                                                                                                                                                                                                                  638 638
638 AA; 69390 MW; 026DB44846AB483F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     713 AA; 76908 MW; 980E392B533E42D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                     51.7%; Score 62; DB 2; I
28.0%; Pred. No. 2.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51.7%; Score 62; DB 2; I
26.9%; Pred. No. 3.2e+02;
:ive 13; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; QUO'AU; TEDM.

GO, GO:0005509; F:calcium ion binding; IEA.
InterPro; IPR000152; Asx_hydroxyl_S.
InterPro; IPR00152; Asx_hydroxyl_S.
InterPro; IPR001439; EGF_Ca.
InterPro; IPR001439; EGF_II.
InterPro; IPR0016209; EGF_II.
FROMOTOS; EGF_I 18.
PRINTS; PR00010; EGFELOD.
SMART; SM00179; EGF_CA; 16.
PROSITE; PS00010; ASX_HYDROXYL; 17.
PROSITE; PS00010; ASX_HYDROXYL; 17.
PROSITE; PS00022; EGF_I; 18.
PROSITE; PS01186; EGF_Z; 18.
PROSITE; PS01186; EGF_Z; 18.
PROSITE; PS01187; EGF_CA; 16.
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01-NOV-1997 (Rel. 35, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                              12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                489 GFTGETCEIEIDECSSSPCQNAGTCV 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 XIXNOXCXOXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30 RLSNHRCIPHCDDCDNGICTKPGYC 54
     EMBL, AARBO1008980; EAA14483.2; -. BMBL, AARBO1008980; EAA14483.2; -. HSSP; P19438; IEXT. InterPro; IPR003341; DUF139. InterPro; IPR006209; EGF like. Pfam; PF02363; C triplex; 15. Pfam; PF0008; EGF; 1. PROSITE; PS01186; EGF 2: 4.
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les 7; Conservative
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Best Local Similarity 7; Conservat
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DLL1_RAT
ID DLL1_RAT
AC P97677,
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Details forced: 46, Late amnotation update)

Details forced: 146, Late annotation update)

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between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00008; EGF; U. PFINTS; PRIOND. PRINTS; PROONDIO; BGFLOOD. PROSITE; PROONDIO; ASX HYDROXYL; 3. PROSITE; PROONDIO; ASX HYDROXYL; 3. PROSITE; PS0108; EGF_1; B. PROSITE; PS01087; EGF_2; B. PROSITE; PS01187; EGF_3; 7. PROSITE; PS01187; EGF_CA; 2. PROSITE; EGF_CA; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4, calcium-binding (Potential).
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R GO; GO: 0005807; C:extracellular; ISS.
R GO; GO: 0005807; C:extracellular; ISS.
R GO; GO: 0005812; F:Notch binding; IPI.
R GO; GO: 0005112; F:Notch binding; IPI.
R GO; GO: 000512; F:protein binding; IPI.
R GO; GO: 0007386; P:compartment specification; IMP.
R GO; GO: 0007386; P:compartment specification; IMP.
R GO; GO: 0007386; P:compartment specification; IMP.
R GO; GO: 0007386; P: Pincre car morphogenesis; NAS.
R GO; GO: 0000912; P:hair cell fate commitment; NAS.
R GO; GO: 0000739; P:hemopoiesis; ISS.
R GO; GO: 0007399; P:nemoropiesis; NAS.
R GO; GO: 0007399; P:notch signaling pathway; ISS.
R GO; GO: 0007219; P:Notch signaling pathway; ISS.
R GO; GO: 00042475; P:compartment of cell adhesion; ISS.
R InterPro; IPR000174; DSL.
R InterPro; IPR00174; DSL.
R INTERPRO; IPR0174; DSL.
R INTERPRO; IPR00174; DSL.
R INTERPRO; IP
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Extracellular (Potential).
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EGF-like 3.
EGF-like 4,
EGF-like 6.
EGF-like 6.
EGF-like 7,
EGF-like 7,
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MGD; MGI:104659; D111.
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HSSP; P00740; 1EDM.
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01-NOV-1997 (Rel. 35, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Delta-like protein 1 precursor (Drosophila Delta homolog 1) (Deltal).
Name-Dlli;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linked (GlcNAc. . .) (Potential)
4B8EE2272BAEA27E CRC64;
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  EGF-like 6.
EGF-like 7, calciu
EGF-like 7, calciu
EGF-like 7, calciu
B similarity.
By similarity.
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28.0%; Pred. No. 3.2e+0;
ive 12; Mismatches
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Best Local Similarity 28.0.
7; Conservative
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DLL1 MOUSE
ID DLL1 MOUSE
AC Q61483;
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SEQUENCE FROM N.A.

SEQUENCE TRAIN=C57BL/6; TISSUE=Mouse;

STRAIN=C57BL/6; TISSUE=Mouse;

STRAIN=C57BL/6; TISSUE=Mouse;

STRAIN=SEASTS; PubMed=124477912; DOI=10.1073/pnas.242603899;

STRAIN=SEASTS; PubMed=124477912; DOI=10.1073/pnas.242603899;

STRAIN=C57BL/6; Feirgold E.A., Grouse L.H., Derge J.G.,

A Strain-SEASTS; Zeeberg B., Buetow K.H., Schemefer C.F., Bhat N.K.,

A Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Heiseh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M.J., Goares M.B., Bonaldo M.F., Gasavant T.L., Scheetz T.B.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Romantel M.J., McEwan N.B., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., McEwan P.J., McKernan K.J., Makek J.A., Gunaratne P.H.,

Richards S., Mocley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Mitting M., Madan A., Young A.C., Shevcheko Y., Bouffard G.G.,

Multing M., I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,

A Norsey K.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Mores S.J., Marra M.A.,

A Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Mones S.J., Marra M.A.,

A Mones S.J., Marra M.A.,

A Mones S.J., Marra M.A.,

A Mones C.D., Shevchman T.S., One full-length human
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Strausberg R.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
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Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                95F581B56DCEC9B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                  Pred. No. 3.2e+02;
                                                                                                                                                                                                                                                                                  51.7%; Score 62; DB 1; 28.0%; Pred. No. 3.2e+02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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                                                                                                                                                                                                                             78448 MW;
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STRAIN=C57BL/6; TISSUE=Mouse;
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05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mouse cDNA sequences.";
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
MEDLINE=99180765; PubMed=10079256;
Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L.,
Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Tsakonas S.;
Human ligands of the Notch receptor.";
Am. J. Pathol. 154:785-794 (1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Han W., Ye Q., Moore M.A.S.;
A soluble form of human delta-like-1 inhibits differentiation of
hematopoietic progenitor cells ";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                            R GO; GO:0005615; C:extracellular space; TAS.
R GO; GO:0016515; C:integral to membrane; TAS.
R GO; GO:0016515; F:protein binding; IPI.
R GO; GO:0007386; P:compartment specification; IMP.
R GO; GO:0007386; P:compartment specification; IMP.
R GO; GO:000737; P:somite specification; IMP.
R InterPro; IPRO0174; DSL.
R InterPro; IPRO0174; DSL.
R InterPro; IPRO0142; EGF_2.
R InterPro; IPRO0143; EGF_1.
R InterPro; IPRO0143; EGF_1.
R InterPro; IPRO0418; EGF_1.
R InterPro; IPRO0429; EGF_1.
R InterPro; IPRO05209; EGF_1.
R Ffam; PFO1414; DSL; 1.
R Pfam; PFO1010; EGF=0.
R PRINTS; RN00011; DSL; 1.
R Pfam; PFO0010; EGF=0.
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000548; Q9NU41; Q9UUV2;
15-JUL-1998 (Rel. 36, Lest sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Delta-like protein 1 precursor (brosophila belta homolog 1)
(H-Delta-) (UNQ146/PR0172).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 722;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
Brathwaite M., Waeltz P., Dudekula D., Nagaraja R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          722 AA; 78449 MW; 9D570B9DC7EEC75E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51.7%; Score 62; DB 2; I 28.0%; Pred. No. 3.2e+02; iive 12; Mismatches 6;
                                                             -! - SIMILARITY: Contains 8 EGF-like domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : :: |: :: | | | | :: | | 433 GFSGRYCEDNVDDCASSPCANGGIC 457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SMO0179; EGF CA; 5.
PROSITE; PS00010; ASX HYDROXYL; 3.
PROSITE; PS00022; EGF 1; 8.
PROSITE; PS01186; EGF 2; 8.
PROSITE; PS01086; EGF 3; 6.
PROSITE; PS01187; EGF CA; 2.
                                                                                          EMBL, BC057400; AAH57400.1; -- BMBL, BC055063; AAH65063.1; -- EMBL, AY497019; AAR30869.1; -- HSSP; P00743; 1APO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 28.0%
les 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00181; EGF;
SMART; SM00179; EGF C
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us-10-627-685a-1.rup

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Q66S04;
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Q66SO4
ID Q66SO
AC Q66SO
                8
                                                                     MEDLINE-22887296; PubMed=12975309; DOI=10.1101/gr.1293003;

MEDLINE-22887296; PubMed=12975309; DOI=10.1101/gr.1293003;

A Clark H.P., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,

Clark H.P., Gurney C., Crowley C., Currell B., Deuel B., Dowd P.,

Baton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,

Huang A., Kim H.S., Klimowski L., Juhn Y., Johnson S., Lee J.,

Huang A., Kim H.S., Klimowski L., Juhn Y., Johnson S., Lee J.,

Beshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagges A.,

Vandlen R., Watanabbe C., Wieand D., Woods K., Xie M.-H., Yansura D.,

A Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,

The secreted profesin discovery initiative (SPDI), a large-scale

for oldentify novel human secreted and transmembrane proteins: a

bioinformatics assessment.",

Genome Res. 13:2265-2270(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropaen Bioinformatics Institute: There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-21464863; PubMed-11581320;
Walleco A.C., Neves H., Hooijberg E., Gameiro P., Clode N., Haury M., Jaleco A.C., Neves H., Hooijberg E., Gameiro P., Clode N., Haury M., Hanrique D., Parreaira L.;
Hanrique D., Parreaira L.;
Injurphoid differentiation.";
J. Exp. Med. 194:991-1001(2001)

J. Exp
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R GG) GG:0005576; C:extracellular; NAS.
R GG; GG:000512; F:Notch binding; IPI.
R GG; GG:0005187; F:Notch binding; IPI.
R GG; GG:0003115; F:Notch binding; IPI.
R GG; GG:0001709; P:cell differentiation; TAS.
R GG; GG:0001709; P:cell fate determination; NAS.
R GG; GG:0001709; P:hair cell fate commitment; ISS.
R GG; GG:0009912; P:hair cell fate commitment; ISS.
R GG; GG:0003097; P:hemopoiesis; NAS.
R GG; GG:0007399; P:neurogenesis; ISS.
R GG; GG:0007319; P:Notch signaling pathway; NAS.
R GG; GG:00042475; P:neurogenesis; (sensu Verrebrata); ISS.
R GG; GG:00042475; P:regulation of cell adhesion; TAS.
R GG; GG:00042475; P:regulation of cell adhesion; TAS.
Oda T., Chandrasekharappa S.C.;
"Human Delta 1 gene sequence.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                Almeida J.,
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF003522; AAB61286.1; --
EMBL; AF196571; AAF05834.1; --
EMBL; A7222310; AAG09716.1; --
EMBL; AY358892; AAQ8251.1; --
EMBL; AL078605; CAB89569.1; --
HSSP; PO0740; JEDM.
Genew; HGNC:2908; DLL1.
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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EGF-like 2.
EGF-like 3.
EGF-like 4.
EGF-like 5.
EGF-like 6.
EGF-like 6.
EGF-like 6.
EGF-like 7.
EGF-like 7.
EGF-like 7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-linked (GICNAc. . .) (Potential).
E -> Q (in Ref. 2).
G -> R (in Ref. 4 and 5).
G -> S (in Ref. 2).
B4EC455FFA32A12B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51.7%; Score 62; DB 1; Length 723; 28.0%; Pred. No. 3.3e+02; iive 12; Mismatches 6; Indels
                                                                                                                                                                                                                                     Delta-like protein 1.
Extracellular (Potential).
                                                                                                                                                                                                                                                                             Cytoplasmic (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                            By similarity. By similarity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77956 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 28.0*
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363
381
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490
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723 AA;
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Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Eucchinoidea; Echinoea; Echinoida; Strongylocentrotidae;
Strongylocentrotus.
NCBI_TaxID=7668;
                                                                                                                                                                                  SEQUENCE FROM N.A.
Pubmed=15343333; DOI=10.1038/nature02709;
Seo H.C., Edvardsen R.B., Maeland A.D., Bjordal M., Jensen M.F.,
Hansen A., Flaat M., Weissenbach J., Lehrach H., Wincker P.,
Reinhardt R., Chourrout D.;
Hox cluster disintegration with persistent anteroposterior order of
expression in Oikopleura dioica.";
Nature 431:67-71(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIJINE=90112459; PubMed=2514273; MEDIJINE=90112459; PubMed=2514273; Delgadillo-Reynoso M.G., Rollo D.R., Hursh D.A., Raff R.A.; Delgadillo-Reynoso M.G., Rollo D.R., Hursh D.A., Raff R.A.; Listuctural analysis of the uEGF gene in the sea urchin strongylocentrotus purpuratus reveals more similarity to vertebrate than to invertebrate genes with EGF-like repeats."; Mol. Evol. 29:314-327(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-1989 (Rel. 10, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Fibropellin I precursor (Epidermal growth factor-related protein 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
                                                      Notch receptor-like protein.
ORFNames=008-50;
Okrames=adoica.
Sukaryota: Metazoa; Chordata; Urochordata; Appendicularia; Oikopleuridae; Oikop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 51.7%; Score 62; DB 2; Length 824; Local Similarity 30.8%; Pred. No. 3.7e+02; es 8; Conservative 12; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    824 AA; 89253 MW; 955AEAE53CCFC86A CRC64;
25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1064 AA.
                                                                                                                                                                                                                                                                                                                                 1 CXIXNOXCXOXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PROBOLO; EGFBLOD.
SWART; SWOOLB1; EGF; 17.
SWART; SWOOLB1; EGF (17.
PROSITE; PSOOLO A AX HYDROXYL; 10.
PROSITE; PSOOLO (UB; 1.
PROSITE; PSOOLO EGF 1; 17.
PROSITE; PSOOLO EGF 1; 17.
PROSITE; PSOOLO EGF 2; 14.
PROSITE; PSOOLO EGF 2; 14.
PROSITE; PSOOLO EGF 3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseaiebaib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isold=P10079-2; Sequence=VSP_000451;
DEVELOPMENTAL STAGE: Moderate levels in unfertilized eggs and DEVELOPMENTAL STAGE: Moderate levels in unfertilized eggs and during early cleavage, then rapidly increases in abundance between late morula and mesenchyme blastula stages to maximal levels maintained through subsequent stages. Expressed both maternally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dev. Biol. 146:89-99(1991).
-!- FUNCTION: Forms the apical lamina, a component of the extracellular matrix.
-!- SUBCELLULAR LOCATION: Extracellular. In vesicles in the cytoplasm of unfertilized eggs, then to the base of the hyalin layer throughout development and finally in the apical lamina in late
                                                                                                                                                                                                                                                                                                  MEDIINE-89196806; PubMed-2784773;
Hunt L.T., Barker W.C.;
"Avidin-like domain in an epidermal growth factor homolog from a sea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHARACTERIZATION.
MEDLINE=91285254; PubMed=2060714;
Bisgrove B.W., Andrews M.E., Raff R.A.;
Bribropellins, products of an EGF repeat-containing gene, form a unique extracellular matrix structure that surrounds the sea urchin
SEQUENCE OF 279-476 AND 781-1064 FROM N.A.
MEDLINE=87319677; PubMed=3498216;
Hursh D.A., Andrews M.E., Raff R.A.;
Harsh D.A., Andrews Gene encodes a polypeptide homologous to epidermal growth factor.";
Science 237:1487-1490(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and zygotically.
--- SIMILARITY: Contains 1 avidin domain.
--- SIMILARITY: Contains 1 CUB domain.
--- SIMILARITY: Contains 21 EGF-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=P10079-1; Sequence=Displayed;
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InterPro; IPR00181; EGF 2.
InterPro; IPR00181; EGF 7.
InterPro; IPR001819; EGF 11.
InterPro; IPR006209; EGF 11.
InterPro; IPR006209; EGF 11.
InterPro; IPR00182; Avidin; 1.
Pfam; PP00181; EGF; 21.
PRINTS; PR00109; EGF; 21.
PRINTS; PR00100; EGFBCDDD.
PROSITE; PS00010; ASX HYDROXYL; 19.
PROSITE; PS001180; CUB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000152; Asx hydroxyl_S.
InterPro; IPR005469; Avidin.
InterPro; IPR005468; Avidin/str.
InterPro; IPR000859; CUB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, L08692, AAA62164.1; --
BMBL, L08692, AAA62163.1; --
EMBL, X17330; CAA35571.1; --
EMBL, M17421; AA30050.1; --
EMBL, X17533; CAA35573.1; --
PIR; A40136; A40136.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             embryos and early larvae. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                           urchin.";
FASEB J. 3:1760-1764(1989).
                                                                                                                                                                                                                                                                      AVIDIN-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=IA;
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Anopheles gambiae str. PEST.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                             (Potential).
(Potential).
(Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A Anopheles Genome Sequencing Consortium;

A Anopheles Genome Sequencing Consortium;

Loudited (MARZ-2002) to the EMBL/GenBank/DDBJ databases.

Loudited (MARZ-2002) to the EMBL/GenBank/DDBJ databases.

-I- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

EMBL, AAABOLO08859; EAA07783.1; --

EMBL; AAABOLO08859; EAA07783.1; --

EMBL; AAABOLO08859; Exalcium ion binding; IEA.

R HSSP; P00740; IEDM.

R InterPro; IPR00152; ARX hydroxyl S.

R InterPro; IPR001620; ESGF Z.

R InterPro; IPR001438; EGF Z.

R InterPro; IPR001438; EGF Z.

R InterPro; IPR00151; Laminin_G.

R InterPro; IPR00151; Laminin_G.

R InterPro; IPR001611; LRR.

R InterPro; IPR001631; LRR.Cterm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;; Score 62; DB 1; Length 1064;
;; Pred. No. 4.6e+02;
13; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    Missing (in isoform IB).
/FTId=VSP_000451.
L -> S (in Ref. 2).
W; 2E569CA012ED6D09 CRC64;
                                                                  By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               205 GFTGRNCEIDIDECASDPCQNGGACV 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 XIXNOXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 26.9%;
Matches 7; Conservative 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             112072
                                                                  279 27
1064 AA;
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SEQUENCE
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                                                                                                                                                                                                 EGF-like 2, calcium-binding (Potential).
EGF-like 4, calcium-binding (Potential).
EGF-like 5, calcium-binding (Potential).
EGF-like 6, calcium-binding (Potential).
EGF-like 7, calcium-binding (Potential).
EGF-like 8, calcium-binding (Potential).
EGF-like 10, calcium-binding (Potential).
EGF-like 11, calcium-binding (Potential).
EGF-like 12, calcium-binding (Potential).
EGF-like 13, calcium-binding (Potential).
EGF-like 13, calcium-binding (Potential).
EGF-like 14, calcium-binding (Potential).
EGF-like 15, calcium-binding (Potential).
EGF-like 16, calcium-binding (Potential).
EGF-like 17, calcium-binding (Potential).
EGF-like 19, calcium-binding (Potential).
EGF-like 10, calcium-binding (Potential).
EGF-like 11, calcium-binding (Potential).
EGF-like 12, calcium-binding (Potential).
EGF-like 13, calcium-binding (Potential).
EGF-like 14, calcium-binding (Potential).
EGF-like 19, calcium-binding (Potential).
EGF-like 19, calcium-binding (Potential).
EGF-like 10, calcium-binding (Potent
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SEQUENCE FROM N.A.
MEDLINE=20144115; PubMed=10677532; DOI=10.1073/pnas.040545897;
MEDLINE=20144115; PubMed=10677532; DOI=10.1073/pnas.040545897;
Smith J.D., Graig A.G., Kriek N., Hudson-Taylor D., Kyes S., Fagen T.,
Pinches R., Baruch D.I., Nawbold C.I., Miller L.H.;
"Identification of a Plasmodium falciparum intercellular adhesion molecule-1 binding domain: a parasite adhesion trait implicated in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmodium falciparum.
Eukaryotai, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51.7%; Score 62; DB 2; Length 1685; 29.6%; Pred. No. 7e+02; ive 13; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1515 AA; 166871 MW; 12FD111277D18D5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 1685 AA; 193671 MW; D1FD426666B0551E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cerebral malaria.";

Proc. Natl Acad. Sci. U.S.A. 97:1766-1771(2000).

EMBL; AF193424; AAF19890.1;

EMBL; AF193424; AF19980.1;

EMBL; AF193424; AF19980.1;

EMBL; AF193424; AF198980.1;

CO; GO:0005539; F:glycosaminos; IEA.

InterPro; IPR00454; Bub ATPase_Csub.

InterPro; IPR00454; Bub ATPase_Csub.

InterPro; IPR00458; PFEMP.

Pfam; PF03011; PFEMP; I.

PROSITE; PS00605; ATPASE_C; UNKNOWN.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Variant surface protein PfEMPI (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1685 AA
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SWART; SW00041; CT; 1.
SWART; SW00179; EGF CA; 1.
SWART; SW00274; FOLK; 3.
R SWART; SW00282; LamG; 1.
R SWART; SW00082; LRRCT; 4.
DR SWART; SW00019; LRRCT; 4.
DR SWART; SW00199; LRRTY; 9.
DR SWART; SW00199; LRR TYP; 9.
DR PROSITE; PS00010; ASX HYDROXYL; 2.
PROSITE; PS01185; CTCK I; UNKNOWN 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1059 VGQQCEQDYNDCLENKCQHGAECV 1082
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                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00022; EGF_1; 9.
PROSITE; PS01186; EGF_2; 7.
PROSITE; PS50026; EGF_3; 8.
PROSITE; PS01187; EGF_CA; 2.
PROSITE; PS50025; LAM_G_DOMAIN; 1.
           Laminin G_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 33.33
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 29.63
Matches 8; Conservative
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                                                                                       Pfam; PF00560; LRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EGF-like domain
SEQUENCE 1515
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X MEDLINE=21098742; PubMed=11161558; DOT=10.1006/dbio.2000.0105;

A FO S.Y., Little M.H., Yamada T., Miyashita T., Halloran M.C.,

Kuwada J.Y., Huh T.L., Okamado H.;

Ruwada J.Y., Huh T.L., Okamado H.;

"Overexpression of a slit homologue impairs convergent extension of T. the mesoderm and causes cyclopia in embryonic zebrafish.";

Dev. Biol. 230:1-17(2001).

R RSBP; AF210320; AAG36772.1; -.

R RSSP; PO1132: 16K5.

R ZPIN; ZDB-GRNE-010306-4; slit3.

R GO; GO:0005509; F:calcium ion binding; IEA.

R GO; GO:0005155; P:call adhesion; IEA.

R InterPro; IPR000152; Asx hydroxyl_S.

InterPro; IPR000152; Ax hydroxyl_S.

InterPro; IPR000152; Ax hydroxyl_S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brachydanio rerio (Zebrafish) (Danio rerio)
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51.7%; Score 62; DB 2; Length 1286; 33.3%; Pred. No. 5.5e+02; ive 10; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1286 AA; 144156 MW; EE919D876B21BB3E CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1515 AA
InterPro; IPR003591; LRR typ.
InterPro; IPR001211; PhospholipaseA2.
                                                       PEAM; PF00008; EGF; 7.
PEAM; PF01463; LRRUT; 3.
PEAM; PF001462; LRRUT; 3.
PEAM; PF00560; LRR 1; 14.
PRINTS; PR00010; EGFBLOOD.
PRINTS; PR00010; EGRICARPT.
PROSITE; PS00010; ASX_HYDROXYL; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                            PS50025; LAM G DOMAIN; 1.
PS00119; PA2 ASP; UNKNOWN 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 XCXQXLDDCCSXXCNXXNXCV 27
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InterPro; IPR00142; EGF 2.
InterPro; IPR001881; EGF Ca.
InterPro; IPR006209; EGF Tike.
InterPro; IPR00545; Fol Nike.
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InterPro; IPR000372; LRR Nterm.
InterPro; IPR003591; LRR Lyp.
InterPro; IPR003129; TSP_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best_Local Similarity 33.3
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                PS00022;
PS01186;
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                                                                                                                                                                                                                                                           PS01185;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGF-like domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=slit3;
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                                                                                                                                                                                                                                                           PROSITE;
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PROSITE;
PROSITE;
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Q9DE37
     DORANGE SERVICE SERVIC
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(AUG-2002) to the EMBL/GenBank/DDBJ databases.
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PROSITE; PSO1086; EGF 2; 27.
PROSITE; PS50026; EGF 3; 35.
PROSITE; PS01187; EGF CA. 22.
ANK repeat; EGF-1ike Gomain.
SEQUENCE 2428 AB.
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                                                         EMBL; AF537369; AAN06819.1;
HSSP; P07207; 10T8.
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NCBI_TaxID=7739;
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0
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Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,

Neoptera, Endopterrygota, Diptera, Nematocera, Culicoidea, Anopheles.

NCBI_TaxID=180454,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anotheles Genome Sequencing Consortium,
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Eukaryota, Metazoa, Arthropoda, Chelicerata, Arachnida, Acari,
Parasitiformes, Ixodida, Ixodidae, Boophilus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0005198; F:calcium ion binding; IEA.
GO; GO:0005198; F:calcium ion binding; IEA.
GO; GO:0005198; F:calcium ion binding; IEA.
GO; GO:0007155; P:cell adhesion; IEA.
InterPro; IPR000152; Asx hydroxyl S.
InterPro; IPR000182; Asx hydroxyl S.
InterPro; IPR000181; EGF Z.
InterPro; IPR001881; EGF Ca.
InterPro; IPR001881; EGF II.
InterPro; IPR001918; EGF II.
InterPro; IPR001791; Laminin G.
InterPro; IPR001791; Laminin G.
InterPro; IPR001791; Laminin G.
InterPro; IPR001791; Laminin G.
                                                                                     01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
AgCP13744 (Fragment).
Name=agCG44966; ORFNames=ENSANGG0000015360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Notch-like protein.
                                        PRT; 2037 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             preliminary data.
EMBL; AAAB01008844; EAA06013.1; -.
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PS00022; EGF 1; 24.
PS01186; EGF 2; 17.
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PS50026; EGE_CA; 13.
PS50025; IAM_G_DOMAIN; 3.
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TISSUE=Whole ticks;
Whitfeld P.L., McNicholas P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00008; EGF; 24.
Pfam; PF07645; EGF CA; 2.
Pfam; PF02210; Laminin G 2
PRINTS; PR00010; EGFBLÖOD.
                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P00740; 1EDM.
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EGF-like domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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Q816X6;
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0816X6

10 0816X1

AC 0816X1

DT 01-MAI

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Gaps
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Bukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 51.7%; Score 62; DB 2; Length 2428; Best Local Similarity 29.2%; Pred. No. 9.8e+02; Matches 7; Conservative 11; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Whole larvae,
Holland L.Z., Burgtorf C., Holland N.D., Lehrach H., Tamme
Abi-Rached L., Pontarotti P., Lardelli M.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          260842 MW; 766A9362CE37CB9F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUB-Whole larvae;
Lardelli M.T.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; Y12539; CAC19873.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO:0030154; P:call differentiation; IEA.
GO; GO:0050793; P:regulation of development; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 2524 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0016020; C:membrane; IEA.
GO; GO:0005509; F:calcium ion binding; IEA
                                                                  InterPro; IPR002110; ANK.
InterPro; IPR00110; ANK.
InterPro; IPR00152; ASK. hydroxyl_S.
InterPro; IPR001881; EGF_2.
InterPro; IPR001881; EGF_II.
InterPro; IPR001838; EGF_III.
InterPro; IPR008297; Nocch.
InterPro; IPR008297; Nocch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 XNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                        PS50088; ANK REPEAT; 4.
PS50297; ANK_REP REGION;
PS00010; ASX_HYDROXYL; 22
PS00022; EGF 1; 34.
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PIR; A32038; A32038.

PDB; LEIT; NMR; @=1-36.

InterPro; IRR00243; Toxin 7.

Pfam; PF05980 Toxin 7; 1.

3D-structure; Anidation; Direct protein sequencing; Neurotoxin; Toxin.

DISULFID 2 17
                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 36;

    I-SSUE SPECIFICITY: Expressed by the venom gland.
    SIMILARITY: Belongs to the mu-agatoxin family.

                                                                                                                                                                                                                                                                                                                                                                                                  4273 MW; 3B973A605B90DE85 CRC64;
                                                                                                                                                                                                                                         Asparagine amide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             471 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51.2%; Score 61.5; I 27.6%; Pred. No. 50; iive 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CXIXNQXCXQXLDDCCS---XXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 CVPENGHCRDWYDECCEGFYCSCRQPPKCI 31
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 61.5;
Pred. No. 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CXIXNQXCXQXLDDCCSXXC---NXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46 CTVDSDFCDPDNHDCCSGRCIDEGGSGVC 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR004214; Conctoxin.
PFam: PF02950; Conctoxin; 1:
SEQUENCE 81 AA: 8697 MW; 99EB013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QBLAG1;
01-OCT-2002 (TrEMBLrel. 22, Created)
    Secreted
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                                                                                                                                                                                                                                                                                                                                                                                                                                          51.2%;
26.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, 01-OCT-2003 (TrEMBLrel. 25,
  SUBCELLULAR LOCATION:
TISSUE SPECIFICITY: EX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conotoxin spaffold VI/VII.
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Best Local Similarity 27.69
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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DISULFID
DISULFID
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Q8LAG1
ID Q8LAG
AC Q8LAG
DT 01-OC
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MEDLINE=8912392; PubMed=2914898;
Skinner W.S., Adams M.E., Quistad G.B., Kataoka H., Cesarin B.J.,
Enderlin F.E., Schooley D.A.; attain of two classes of neurotoxins from
"purification and characterization of two classes of neurotoxins from
the funnel web spider, Agelenopsis aperta.";
J. Biol. Chem. 264:2150-2155(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=96182019; PubMed=8608119; DOI=10.1021/bi952605r; Omecinsky D.O., Holub K.E., Adams M.E., Reily M.D.; "Three-dimensional structure analysis fmu-agatoxins: further evidence for common motifis among neurotoxins with diverse ion channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gpedificities.";
Biochemistry 35.2836-2844(1996).
Biochemistry 35.2836-2844sersible paralysis in lepidopterous insects
-!-PUNCTION: Causes irreversible paralysis in lepidopterous insects
by massive transmitter release (which is mediated by glutamate
receptors) from presynaptic stores at neuromuscular junctions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Būkaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
Araneomorphae; Entelegynae; Agelenidae; Agelenopsis.
NCBI_TaxID=6908;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 62; DB 2; Length 2524;
Pred. No. 1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00022; EGF_1; 34. PROSITE; PS01186; EGF_2; 28. PROSITE; PS50026; EGF_3; 36. PROSITE; PS10187; EGF_A; 22. ANK repeat; EGF_1ike Gomain; Receptor. SEQUENCE 2524 AA; 270970 MW; C2CA57E306D23EC9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUL-1989 (Rel. 11, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
F:receptor activity; IEA. P:cell differentiation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50089; ANK REPEAT; 4.
PROSITE; PS50297; ANK REP REGION; 1.
PROSITE; PS00010; ASX_HYDROXYL; 23.
PROSITE; PS00190; CYTOCHROWE_C; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  925 GFGGTNCEEDIDECYSNPCQNGGQCI 950
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                                                     InterPro; IPR000152; ABX hydroxyl S. InterPro; IPR008985; ConA like_lec_gl. InterPro; IPR000345; CytC_heme_BS.
                                                                                                                              01-JUL-1989 (Rel. 11, Created)
                                                                                                                                                                                                                                   Pfam; PP00008; EGF; 34.
Pfam; PP0066; EGF; CA; 2.
Pfam; PP0066; NOtCh; 3.
PRINTS; PR01415; ANKYRIN.
PRINTS; PR00010; EGFBLOOD.
PRINTS; PR01452; NOTCH.
SMART; SM00248; ANK; 6.
SMART; SM00179; EGF CA; 21.
                                                                                               InterPro; IPR000345; CytC
InterPro; IPR000742; EGF
InterPro; IPR001881; EGF
InterPro; IPR001438; EGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 23.1 es 6; Conservative
                                         InterPro; IPR002110; ANK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                Pfam; PF00023; Ank;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRUCTURE BY NMR.
GO; GO:0004872;
GO; GO:0030154;
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P11057;
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Gaps

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Indels

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B
                                                                                     Conus arenatus (Sand-dusted cone).
Bukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidae; Conus.
                                                                                                                                                                                                                                                                                                      MEDLINE=21105969; PubMed=11158371;
Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
Fainzilber M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 81;
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EMBL. AF215061; AAG6499.1;
GO; GO:0005576; C:extracellular; IEA.

GO; GO:0008200; P:ion channel inhibitor activity; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8697 MW; 99EB0139D26851D5 CRC64;
Last sequence update)
Last annotation update)
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Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamina A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J., Sakurai T., Satou M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Saki M., Shinn P., Southwick A., Shinozaki K., Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AY065014; AAL57658.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AY096601; AAM20251.1; -.
EMBL; AY142043; AAM98307.1; -.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 22.28
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ecker J.R.;
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Q9ZVZ7;
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                                   셤
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                                                                                                      Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II, Brassicales; Brassicaceae; Arabidopsis.
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SEQUENCE FROM N.A.

Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,

Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,

Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,

Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,

Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,

Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Mixanda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou P.
Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=22088475; PubMed=12093376;
Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N., Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
"Full-length messenger RNA sequences greatly improve genome annotation.";
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د.
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Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 471;
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY087835; AAM65388.1;
Hypothetical protein.
SEQUENCE 471 AA; 53428 MW; 3573C789C54FB28A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51.2%; Score 61.5; DB 2; Length 4 22.2%; Pred. No. 2.5e+02; ive 12; Mismatches 7; Indels
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Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
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Theologis A.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                           Last annotation update)
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                    Last sequence update)
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150 CKAGNEKCRSLMPQCEAETL.PAMPCDICCGERKFCV 185
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01-OCT-2002 (TrEMBLrel. 22, Last sequenc
01-MAR-2003 (TrEMBLrel. 23, Last annotat
Hypothetical protein.
Arabidopsis thaliana (Mouse-ear cress)
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Best Local Similarity 22.23
Matches 8; Conservative
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08VZES
1D 08VZES
DT 08VZES
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GN NCBI
RN ATABL
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RA BOWE
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Kim C.J., Chen H., Cheuk R., Shinn P., Bowser L., Carninci P., Chen M., Chang C.H., Dale J.M., Deng J.M., Hayashizaki Y., Hsuan V.W., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Wallender E.K., Wong C., Wu H.C., Yamada K., Yu G., Yuan S., Davis R.W., Theologis A., Ecker J.R.; Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
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Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,
Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosićeurosids II, Brassicales, Brassicaceae, Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                    Length 471;
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                                                                                                                                                                                                                                                                                                                   al protein.
471 AA; 53368 MW; 582512E495010DDA CRC64;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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150 CKAĞNBKCRSLMPQCEAETLPAMPCDICCGERKFCV 185
                                                                                                                                                                                                                                                                                                                                                                                            51.2%; Score 61.5; DB 2; 22.2%; Pred. No. 2.5e+02; ive 12; Mismatches 7;
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Job time : 121 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDZINE=2255705; PubMed=12368864; DOI=10.1038/nature01097; Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W., Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K., Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Chan M.S., Nene V., Shallon S.J., Shu B., Peterson J., Angiuoli S., Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B., Martin D.M., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., Werter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W., Fraser C.M., Barrell B.;
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MEDLINE=94150815; Pubmed=8107968; DOI=10.1016/0028-3908(93)90008-Q;
Monje V.D., Haack J.A., Naisbitt S.R., Miljanich G., Ramachandran J.,
                                                                                                                                                                                                                                                                      Gaps
Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
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Neogastropoda; Conoidea; Conidae; Conus.
NCBI_TaxID=6492;
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Pred. No. 9.4e+02;
                                                                                                                                                                                                     Length 481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium faĪciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
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                                     Theologis A., Ecker J.; Submitted (UUN-2000) to the EMBL/GenBank/DDBJ databases. Submit Actod (UUN-2000) to the EMBL/GenBank/DDBJ databases. SEQUENCE 481 AA; S4484 MW; 409BE67FF55068E1 CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                              51.2%; Score 61.5; DB 2;
22.2%; Pred. No. 2.5e+02;
tive 12; Mismatches 7;
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32.1%; Pred. No. >...
've 14; Mismatches
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15-DEC-1998 (Rel. 37, Last sed
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Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 419:498-511 (2002)
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Thaveri A.,
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Q26350;
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LD CXOD AC
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1081KO3
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                                                                                                                                                                                                                                                  "Solution structure determination by two-dimensional 1H NMR of omega-
conotoxin MVIID, a calcium channel blocker peptide.";
Biochem. Biophys. Res. Commun. 254:32-35(1999).
--- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bin
and block voltage-sensitive calcium channels (VSCC). This toxin
blocks channels of the N-type as well as other types.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                             Civera C., Vazquez A., Sevilla J.M., Bruix M., Gago F., García A.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the venom duct.
-!- SIMILARITY: Belongs to the conotoxin O-superfamily. Omega-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cysteine amide (G-29 provides amide
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InterPro; 198004214; Conotoxin.
Amidation; Calcium channel inhibitor; Ionic channel inhibitor;
Neurotoxin; Presynaptic neurotoxin; Toxin.
                                                                                                                                  STRUCTURE BY NMR.
MEDLINE=99121185; PubMed=9920728; DOI=10.1006/bbrc.1998.9878;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 61; DB 1; Length 29;
Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Indels
Nasdasdi L., Olivera B.M., Hillyard D.R., Gray W.R.; "A new Conus peptide ligand for Ca channel subtypes."; Neuropharmacology 32:1141-1149(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           group).
9E04B2EA3779CB22 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CXIXNOXCXQXLDDCCSXXCNXXNX 25
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28.0%;
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204 Shail 342 Conus 344 Conus 336 Conus 339 Conus 345 Conus 345 Conus	Aac38356 Conus pur Aac38356 Conus pur Aau10213 Snail Kap Aau10219 Snail Kap Aau10219 Snail Kap Aau10215 Snail Kap Aau10215 Snail Kap Aau10215 Snail Kap Aau10215 Snail Kap Aau10215 Snail Kap	Conus Conus Conus Conus Snail Conus Omega- Omega- SNX-20 SNX-20 SNX-20 SNX-20 Omega- Conus	Aay56496 Analogue Aab14370 Omega-con Aab19462 Sequence Abb96887 Omega-con Abb96679 Omega-con Abb9666 Omega-con Abb9666 Omega-con Aar39615 SVIB/SNX- Aar39760 SVIB/SNX- Aar39760 SVIB/SNX- Aar19551 Natural o Aav12674 Omega-con Aav56780 Natural o Aab14359 Omega-con Aab5480 Natural o Aab14359 Omega-con Aab14359 Omega-con Aab14359 Omega-con	Aao15126 Cone enai Abb96680 Omega-con Abb96680 Omega-con Abb96780 Omega-con Abb96772 Omega-con Abb96874 Omega-con Abb96874 Omega-con Abb968874 Omega-con Abb968879 Cones bet Abb96774 Omega-con Abb96774 Omega-con Abb96774 Omega-con Abb96774 Omega-con Abb96774 Omega-con Abb96774 Omega-con Aar39616 MVIIC/SNX Aar39616 Abbraral O Aar37761 MVIIC/SNX Aar39616 Omega-con Aar3761 Omega-con Aar3761 Omega-con Aar3761 Omega-con Aar3761 Omega-con Aar3761 Omega-con Aar3761 Omega-con Aar37761 Omega-con Aar37761 Omega-con Aar37761 Omega-con Aar37761 Omega-con Aar35572 Omega-con Aav95573 Omega-con
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	ates/sec 33 33 33 33 34 4 4 4 4 4 4 4 4 4 4 4 4	2105692 2105692 4 4 4 4 4 4 8 4 8 8 8 8 8 8 8 8 8 8 8 8	y chance to have a 65 61 62 62 63 64 64 65 65 65 65 65 65 65 65 65 65 65 65 65	Aaw35723 Kappa-con 74 Aau10218 Snail Kap 75 Aau10212 Snail Kap 76 Aau10205 Snail Kap 77 Aau10205 Snail Kap 77 Aau10205 Snail Kap 80 Aau10207 Snail Kap 81 Aau10207 Snail Kap 84 Aau10217 Snail Kap 84 Aau10217 Snail Kap 86 Aau10218 Snail Kap 86 Aau10218 Snail Kap 88 Aau10200 Snail Kap 89 Aau10205 Snail Kap 91 Aau10205 Snail Kap 94 Aau10205 Snail Kap 94 Aau10205 Snail Kap 94 Aau10205 Snail Kap 94 Aau10207 Snail Kap 94 Aau10207 Snail Kap 96 Aau10210 Snail Kap 96 Aau10210 Snail Kap 97
GenCore versic Copyright (c) 1993 - 2005 protein - protein search, using sw model	7-685A-26 KCFQHLDDCCSRK DX Gapext 0	105692 seqs, 386760381 residues its satisfying chosen parameters: ngth: 0 ngth: 2000000000 Minimum Match 0% Maximum Match 100% Listing first 100 summaries A_Geneseq_16Dec04:* : geneseq_16Dec04:* : geneseq_16Dec08:*	geneseqp2000s:* geneseqp200s:* geneseqp2003s:* geneseqp2003as:* geneseqp2003as:* geneseqp2004s:* the number of results predicted lar than or equal to the score of the by analysis of the total score cry	1 161 100.0 27 2 AAW35723 2 161 100.0 27 4 AAU10218 4 158 98.1 27 4 AAU10216 6 158 98.1 27 4 AAU10205 6 158 98.1 27 4 AAU10205 7 158 98.1 27 4 AAU10205 9 158 98.1 27 6 AAE3835 10 157 97.5 27 4 AAU10207 11 157 97.5 27 4 AAU10207 12 157 97.5 27 4 AAU10207 13 157 97.5 27 4 AAU10207 14 156 96.9 27 4 AAU10198 15 156 96.9 27 6 AAE38354 16 156 96.9 27 6 AAE38354 17 156 96.9 27 6 AAE38354 18 155 96.3 27 4 AAU10205 20 155 96.3 27 4 AAU10205 21 155 96.3 27 4 AAU10205 22 155 96.3 27 4 AAU10205 23 155 96.3 27 4 AAU10205 24 155 96.3 27 4 AAU10205 25 155 96.3 27 4 AAU10205 27 4 AAU10205 28 155 96.3 27 4 AAU10205 29 155 96.3 27 4 AAU10205 20 155 96.3 27 4 AAU10205 21 155 96.3 27 4 AAU10205 22 155 96.3 27 4 AAU10205 23 155 96.3 27 4 AAU10205 24 155 96.3 27 4 AAU10205

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/note= "Optionally 4-trans-hydroxyproline, hydroxyproline or proline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a new kappa-conotoxin PVIIA which targets potassium channels and can be used to augment neurotransmitter release in pathological situations such as autoimmune diseases, e.g. Alzheimer's disease, Lambert-Eaton syndrome or myasthenia gravis. This peptide inmobilize fish which are injected with the two peptides. Injection of kappa-conotoxin PVIIA and synergistically to rapidly kappa-conotoxin PVIIA alone results in different symptoms with an injected fish becoming hyperactive and then contracting and suddenly extending all major fins. This "fin-popping" occurs repeatedly resulting in a series of jerky movements, but injection of only kappa-conotoxin PVIIA does not immobilize or kill the fish
       Aay43715 Amino aci
Aab14377 Omega-con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New kappa-conotoxin peptides - which target potassium channels and can be used to augment neurotransmitter release in e.g. autoimmune diseases.
                                                                                                                                                                                                                            Kappa-conotoxin PVIIA; potassium channel; neurotransmitter release; cone snail; venom; goldfish; delta-conotoxin PVIIA; disulphide.
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                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                         note= "disulphide bond"
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/note= "disulphide bond"
    AAY43715
AAB14377
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                                                                                                                    AAW35723 standard; peptide; 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 23; 29pp; English.
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                                                                                                                                                                                                   Kappa-conotoxin PVIIA.
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  37.9
37.9
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Disulfide-bond
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  61
                                                                                                                                             AAW35723;
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                                                                                                            Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; O4A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappaconotoxin PVIIA peptide.
                                                                                                                                                                                                                                                                  /note= "The C-terminus is either a carboxyl group or amide group"
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Pred. No. 1e-10;
1; Mismatches
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                                                                                Snail Kappa-conotoxin PVIIA analogue 04A.
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                                                                                                                                                                                                              Location/Qualifiers
AAU10218 standard; peptide; 27 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cornell-Bell AH, Pemberton KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 28; 46pp; English.
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20-JUL-2000; 2000US-0219438P.
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es 26; Conservative
                                                         (first entry)
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                                                                                                                                                                     purpurascens
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Modified-site
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                                                       16-JAN-2002
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Synthetic.
                             AAU10218;
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Matches
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AAE38358 standard; peptide; 27 AA.

RESULT 3 AAE38358 ID AAE3

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Gaps ; 0

2; Length 27; Indels

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100.0%; Score 161; DB 2 96.3%; Pred. No. 1e-10; tive 1; Mismatches

CRIXNOKCFOHLDDCCSRKCNRFNKCV 27

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Conservative

Local Similarity les 26; Conserv

Query Match Matches

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cerebral ischaemia; ocular ischaemia; asthma; S17A.
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                                                                  Modified-site
                                                                                         Modified-site
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                                   Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to kappa-PVIIA-related conotoxins and their use as organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, neuropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral exerappanting subarachnoid haemorrhage, anxiety disorder, cerebral ischaemia, coronary artery bypass graft (GASG) surgery, ischaemic heart disease, asthma, and congestive heart failure. The present
                                                                          Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
                                                                                                                                                                                                                                                                                                                                                         Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
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                                                       Conus purpurascens kappa-PVIIA analogue peptide, Q4A.
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                                                                                                                                                                                                                                                                                                  Jones RM,
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96.3%; E
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                                                                                                                                                                                                                                         29-JAN-2002; 2002US-0352219P.
                                                                                                                                                                                                                                                               (COGN-) COGNETIX INC.
(UTAH ) UNIV UTAH RES FOUND.
                                 (first entry)
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Les 26; Conservative
                                                                                                                                                                                                                                                                                                 Pemberton-Goodman KE,
                                                                                                                                                                                                                                                                                                                                    WPI; 2003-679464/64.
                                                                                                                                                Conus purpurascens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 27 AA;
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                                 20-NOV-2003
                                                                                                                                                                                            07-AUG-2003
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           AAE38358
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The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with channel, especially cardiac ischaeme by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappa-conotoxin PVIIA peptide.
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                                                                                                                                                                                                        /note= "The C-terminus is either a carboxyl group or an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98.1%; Score 158; DB 4; 96.3%; Pred. No. 2.2e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
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                                                                                                                                               /note= "Hyroxyproline"
                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                           amide group"
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Best Local Similarity 96.3
Matchès 26, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (COGN-) COGNETIX INC.
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Conus purpurascens
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Synthetic.
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amide group"

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28-JAN-2003; 2003WO-US002384.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappa-
                                                                                                                                                                          /note= "The C-terminus is either a carboxyl group or an amide group"
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cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
cerebral ischaemia; ocular ischaemia; asthma; R2K.
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        Location/Qualifiers
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Modified-site
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The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprishing administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappaconotoxin PVIIA peptide.
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WO200121648-A1
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                                                                                                                                                                             Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
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Pred. No. 2.2e-10;
                                                                                                Mcintosh JM;
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                                                                                                  Temple DL,
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                                                                                                                                                                                                                              Disclosure; Page 7; 32pp; English.
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                                                                                                  Jones RM,
               29-JAN-2002; 2002US-0352219P.
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92.6%;
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                                             (COGN-) COGNETIX INC.
(UTAH ) UNIV UTAH RES FOUND.
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es 25; Conservative
                                                                                                Pemberton-Goodman KE,
                                                                                                                                            WPI; 2003-679464/64.
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                                                                                                                Olivera BM;
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AAE38346
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Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
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               Mcintosh JM;
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               Temple DL,
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                                                                                                                                           Disclosure; Page 7; 32pp; English.
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               Jones RM,
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(UTAH ) UNIV UTAH RES FOUND.
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Matches 25; Conservative
               Pemberton-Goodman KE,
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                                                              WPI; 2003-679464/64.
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                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 27 AA;
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Modified-site
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                               Olivera
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AAE38343
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(COGN-) COGNETIX INC.
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                                                                     Best Local Similarity
                                                                                                                                       Conus purpurascens.
Synthetic.
                                                                                                                                                                                                      Cornell-Bell AH,
                                                            Sequence 27 AA;
                                                                                                                                                                     WO200121648-A1
                                                                                                                                                Key
Modified-site
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                                                                                                               16-JAN-2002
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                                                                  Query Match
                                                                                                         AAU10207:
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The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conctoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conctoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, errebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conctoxin PVIIA analogue of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; V27A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "The C-terminus is either a carboxyl group or an
activating a KATP channel by administering to an individual a kappa-conotoxin PVIIA peptide.
                                                                                                                                                                                                                                                                                                                                  Length 27;
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Pred. No. 2.8e-10;
                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Snail Kappa-conotoxin PVIIA analogue V27A.
                                                                                                                                                                                                                                                                                                                                                                                                                            1 CRIXNOKCFQHLDDCCSRKCNRFNKCV 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                      Claim 1; Page 28; 46pp; English.
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20-JUL-2000; 2000US-0219438P.
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                                                                                                                                                                                                                                                                                      Sequence 27 AA;
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Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
                                                                                     The invention relates to kappa-PVIIA-related conotoxins and their use as organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, treatment of arrivhthmia, urinary incontinence, reperfusion injury, treatment of arrivhthmia, urinary incontinence, reperfusion injury, peripheral circulation disturbances, hypertension, angina, cerebral escribaral ischaemia, coronary artery bypass graft (CABG) surgery, ischaemia, coronary artery bypass graft (CABG) surgery, sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
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cardioactive; antiasthmatic; KATP charnel activation; cardiac ischaemia;
cerebral ischaemia; ocular ischaemia; asthma; R2Q.
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                                                      Disclosure; Page 7; 32pp; English.
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20-JUL-2000; 2000US-0219438P.
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Mccabe RT;

Claim 1; Page 28; 46pp; English.

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The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-concorxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conctoxins are used for treating disorders associated with channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
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(UTAH ) UNIV UTAH RES FOUND.
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                                                                                                                                                analogue of the invention
                                                                                                                                                                                                                                                      26; Conservative
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                                                                                                                                                                                                                                      Best Local Similarity
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                                                                                                                                                                                 Sequence 27 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a mammal comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to kappa-PVIIA-related conotoxins and their use as
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cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
ischaemic heart disease, asthma and congestive heart failure. The preser
sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
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                                                                                                                   Length 27;
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                                                                                                                                                                                                                                                                                                                                                                                                          Conus purpurascens kappa-PVIIA analogue peptide, R2Q.
                                                                                                               Score 157; DB 6;
Pred. No. 2.8e-10;
1; Mismatches 0
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                                                                                                                                                                                                                     1 CRIPNOKCFOHLDDCCSRKCNRFNKC 26
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                                                                                                               97.5%;
96.2%;
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                                                                                                                                                                                                                                                                                                       AAE38347 standard; peptide;
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                                                                                                                                                    Conservative
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                                                                                                 Query Match
Best Local Similarity
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Modified-site
                                                                                  Sequence 27
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                                                                                                                                                                                                                                                                     Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; L12A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular analogue of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappa-
                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "The C-terminus is either a carboxyl group or an
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               97.5%; Score 157; DB 6; Length 27; llarity 92.6%; Pred. No. 2.8e-10; Conservative 2; Mismatches 0; Indels
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96.3%; Pred. No. 3.6e-10;
ive 0; Mismatches 1;
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                                                                    1 CRIXNOKCFQHLDDCCSRKCNRFNKCV 27
                                                                                  note= "Hyroxyproline"
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                                                                                                                                                             AAU10214 standard; peptide; 27
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20-JUL-2000; 2000US-0219438P.
                                                                                                                                                                                                                                                                                                                                                                                                                                     amide group"
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conotoxin PVIIA peptide.
Query Match
Best Local Similarity
Then 25; Conserve
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Synthetic.
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les 26; Conserv
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The invention relates to treating disorders associated with radical comprisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-contoxin PVIIA (Kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
                                                                                                                                                                                                       Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
cerebral ischaemia; ocular ischaemia; asthma; I3A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappaconotoxin PVIIA peptide.
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 CRIXNOKCFOHLDDCCSRKCNRFNKCV
                  CRIXNOKCFQHADDCCSRKCNRFNKCV
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                                                                                          AAU10198 standard; peptide;
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es 26; Conservative
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Synthetic.
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ischaemic heart disease, cerebral ischaemia; anxiety disorder; diabetes; organ protectent, arrhythmia; reperfusian injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure;

Location/Qualifiers

Conus purpurascens.

/label= Hyp

Modified-site

WO2003063782-A2

07-AUG-2003

28-JAN-2003; 2003WO-US002384.

Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;

Conus purpurascens kappa-PVIIA analogue peptide, L12A.

20-NOV-2003 (first entry)

AAE38354;

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                                                                                                                                                                       Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
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                                 AAE38338 standard; peptide; 27 AA.
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Matches 25; Conservative
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(UTAH ) UNIV UTAH RES FOUND.
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Matches 25; Conserv
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8X4X5X8
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CRAPNOKCFOHLDDCCSRKCNRFNKCV 27

AAE38354 standard; peptide; 27 AA

RESULT 17 AAE38354 ID AAE3 XX

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The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active radical depolarisation of excitable membrane by activatival depolarisation of excitable membrane by activating a specially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention
               Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
cardicactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
cerebral ischaemia; ocular ischaemia; asthma; R2A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappa-
                                                                                                                                                                                  /note= "The C-terminus is either a carboxyl group or an amide group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Purple cone snall, kappà-conotoxin PVIJA analogue; circulatory;
cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
cerebral ischaemia; ocular ischaemia; asthma; Q10A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96.3%; Score 155; DB 4; Length 27; 96.3%; Pred. No. 4.7e-10;
                                                                                                                                                                                                                                                                                                                                                                                             Temple DL, Layer RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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                                                                                                                                                     'note= "Hyroxyproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CRIXNOKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAIXNQKCFQHLDDCCSRKCNRFNKCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU10216 standard; peptide; 27 AA.
                                                                                                                                                                                                                                                                                                                                                                                          Cornell-Bell AH, Pemberton KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 27; 46pp; English.
                                                                                                                                                                                                                                                                                                                   22-SEP-1999; 99US-0155135P.
20-JUL-2000; 2000US-0219438P.
                                                                                                                                                                                                                                                                                      21-SEP-2000; 2000WO-US025827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  conotoxin PVIIA peptide.
                                                                                                                                                                                                                                                                                                                                                               (COGN-) COGNETIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-648090/74.
                                                                          Conus purpurascens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
les 26; Conser
                                                                                                                                                                                                                           WO200121648-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 27 AA;
                                                                                                                                  Modified-site
                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                        29-MAR-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                             Jones RR;
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Mccabe RT;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
cerebral ischaemia; ocular ischaemia; asthma; F9M.
                                                                                                                                                                                                                                                                                                                                          Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprise activating a KATP channel by administering to an individual a kappaconotoxin PVIIA peptide.
                                                                                                   or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                           C-terminus is either a carboxyl group
                                                                                                                                                                                                                                                                                    Mccabe RT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96.3%; Score 155; DB 4; Length 27; 96.3%; Pred. No. 4.7e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                    Layer RT,
                                                                                                                                                                                                                                                                                 Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Snail Kappa-conotoxin PVIIA analogue F9M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CRIXNOKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27
                                                                 note= "Hyroxyproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRIXNQKCFAHLDDCCSRKCNRFNKCV
                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU10205 standard; peptide; 27 AA.
                                                                                                                                                                                                                                                                               Pemberton KE,
                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 28; 46pp; English.
                                                                                                                                                                                   21-SEP-2000; 2000WO-US025827.
                                                                                                                                                                                                            22-SEP-1999; 99US-0155135P.
20-JUL-2000; 2000US-0219438P.
                                                                                                           amide group"
                                                                                           /note= "The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 96.3
Matches 26; Conservative
                                                                                                                                                                                                                                                   (COGN-) COGNETIX INC.
 Conus purpurascens.
Synthetic.
                                                                                                                                                                                                                                                                                                                    WPI; 2001-648090/74.
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Synthetic.
                                                                                                                                                                                                                                                                           Cornell-Bell AH,
                                                                                                                               WO200121648-A1
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                                       Key
Modified-site
                                                                           Modified-site
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Modified-site
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                                                                                                                                                                                                                                                                                            Jones RR;
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21-SEP-2000; 2000WO-US025827.
                                                                                        (COGN-) COGNETIX INC.
                                                                                                                                           WPI; 2001-648090/74.
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Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conus purpurascens.
Synthetic.
                                                                                                            Cornell-Bell AH,
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   WO200121648-A1.
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Modified-site
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                                                            22-SEP-1999;
                      29-MAR-2001
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                                                                                                                       Jones RR
                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 22
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                                                                                                                                                                                                                                                                                 The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with channel, especially cardiac ischaemia, cerebral ischaemia, octobar ischaemia, octobar ischaemia, octobar ischaemia, octobar ischaemia, pviiA
                                                                                                                                                                                                              depolarization of excitable ischemia and asthma comprises to an individual a kappa-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; K19A.
                  /note= "The C-terminus is either a carboxyl group or an
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                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                               Mccabe RT;
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0
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Pred. No. 4.7e-10;
0; Mismatches 1; Indels
                                                                                                                                                               Temple DL, Layer RT,
                                                                                                                                                                                                              Treating disorders associated with radical membrane e.g. cardiac, cerebral and ocular activating a KATP channel by administering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Snail Kappa-conotoxin PVIIA analogue K19A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRIXNOKCMOHLDDCCSRKCNRFNKCV 27
/note= "Hyroxyproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "Hyroxyproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ź
                                                                                                                                                                                                                                                                Claim 1; Page 28; 46pp; English.
                                                                                                                                                              Pemberton KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU10199 standard; peptide; 27
                                                                                                                                                                                                                                                                                                                                                                                                         96.3%;
                                                                                                            22-SEP-1999; 99US-0155135P.
20-JUL-2000; 2000US-0219438P.
                                                                                         21-SEP-2000; 2000WO-US025827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amide group"
                                amide group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                  analogue of the invention
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 96.3
                                                                                                                                                                                                                                  activating a KATP channe
conotoxin PVIIA peptide
                                                                                                                                           (COGN-) COGNETIX INC
                                                                                                                                                                                           WPI; 2001-648090/74.
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                                                                                                                                                             Cornell-Bell AH,
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 27 AA;
                                                   WO200121648-A1
           Modified-site
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                                                                      29-MAR-2001
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                                                                                                                                                                         Jones RR;
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                                                                                                                                                                                                                                                                                                                                                         Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappaconotoxin PVIIA peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; R18A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "The C-terminus is either a carboxyl group or an
amide group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gape
                                                                                                                                                                                                            Mccabe RT;
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                                                                                                                                                                                                               Layer RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96.3%; Score 155; DB 4;
llarity 96.3%; Pred. No. 4.7e-10;
Conservative 0; Mismatches 1.
                                                                                                                                                                                                            Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Snail Kappa-conotoxin PVIIA analogue R18A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRIXNOKCFQHLDDCCSRACNRFNKCV
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                                                                                                                                                                                                            Pemberton KE,
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21-SEP-2000; 2000WO-US025827
                                                           99US-0155135P
                                                                                       20-JUL-2000; 2000US-0219438P
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                                                                                                                        Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappa-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; K25A.
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                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "The C-terminus is either a carboxyl group or
                                                                         Mccabe RT;
                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                            Score 155; DB 4; Length 27;
Pred. No. 4.7e-10;
0; Mismatches 1; Indels
                                                                        Layer RT,
                                                                      Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Snail Kappa-conotoxin PVIIA analogue K25A.
                                                                                                                                                                                                                                                                                                                                                                                     1 CRIXNOKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                               27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Hyroxyproline"
                                                                                                                                                                                                                                                                                                                                                                                                         CRIXNOKCFOHLDDCCSAKCNRFNKCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                Claim 1; Page 27; 46pp; English.
                                                                  Pemberton KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU10202 standard; peptide; 27
            22-SEP-1999; 99US-0155135P.
20-JUL-2000; 2000US-0219438P.
                                                                                                                                                                                                                                                                                                                                             96.3%;
96.3%;
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20-JUL-2000; 2000US-0219438P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amide group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-SEP-2000; 2000WO-US025827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 96.3
Matches 26; Conservative
                                                                                                                                                              conotoxin PVIIA peptide
                                           (COGN-) COGNETIX INC.
                                                                                                   WPI; 2001-648090/74.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          purpurascens
                                                                 Cornell-Bell AH,
                                                                                                                                                                                                                                                                                                                    Sequence 27 AA;
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                                                                              Jones RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU10202;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 23
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The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention
                                                                                  membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappa-conotoxin PVIIA peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
cerebral ischaemia; ocular ischaemia; asthma; Q6A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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           Mccabe RT;
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                                                                                                                                                                                                                                                                                                                                                                                                                96.3%; Score 155; DB 4; Length 27 llarity 96.3%; Pred. No. 4.7e-10; Conservative 0; Mismatches 1; Indels
         Layer RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Layer RT,
       Temple DL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CRIXNQKCFQHLDDCCSRKCNRFNACV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "Hyroxyproline"
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Cornell-Bell AH, Pemberton KE,
                                                                                                                                                                       Claim 1; Page 27; 46pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU10210 standard; peptide; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amide group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-SEP-2000; 2000WO-US025827.
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20-JUL-2000; 2000US-0219438P.
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                                                 WPI; 2001-648090/74.
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Best Local Similarity
Matches 26; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                 Sequence 27 AA;
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                  Jones RR;
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                                                                                                        The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention
           disorders associated with radical depolarization of excitable e.g. cardiac, cerebral and ocular ischemia and asthma comprises a KATP channel by administering to an individual a kappa-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappaconotoxin PVIIA peptide.
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                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "The C-terminus is either a carboxyl group or
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                                                                                                                                                                                                                                                                              96.3%; Score 155; DB 4; Length 27; 96.3%; Pred. No. 4.7e-10;
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                                                                                                                                                                                                                                                                                                                                     1 CRIXNOKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                      CRIXNAKCFOHLDDCCSRKCNRFNKCV 27
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                                                                               Claim 1; Page 28; 46pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU10197 standard; peptide; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-SEP-2000; 2000WO-US025827.
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20-JUL-2000; 2000US-0219438P
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les 26; Conservative
                                                    conotoxin PVIIA peptide
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Synthetic.
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                                          activating
                           membrane
                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU10197,
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                              The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac isochemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; K7A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappa-
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                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                        1; Indels
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                                                                                                                                                                                                                                       Score 155; DB 4;
Pred. No. 4.7e-10;
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                                                                                                                                                                                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                                                                                        27
                                                                                                                                                                                                                                                                                                        1 CRIXNOKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note= "Hyroxyproline"
                                                                                                                                                                                                                                                                                                                              1 CRIXNQKCFQHLDDCCSRKCNAFNKCV
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Claim 1; Page 27; 46pp; English.
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                                                                                                                                                                                                                                       96.3%;
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20-JUL-2000; 2000US-0219438P.
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                                                                                                                                                                                                                                                                                                                                                                                                                            AAU10204 standard; peptide;
                                                                                                                                                                     analogue of the invention
                                                                                                                                                                                                                                       Query Match
Best Local Similarity 96.3
Matches 26; Conservative
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                                                                                                                                                                                                       Sequence 27 AA;
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kappa-conotoxin PVIIA (kappa-

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a mammal comprises
comprising administering to an individual a kappa-conotoxin PVIIA (kap PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention
                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                Length 27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conus purpurascens kappa-PVIIA analogue peptide, K25A.
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use of a compound binding to kappa-PVIIA-binding site.
                                                                                                                                                                         Score 155; DB 4;
Pred. No. 4.7e-10;
0; Mismatches 1;
                                                                                                                                                                                                                                         1 CRIXNOKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                             27
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                                                                                                                                                                                                                                                                                                                                                           AAE38342 standard; peptide; 27
                                                                                                                                                                  Query Match 96.3%;
Best Local Similarity 96.3%;
Matches 26; Conservative
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(UTAH ) UNIV UTAH RES FOUND.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conus purpurascens.
                                                                                                                                    Sequence 27 AA;
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AAE38342
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sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protection and preservation of an organ e.g. heart of a mammal comprises
use of a compound binding to kappa-PVIIA-binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to kappa-PVIIA-related conotoxins and their use as organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, treatment of arrhythmia, utinary incontinence, reperfusion in for the diabetes, retinopathy, neuropathy, neuropathy, nephropathy, acute heart failure, vasospasa accomparing subarachnoid haemorrhage, anxiety disorder, vasospasa accomparing subarachnoid haemorrhage, anxiety disorder, ischaemia, coronary artery bypass graft (GABG) surgery, ischaemic heart disease, asthma and congestive heart failure. The presensequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
                                                                                                                   Gaps
                                                                                                                 ;
0
                                                                                   Length 27
                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mcintosh JM;
                                                                                                                                                                                                                                                                                                                                 Conus purpurascens kappa-PVIIA analogue peptide, K7A.
                                                                                Score 155; DB 6;
Pred. No. 4.7e-10;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Temple DL,
                                                                                                                                      1 CRIXNOKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                       27
                                                                                                                                                        CRIPNOKCFOHLDDCCSRKCNRFNACV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                          AAE38344 standard; peptide; 27 AA.
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                                                                              96.3%;
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                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                            Conservative
                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conus purpurascens
                                               Sequence 27 AA;
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Modified-site
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a mammal comprises
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to kappa-PVIIA-related conotoxins and their use as
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                                      Gaps
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   DB 6; Length 27; 4.7e-10;
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                                   1; Indels
                                                                                                                                                                                                                                                                              Conus purpurascens kappa-PVIIA analogue peptide, R18A.
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96.3%; Score 155; DB
92.6%; Pred. No. 4.7e
tive 1; Mismatches
                                                                   1 CRIXNOKCFQHLDDCCSRKCNRFNKCV 27
                                                                                  Location/Qualifiers
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                                                                                                                                                                                AAE38336 standard; peptide; 27
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(UTAH ) UNIV UTAH RES FOUND.
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Best Local Similarity 92.00,
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                                   Conservative
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                    Similarity
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Modified-site
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     Query Match
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                    Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to kappa-PVIIA-related conotoxins and their use as organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-
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                                                                                                                                                                                               Conus purpurascens kappa-PVIIA analogue peptide, K19A.
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CRIPNOKCFQHLDDCCSAKCNRFNKCV
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                                                                                               AAE38339 standard; peptide; 27
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(UTAH ) UNIV UTAH RES
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Modified-site
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Matches
                                                                    RESULT 30
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Gaps

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Score 155; DB 6; Length 27; Pred. No. 4.7e-10; 1; Mismatches 1; Indels

96.3%; 92.6%;

Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischeamic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.

Location/Qualifiers

Conus purpurascens

/label= Hyp

Modified-site

WO2003063782-A2

07-AUG-2003.

Conus purpurascens kappa-PVIIA analogue peptide, R22A.

(first entry)

20-NOV-2003

us-10-627-685a-26.rag

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ischaemic heart disease, cerebral ischaemia, anxiety disorder; diabetes, organ protectant, arrhythmia, reperfusion injury; hypertension, angina; retinopathy, coronary artery bypass graft surgery, acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
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                                                                                        Purple cone snail, kappa-PVIIA-related conotoxin, urinary incontinence,
                                                                                                                                                                                                                                                                                                                                        Mcintosh JM;
                                                                    Conus purpurascens kappa-PVIIA analogue peptide, F9M.
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                                                                                                                                                                               Location/Qualifiers
       AAE38345 standard; peptide; 27 AA
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                                                                                                                                                                                                                                                                                                                                       Jones RM,
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) UNIV UTAH RES FOUND.
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                                                                                                                                                          purpurascens
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Modified-site
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                             AAE38345;
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AAE38345
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Mcintosh JM;

Temple DL,

Jones RM,

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(COGN-) COGNETIX INC. (UTAH) UNIV UTAH RES Pemberton-Goodman KE,

28-JAN-2003; 2003WO-US002384. 29-JAN-2002; 2002US-0352219P.

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organ protectants The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The invention also relates to a method of arresting, protecting or preserving somatic cells. The invention is for the protecting or preserving somatic cells. The invention is for the readment of arrhythmia, urinary incontinence, reperfusion injury, peripheral circulation disturbances, hypertension, angina, cerebral vasospasm accompanying subarachnoid haemorrhage, arxiety disorder, cerebral ischaemia, coronary artery bypass graft (CABG) surgery, ischaemic heart disease, asthma and congestive heart failure. The present endiance is Conus purpurascens (purple cone snail) kappa PVIIA analogue.
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AAE38340;
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AAE38340
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Query Match
96.3%; Score 155; DB 6; Length 27;
Best Local Similarity 92.6%; Pred. No. 4.7e-10;
Matches 25; Conservative 1; Mismatches 1; Indels
                                                               1 CRIXNOKCFQHLDDCCSRKCNRFNKCV 27
                                                                               1 CRIPNOKCMOHLDDCCSRKCNRFNKCV 27
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RESULT 32

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XXEX BX SX
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The invention relates to kappa-PVIIA-related conotoxins and their use as organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, nephropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral ovasospasm accompanying subarachnoid haemorrhage, anxiety disorder, ischaemia, coronary artery bypass graft (GABG) surgery, ischaemic heart disease, asthma and congestive heart failure. The present sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
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   cerebral ischaemia; anxiety disorder; diabetes;
                organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive,heart failure; neuropathy; nephropathy; CABG.
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                                                                                                                           Location/Qualifiers
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(UTAH ) UNIV UTAH RES FOUND.
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ischaemic heart disease;
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hes 25, Conservative
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                                                                                           Conus purpurascens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure;
                                                                                                                                                                                                                                                                                                                                                                                                                               organ protectants. The invertion also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, nephropathy, acute heart fallure, peripheral circulation disturbances, hypertension, angina, cerebral vasospasm accompanying subarachnoid haemorrhage, anxiety disorder, escebbal ischaemia, coronary artery bypass graft (CABG) surgery, ischaemic heart disease, asthma and congestive heart failure. The presen sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               snail; kappa-PVIIA-related conotoxin; urinary incontinence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                             Mcintosh JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                        Protection and preservation of an organ e.g. heart of
use of a compound binding to kappa-PVIIA-binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conus purpurascens kappa-PVIIA analogue peptide, Q6A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 155; DB 6;
Pred. No. 4.7e-10;
                                                                                                                                                                                                                                                           Jones RM, Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27
                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                       Disclosure, Page 8; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE38350 standard; peptide; 27 AA.
                                                                                                                                                     28-JAN-2003; 2003WO-US002384.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96.3%;
92.6%;
                                                                                                                                                                                  29-JAN-2002; 2002US-0352219P
                                                           /label= Hyp
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                                                                                                                                                                                                                (COGN-) COGNETIX INC. (UTAH ) UNIV UTAH RES
                                                                                                                                                                                                                                                               Pemberton-Goodman KE,
                                                                                                                                                                                                                                                                                                          WPI; 2003-679464/64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
es 25; Conserv
 Conus purpurascens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conus purpurascens.
                                                                                         WO2003063782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 27 AA;
                                           Modified-site
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                                                                                                                                                                                                                                                                             Olivera BM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide
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The invention relates to kappa-PVIIA-related conotoxins and their use as organ protectants. The invention also relates to a method of arresting, related conotoxins and reconstructing and/or preserving an organ of a mammal using kappa-PVIIA-protecting and/or preserving an organ of a mammal using kappa-PVIIA-protecting or preserving somatic cells. The invention is for the diabetes, retinopathy, neuropathy, incontinence, reperfusion injury, acute heart failure, vasospasm accompanying subarachnoid haemorrhage, anxiety disorder, vasospasm accompanying subarachnoid haemorrhage, anxiety disorder, ischaemia, coronary artery bypass graft (CABG) surgery, sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
                                                                                                                                                                                                                               Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
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cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
cerebral ischaemia; ocular ischaemia; asthma; N24A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note=,"The C-terminus is either a carboxyl group or an
amide group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                    Mcintosh JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 155; DB 6; Length 27; Pred. No. 4.7e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                   Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Snail Kappa-conotoxin PVIIA analogue N24A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CRIXNOKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "Hyroxyproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                     Disclosure, Page 7; 32pp; English.
                                                                                                                                                                 Jones RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU10213 standard; peptide; 27 AA
                                                                 28-JAN-2003; 2003WO-US002384.
                                                                                           29-JAN-2002; 2002US-0352219P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96.3%;
                                                                                                                     (COGN-) COGNETIX INC.
(UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25; Conservative
                                                                                                                                                             Pemberton-Goodman KE,
                                                                                                                                                                                                     WPI; 2003-679464/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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Synthetic.
              WO2003063782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 27 AA;
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                                        07-AUG-2003
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                                                                                                                                                                             Olivera BM;
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Matches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; D14A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "The C-terminus is either a carboxyl group or an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                        Mccabe RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 153; DB 4; Length 27;
Pred. No. 7.7e-10;
0; Mismatches 1; Indels
                                                                                                                       Layer RT,
                                                                                                                     Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Snail Kappa-conotoxin PVIIA analogue D14A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CRIXNQKCFQHLDDCCSRKCNRFAKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "Hyroxyproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CRIXNOKCFQHLDDCCSRKCNRFNKCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                 Pemberton KE,
                                                                                                                                                                                                                                              Claim 1; Page 28; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU10209 standard; peptide; 27
                          21-SEP-2000; 2000WO-US025827.
                                                 22-SEP-1999; 99US-0155135P.
20-JUL-2000; 2000US-0219438P.
                                                                                                                                                                                                                                                                                                                                                                                                                                  95.0%;
96.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amide group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                       (COGN-) COGNETIX INC
                                                                                                                                                      WPI; 2001-648090/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
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                                                                                                                 Cornell-Bell AH,
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 27 AA;
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 29-MAR-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         26;
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                                                                                                                                Jones RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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ID AAU1
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99US-0155135P.

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The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia, and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention
                                                                             Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappa-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; F9A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Treating disorders associated with radical depolarization of excitable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "The C-terminus is either a carboxyl group or
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 153; DB 4;
Pred. No. 7.7e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Snail Kappa-conotoxin PVIIA analogue F9A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CRIXAQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "Hyroxyproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                        Claim 1; Page 28; 46pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27
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20-JUL-2000; 2000US-0219438P.
                                                                                                                                                                                                                                                                                                                                                                                                                                             95.0%;
96.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26; Conservative
                                                                                                                                   conotoxin PVIIA peptide
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                                         WPI; 2001-648090/74.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 27 AA;
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     Jones RR;
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                                                                                                                                                                                                                                                                                                   The invention relates to treating disorders associated with radical comprisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
                                                                                                                                                                    Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappaconotoxin PVIIA peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; NSA.
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                                                                             Mccabe RT;
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                                                                             Layer RT,
                                                                           Temple DL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRIXNOKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRIXNQKCFQHLDACCSRKCNRFNKCV 27
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                                                                           Pemberton KE,
                                                                                                                                                                                                                                                                    Claim 1; Page 28; 46pp; English.
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20-JUL-2000; 2000US-0219438P.
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20-JUL-2000; 2000US-0219438P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-SEP-2000; 2000WO-US025827
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                                     (COGN-) COGNETIX INC
                                                                                                                               WPI; 2001-648090/74.
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Best Local Similarity
Matches 26; Consera
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                                                                     Cornell-Bell AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 27 AA;
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                                                                                           Jones RR;
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RESULT 38 AAU1021

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The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with channel, especially cardiac ischaemia, cerebral ischaemia, ocular analogue of the invention
membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappa-conotoxin PVIIA peptide.
                                                                                                                                                    95.0%; Score ....
96.3%; Pred. No. 7.7e-J
                                                                                                                                                                                                                                                                                                                            Snail Kappa-conotoxin PVIIA analogue D13A.
                                                                                                                                                                                                        1 CRIXNOKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                    1 CRIXNQKCAQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                           Ą.
                                   Claim 1; Page 27; 46pp; English.
                                                                                                                                                                                                                                                                     AAU10215 standard; peptide; 27
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                                                                                                                                                                                    26; Conservative
                                                                                                                                                                             Best Local Similarity
Matches 26; Conserv
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Synthetic.
                                                                                                                                                 Sequence 27 AA;
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                                                                                                                                                                    Query Match
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Length 27;

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Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; D13A.
                                                                                                                                                                                                                                                                           C-terminus is either a carboxyl group or an
                                                                                                                                                                                                                              /note= "Hyroxyproline"
                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                           /note= "The
                                                                                                                                                                                                                                                                                                          amide group"
                                                                                                                                                                                               Modified-site
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21-SEP-2000; 2000WO-US025827 WO200121648-A1 29-MAR-2001

Temple DL, Cornell-Bell AH, Pemberton KE, (COGN-) COGNETIX INC.

22-SEP-1999; 99US-0155135P. 20-JUL-2000; 2000US-0219438P.

Mccabe RT;

Layer RT,

WPI; 2001-648090/.74. Jones RR;

disorders associated with radical depolarization of excitable e.g. cardiac, cerebral and ocular ischemia and asthma comprises ng a KATP channel by administering to an individual a kappaconotoxin PVIIA peptide. activating Treating membrane

Claim 1; Page 28; 46pp; English

The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active

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The invention relates to treating disorders associated minimizering depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention
                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                             Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; N2IA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappaconotoxin PVIIA peptide.
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                                                                                                                                                                         Length 27;
                                                                                                                                                        Layer RT,
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                                                                                                                                                                                                                    1 CRIXNOKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                        1 CRIXNQKCFQHLADCCSRKCNRFNKCV 27
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20-JUL-2000; 2000US-0219438P.
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                                                                                                                                                                                              Conservative
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                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conus purpurascens.
                                                                                                                                         Sequence 27 AA;
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                                                                                                                                                                                          26;
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Best Local (
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Best Local Similarity
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                  Sequence 27 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Olivera BM;
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                                                                                                                                                      RESULT 43
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                                                                                                                                                                                                                                                                                                                                                      ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a mammal comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to kappa-PVIIA-related conotoxins and their use as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, nephropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral vasospasm accompanying subarachnoid haemorrhage, anxiety disorder, cerebral ischaemia, coronary artery bypass graft (CABG) surgery, ischaemic heart disease, asthma and congestive heart failure. The presen sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting,
                                                                                                                                                                                                                                                                                                                                          Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
salt. The conotoxing are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
                                                                                                                              Gaps
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                                                                                                    Score 153; DB 4; Length 27; Pred. No. 7.7e-10;
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                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                    Conus purpurascens kappa-PVIIA analogue peptide, N24A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protection and preservation of an organ e.g. heart of
use of a compound binding to kappa-PVIIA-binding site.
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                                                                                                                             0; Mismatches
                                                                                                                                                     1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                           1 CRIXNOKCFOHLDDCCSRKCARFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 7; 32pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pemberton-Goodman KE, Jones RM,
                                                                                                                                                                                                                                          AAE38353 standard; peptide; 27
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                                                                                                     95.0%;
96.3%;
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(UTAH ) UNIV UTAH RES FOUND
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                                                    analogue of the invention
                                                                                                                             26; Conservative
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                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                    Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2003063782-A2
                                                                              Sequence 27 AA;
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                                                                    Gaps
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   Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mcintosh JM;
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                                                                    Indels
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Score 153; DB 6; Le
Pred. No. 7.7e-10;
1; Mismatches 1;
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Pred. No. 7.7e-10;
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                                                                                                                                                                                                1 CRIPNOKCFOHLDDCCSRKCNRFAKCV 27
                                                                                                                                     1 CRIXNOKCFOHLDDCCSRKCNRFNKCV 27
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92.6%;
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   Query Match
Best Local Similarity 92.6%;
Matches 25; Conservative
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Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure;

Location/Qualifiers

Conus purpurascens.

/label= Hyp

Modified-site

WO2003063782-A2.

07-AUG-2003

28-JAN-2003; 2003WO-US002384. 29-JAN-2002; 2002US-0352219P

Conus purpurascens kappa-PVIIA analogue peptide, D13A.

(first entry)

20-NOV-2003

AAE38355;

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AAE38355 standard; peptide; 27

RESULT 45

AAE38355

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                                                                                                                                                                                                                                                                 ischaemic herrit nappa-rvllA-related conotoxin; urinary incontinence; organ protectant disease; crebral ischaemia; anxiety disorder; diabetes; retinopath; arrhythma; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to kappa-PVIIA-related conotoxins and their use as organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the diabetes, retinopathy, neuropathy, nephropathy, acute heart failure, peripheral circulation disturbance, hypertension, angina, cerebral vassospasa accompanying subarachnoid haemorrhage, anxiety disorder, sectebral ischaemia, coronary artery bypass graft (CABG) surgery, bechaemic heart disease, asthma and congestive heart failure. The present accompanying subarachnoid congestive heart failure. The present schaemic heart disease, asthma and congestive heart failure. The present accompanying superpursacens (purple cone snail) kappa PVIIA analogue
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                                                                                                                                                                                                                                 purpurascens kappa-PVIIA analogue peptide, F9A,
         1;
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Pred. No. 7.7e-10;
1; Mismatches 1;
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      1; Mismatches
                               CRIXNOKCFQHLDDCCSRKCNRFNKCV 27
                                                                 27
                                                    1 CRIPNQKCFQHLDDCCSRKCARFNKCV
                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                     AAE38341 standard; peptide; 27
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UNIV UTAH RES FOUND.
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                                                                                                                                                                                                     (first entry)
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pemberton-Goodman KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-679464/64.
                                                                                                                                                                                                                                                                                                                                                          Conus purpurascens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2003063782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 27 AA;
                                                                                                                                                                                                 20-NOV-2003
 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Olivera BM;
                                                                                                                                                                    AAE38341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (COGN-)
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                            Protection and preservation of an organ \mathbf{e},\mathbf{g}, heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                                                                       Mcintosh JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 153; DB 6; Length 27;
Pred. No. 7.7e-10;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                       Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CRIXNOKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 8; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE38349 standard; peptide; 27 AA.
                                                                                                                                                                                                                                                                                                                                                                      Jones RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95.04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25; Conservative
                                                                                                                                                                                                                                                                                                                              COGNETIX INC.
UNIV UTAH RES
                                                                                                                                                                                                                                                                                                                                                                   Pemberton-Goodman KE,
                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-679464/64.
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                                                                                                                                                                                                                                                                                                                                                                              Olivera BM;
                                                                                                                                                                                                                                                                                                                              (COGN-)
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Matches
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ID AAE3
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1 CRIXNOKCFQHLDDCCSRKCNRFNKCV 27 CRIPNOKCAQHLDDCCSRKCNRFNKCV 27

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Best Local Similarity 92.6 Matches 25, Conservative

Length 27; 1; Indels

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ischaemic heart diseañe; cerebral ischaemia; anxiety disorder; diabetes; organ protectant, arrhythmia; reperfuaion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to kappa-PVIIA-related conotoxins and their use as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organ protectants. The invertion also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, nephropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral ecebral schemmia, coronary artery bypass graft (CARG) surgery, ischaemic heart disease, asthma and congestive heart failure. The presensequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; H11A.
                                          snail; kappa-PVIIA-related conotoxin; urinary incontinence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       snail; kappa-conotoxin PVIIA analogue; circulatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mcintosh JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protection and preservation of an organ e.g. heart of
use of a compound binding to kappa-PVIIA-binding site.
Conus purpurascens kappa-PVIIA analogue peptide, NSA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 153; DB 6;
Pred. No. 7.7e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Snail Kappa-conotoxin PVIIA analogue H11A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CRIXNOKCFOHLDDCCSRKCNRFNKCV
                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 8; 32pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jones RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
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                                                                                                                                                                                                                                                                                                                                                                                                                               29-JAN-2002; 2002US-0352219P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU10208 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COGNETIX INC.
UNIV UTAH RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pemberton-Goodman KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-679464/64.
                                                                                                                                                                     purpurascens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                  WO2003063782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 27 AA;
                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                            07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Olivera BM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Si
Matches 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU10208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COGN-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UTAH )
                                            Purple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Purple
                                                                                                                                                                     Conus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 48
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to kappa-PVIIA-related conotoxins and their use as organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, nephropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral wasospasm accompanying subarachnoid haemorrhage, anxiety disorder, cerebral ischaemia, coronary artery bypass graft (CABG) surgery, ischaemic heart disease, asthma and congestive heart failure. The present sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
                                                                                                                                        Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.0%; Score 153; DB 6; Length 27; 92.6%; Pred. No. 7.7e-10; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mcintosh JM,
                                                                                                  Conus purpurascens kappa-PVIIA analogue peptide, D14A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRIPNOKCFQHLDACCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 7; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jones RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE38359 standard; peptide; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JAN-2002; 2002US-0352219P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-JAN-2003; 2003WO-US002384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (COGN-) COGNETIX INC. (UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                                                                                                              /label= Hyp
                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-NOV-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pemberton-Goodman KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-679464/64.
                                                                                                                                                                                                                                                                         Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                         WO2003063782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                       20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Olivera BM;
                 AAE38349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE38359;
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Gaps

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1; Indels

RESULT 47
AAE38359
ID AAE38:
XX
AC AAE38:
XX
DT 20-NO'
XX

Matches

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Length 27;

present

a mammal comprises

Location/Qualifiers

Key Modified-site

/label= Hyp

WO2003063782-A2

07-AUG-2003

28-JAN-2003; 2003WO-US002384. 29-JAN-2002; 2002US-0352219P (COGN-) COGNETIX INC. (UTAH) UNIV UTAH RES FOUND.

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Purple come snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conus purpurascens kappa-PVIIA analogue peptide, H11A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE38348 standard; peptide; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
          Conus purpurascens.
                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                         WO200121648-A1
                                                                                                                                                                                                                                                                                                                                                                  Sequence 27 AA;
                                        Modified-site
                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-NOV-2003
                                                                                                          29-MAR-2001
                  Synthetic
                                                                                                                                                                                          Jones RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE38348;
                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE38348
XX
AC AAE3
XX
AC AAE3
XX
DT 20-N
XX
XY
XW PULF
XW iscl
XW refi
XW refi
XW cong
XX
XX
XX
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XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                         Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappa-conotoxin PVIIA peptide.
                                                                                                       /note= "The C-terminus is either a carboxyl group or an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                          Mccabe RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93.8%; Score 151; DB 4; Length 27; 96.3%; Pred. No. 1.3e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 i; Indels
                                                                                                                                                                                                                                                                                                                      Temple DL, Layer RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                           'note= "Hyroxyproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CRIXNOKCFQHLDDCCSRKCNRFNKCV
                                                                                                                                                                                                                                                                                                                      Pemberton KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 28; 46pp; English.
                                                                                                                                                                                                            21-SEP-2000; 2000WO-US025827.
                                                                                                                                                                                                                                           22-SEP-1999; 99US-0155135P.
20-JUL-2000; 2000US-0219438P.
                                                                                                                         amide group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26; Conservative
                                                                                                                                                                                                                                                                                      (COGN-) COGNETIX INC.
                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-648090/74.
                                                                                                                                                                                                                                                                                                                 Cornell-Bell AH,
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a mammal comprises

Protection and preservation of an organ e.g. heart of use of a compound binding to kappa-PVIIA-binding site.

Disclosure; Page 7; 32pp; English.

Mcintosh JM;

Jones RM, Temple DL,

Pemberton-Goodman KE,

Olivera BM;

(COGN-) COGNETIX

WPI; 2003-679464/64.

The invention relates to kappa-PVIIA-related conotoxins and their use as

organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-FVIIA. Protecting and/or preserving an organ of a mammal using kappa-FVIIA. Protecting or preserving somatic cells. The invention is for the diabetes, retinopathy, neuropathy, nephropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral cerebral isohaemia, coronary artery bypass graft (CARG) surgery, ischaemic heart disease, asthma and congestive heart failure. The present sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue

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                                                                                                                                                                                                                                                                                                                                                                         neuroprotective; cerebroprotective; cardiovascular; antiinflammatory; antignatule; antidnabetic; tranquiliser; vulnerary; antipsychotic; anxiolytic; neuroleptic; tranquiliser; vulnerary; antipsychotic; neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia; stroke; cerebrovascular accident; brain trauma; spinal chord trauma; stroke; suffocation; perinatal asphyxia; hypoglycaemic event; pain; migraine; inflammation; cardiovascular disorder; psychosis; anxiety; schizophrenia.
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                         Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiant;
                                                                             ..
0
                                    93.8%; Score 151; DB 6; Length 27; 92.6%; Pred. No. 1.3e-09; ive 1; Mismatches 1; Indels
                                                                                                   1 CRIXNOKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                       Omega-conopeptide E6.2 toxin sequence.
                                                                                                                                                                                                                     ABB96846 standard; peptide; 27 AA.
                                                                                                                                                                                                                                                                                        12-JUL-2002. (first entry)
                                               Similarity 92.6
25; Conservative
Sequence 27 AA;
                                Query Match
Best Local Si
Matches 25;
                                                                                                                                                                                                   ABB96846
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WO200207675-A2.

Conus purpurascens

Shon K;

Garrett JE,

Cartier GE;

us-10-627-685a-26.rag

31-JAN-2002

Jacobsen R,

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The invention relates to isolated omega-conopeptides, nucleic acid sequences encoding them, and propeptide sequences. The activity of the peptides of the invention may be described as, analgesic, anticonvulsant, vasotropic, cardiant, neuroprofective, cerebroprotective, cardiovascular, antinflammatory, antimigraine, antidiabetic, tranquiliser, vulnerary, antinflammatory, antimigraine, antidiabetic, tranquiliser, vulnerary, antinflammatory, antimigraine, antidiabetic, tranquiliser, vulnerary, by modulating the activity of voltage gated ion channels. They may be used for treating or preventing disorders, e.g. seizure (associated ion channels such as neurological disorders, e.g. seizure (associated with epilepsy), neurotoxic injury associated with conditions of hypoxia, anoxia, ischaemia, stroke, cerebrovascular accident, brain or spinal chord trauma, drowning, suffecation, perinatal asphyxia or hypoglycaemic events; pain e.g. migraine; inflammation or cardiovascular disorders. They may also be used for treating psychiatric disorders e.g. psychosis, anxiety or schizophrenia. The analgesic agents of the invention show diminished side effects and toxicity, and are non-addictive. The sequences given in records ABB96595-ABB96697 represent omega-conopeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New omega-conopeptides useful for treating disorders associated with voltage gated ion channels e.g. pain, inflammation, neurologic or cardiovascular disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Omega conopeptide; OCT; analgesia; inhibition; voltage-gated; calcium channel; neurone; contraction; guinea pig; ileum; WVIIA; binding site; toxin; marine; snail; Conus; opiod; chronic pain; narcotics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48.8%; Score 78.5; DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.2%; Pred. No. 0.22
ive 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |:::||| | |||::|| | :||
47 CKPKGRKCFPHQKDCCNKTCTR-SKC 71
                                                                                                                                                                                                                                                                                                                                Mcintosh JM, Watkins M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1(c); Page 42; 195pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR39628 standard; peptide; 26 AA.
                                                                                                                                                                       21-JUL-2000; 2000US-0219616P. 05-FEB-2001; 2001US-0265888P.
                                                                                                                    33-JUL-2001; 2001WO-US023041
                                                                                                                                                                                                                                                 UTAH ) UNIV UTAH RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 46.2
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                        Jones RM,
                                                                                                                                                                                                                                                                              COGN-) COGNETIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            propeptide sequences
                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-257318/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ABL98897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 72 AA;
                                                                       31-JAN-2002
                                                                                                                                                                                                                                                                                                                              Olivera BM,
                                                                                                                                                                                                                                                                                                                                                        Jacobsen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-2003
20-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR39628;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNX-202.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR39628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to isolated omega-conopeptides, nucleic acid sequences encoding them, and propeptide sequences. The activity of the peptides of the invention may be described as, analgeaic, anticonvulsant, vasocropic, cardiant, neuroprotective, crebroprotective, cardiovascular, antiinflammatory, antimigraine, antidiabetic, tranquiliser, vulnerary, antipsychotic, anxiolytic and neuroleptic. Peptides of the invention act by modulating the activity of voltage gated ion channels. They may be used for treating or preventing disorders associated with voltage gated ion channels such as neurological disorders, e.g. seizure (associated with epilepsy), neurotoxic injury associated with conditions of hypoxia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anoxia, ischaemia, stroke, cerebrovascular accident, brain or spinal chord trauma, drowning, suffocation, perintatal asphyxia or hypoglycaemic events; pain e.g. migraine; inflammation or cardiovascular disorders. They may also be used for treating psychiatric disorders e.g. psychosis, anxiety or schizophrenia. The analysesic agents of the invention show diminished side effects and tooxicity, and are non-addictive. The sequences given in records ABB96807-ABB96905 represent omega-conopeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiant; neuroprotective; cerebroprotective; cardiovascular; antinflammatory; antipagraine; antidiabelic; tranquilises; vulnerary; antipaychotic; anxiolytic; neuroleptic; voltage gated ion channel; seizure; epilepsy; neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia; stroke; cerebrovascular accident; brain trauma; spinal chord trauma; drowning; sulfocation; perinatal asphyxia; hypoglycaemic event; pain; migraine; inflammation; cardiovascular disorder; psychiatric disorder; psychosis; anxiety; schizophrenia.
                                                                                                                                                                                                                                                                                                                                                                                                New omega-conopeptides useful for treating disorders associated with voltage gated ion channels e.g. pain, inflammation, neurologic or cardiovascular disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48.8%; Score 78.5; DB 5; Length 27; 46.2%; Pred. No. 0.098; ive 6; Mismatches 7; Indels
                                                                                                                                                                                                                                                                              Shon K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Indels
                                                                                                                                                                                                                                                                              Garrett JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M, Watkins M,
Cartier GE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CRIXNQKCFQHLDDCCSRKCNRFNKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1(a); Page 71; 195pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Omega-conopeptide E6.2 propeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB96638 standard; peptide; 72 AA.
                                                                                                                    21-JUL-2000; 2000US-0219616P.
05-FEB-2001; 2001US-0265888P.
                                                                       23-JUL-2001; 2001WO-US023041
                                                                                                                                                                                                 UNIV UTAH RES FOUND.
COGNETIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                              Mcintosh JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 46.2
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                        Jones RM,
                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-257318/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       toxin sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 27 AA;
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                                                                                                                                                                                                 (UTAH ) UNIV
(COGN-) COGNE
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                                                                                                                                                                                                                                                                              Olivera BM,
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Query Match

ò g ABB96638;

RESULT 51 ABB96638

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Gaps

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DB 5; Length 72; 7; Indels

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WO9310145-A1
                                27-MAY-1993.
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Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-OCT-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequences given in AAR39608-30 are omega conopeptides (OCTs) and derivatives of these, which may be used to produce analgesia in a mammal. These OCTs inhibit voltage-gated calcium channels selectively in neuronal tissue. This is shown by the peptides ability to stimulate contraction in neuronal tissue. OCTs are components of peptide toxins derived from marine snails of the genus Comus, and act as calcium channel blockers. These OCTs may be used to replace opiods in the treatment of chronic pain or to reduce the opiod dosage required. This helps to reduce dependence on and tolerance to opiod narcotics. (Updated on 25-MAR-2003 to correct py field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
                                                                                                                                                                                                                                                                Use of omega-cono-peptide(s) which selectively inhibit voltage-gated calcium channels - to induce analgesia, enhance opiate analgesics, treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ischaemia; neuronal; omega-conotoxin; OCT; MVIIA; MVIIC; MVIID; MVIIB; GVIA; GVIIA; RVIA; SVIA; TVIA; SVIB; SNX-207; stroke; delayed treatment; antihistamine; blood pressure; N-type voltage-gated Ca currents;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                   Valentino KL, Miljanich GP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46.6%; Score 75; DB 2; Length 26; 42.3%; Pred. No. 0.23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10; Indels
                                                          /note= "Amidated C-terminal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-channel mediated neurotransmitter release
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CKLKGQSCSRLMYDCCSGSCGRSGKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR37774 standard; peptide; 26 AA.
                                                                                                                                                                                                                   Gohil K,
                                                                                                                                                                                                                                                                                                                 Claim 1; Fig 2; 90pp; English.
                                                                                                                                       92WO-US011349
                                                                                                                                                              91US-00814759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 42.33
Matches 11; Conservative
                                . 26
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(first entry)
            .1. .16
8. .20
                                                                                                                                                                                                                 Singh T,
                                                                                                                                                                                      (NEUR-) NEUREX CORP.
                                                                                                                                                                                                                                         WPI; 1993-227270/28
        Disulfide-bond
                    Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 26 AA;
                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disulfide-bond
Disulfide-bond
Disulfide-bond
                                                                                                                                   30-DEC-1992;
                                                                                                                                                            30-DEC-1991;
                                                                                  WO9313128-A1
                                                                                                          08-JUL-1993.
                                                                                                                                                                                                                Justice A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-2003
08-SEP-1993
                                                                                                                                                                                                                                                                                             pain etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR37774;
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The C-terminal is amidated. Ischaemia-related neuronal damage in mammals is reduced by admin., 4-24 hr after onset of ischaemia, of a cpd. (I) which binds selectively to an omega-conotoxin (OCT) WVIA site in neuronal tissue. (I) has selectivity at least 100 expressed as ratio of binding affinity for the MVIA site to that for the MVIC site. (I) is come of the OCTS MVIA. WVIB. (GVIA) or RVIA or It is the cpd. SNX-C 207. (I) is esp. used to reduce neuronal damage caused by stroke. By within 1 hr of the onset of ischaemia) a greater redn. in neuronal damage of station at 0.1-20 microg/kg, but can also be given iv. (opt. after treatment with antihistandnes to minimise redn. in blood pressure caused by (I)). (I) is also at least as effective as the specified conotoxins control tissue and (2) selective inhibition of N-type voltage-gated ca currents in neuronal tissue and (2) selective inhibition of N-type voltage-gated ca currents in neurorial tissue and (2) selective inhibition of N-type voltage-gated ca currents in currents and tissue and (2) selective inhibition of N-type voltage-gated Ca currents of neurorial tissue and (2) selective inhibition of N-type voltage-gated Ca currents of neurorial tissue. Primary sequences of omegaconopeptides are given in AAR37752-62. Several analog omega-conopeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                 Redn. of neuronal damage caused by ischaemia - by admin. of cpds. that bind specifically to omega-conotoxin MVIIA binding sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                      Bitner RS;
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N-type voltage-sensitive calcium channel; block; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNX-202, omega conopeptide derivative used for pain relief.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 46.6%; Score 75; DB 2; Length 26; l Similarity 42.3%; Pred. No. 0.23; l1; Conservative 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                  Fox JA, Valentino KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CRIXNOKCFOHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 2; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW19570 standard; peptide; 26 AA.
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   92WO-US009766
                                                                         91US-00789913
92US-00916478
                                                                                                                                                                                                                                                           Bowersox SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                               WPI; 1993-182487/22.
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Matches 11; Conserva
                                                                                                                                                                             (NEUR-) NEUREX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 26 AA;
                                                                                                                                                                                                                                                   Miljanich GP,
Yamashiro DH;
12-NOV-1992;
                                                                     12-NOV-1991;
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Singh T;

Justice A,

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Valentino KL,
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93US-00049794.
96US-00675354.
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                                                                                                                                                                                                                                  46.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                  (revised)
(first entry)
 Miljanich GP,
                                                                                                                                                                                                                                                            11; Conservative
                                                  Omega cono:peptide(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-582596/49.
                         WPI; 1997-064830/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORP
                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                              neuropathic pain
                                                                                                                                                                                                         Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NEUR-) NEUREX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-DEC-1991;
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06-JAN-1999
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                                                                                                                                                                                PF field.)
Gohil KC,
                                                                                                                                                                                                                                                                                                                                                                                                         AAW72625;
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Matches
                                                                                                                                                                                                                                                                                                                                                      RESULT 56
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                                                                                                                                                                                                                              AAW19555-W19572 are omega conopeptides (OCB) derived from natural peptides from Conus sp. (cone snails). The peptides and their analogues are used as analgesics acting by blocking N-type voltage-esnsitive calcium channels. The OCB can be used to treat neuropathic pain as a result of e.g. insult to the spinal cord or peripheral nerves, cancer, bone degenerative diseases, AIDS, reflex sympathetic dystrophy, herpess coster neuropathy, diabetic neuropathy, hyperesthesia, allodynia or hyperalgesia. The OCB are preferably administered in a medicament via an epidural route in a continuous infusion or sustained release formulation. The OCB can provide pain relief when administered epidurally in the absence of a permeation enhancer, at doses that are comparable to effective analgesic doses using intrathecal administration. OC cormulations comprising an OC and a carboxylic acid buffer anti-oxidant. They also confer stability to solutions containing them for prolonged treatment methods and long-term storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                  Stable omega conopeptide compositions - for producing analgesia and for inhibiting progression of neuropathic pain disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      conopeptide; analgesic; treatment; neuropathic pain; inhibition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                    Kristipati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neuronal damage; schizophrenia; tardive dyskinesia; analgesia;
acute dystonic reactions; inflammation; epilepsy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 46.6%; Score 75; DB 2; Length 26; Local Similarity 42.3%; Pred. No. 0.23; les 11; Conservative 5; Mismatches 10; Indels
                                                                                                  , Gohil K, Adriaenssens PI,
Luther RR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CKLKGQSCSRLMYDCCSGSCGRSGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CRIXNOKCFQHLDDCCSRKCNRFNKC
                                                                                                                                                                                                         Disclosure; Fig 4; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW12985 standard; peptide; 26
            96WO-US011041.
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                                    95US-00496847
96US-00613400
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                                                                                                    Bowersox SS,
Pettus MR, Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Omega conopeptide SNX-202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (revised)
                                                                          (NEUR-) NEUREX CORP.
                                                                                                                                        WPI; 1997-100012/09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 26 AA;
                                     27-JUN-1995;
                                                  08-MAR-1996;
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                                                                                                  Amstutz GA,
Gadbois T,
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22-APR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Omega
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Conus genus, marine snail; cone snail; omega-conopeptide; analgesia; nociceptive pain; neuropathic pain; neuronal tissue; conocoxin; inflammation; schizophrenia; tardive dyskinesia; acute dystonic reaction; rheumatoid arthritis; epilepsy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treatment of inflammation, comprises administration of omega-conopeptide - effective to block voltage-gared calcium channels, bind with high affinity to omega-conopeptide binding site, and inhibit neuro-transmitter
                                                                                                                                                                                                                                     especially for treating neuropathic pain. The peptide, which can be prepared by solid phase synthesis, can also be used to inhibit neuronal damage and treat schizophrenia, tardive dyskinesia, acute dystonic reactions, inflammation and epilepsy. (Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gapa
                                                                                                                                                                                               The present peptide is an omega conopeptide, useful as an analgesic,
- useful as analgesics, esp. for treating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Length 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conus genus analogue omega-conopeptide SNX-202.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 75;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gohil KC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CKLKGÓSCSRLMYDCCSGSCGRSGKC 26
                                                                                                                Disclosure; Col 51-52; 58pp; English
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inflammation and associated pain. The treatment can also be used to produce analgesia (especially in subjects experiencing neuropathic pain); and to treat schizophrenia, tardive dyskinesia and acute dystonic reactions, rheumatoid arthritis, and epilepsy. The present sequence represents an analogue omega-conopeptide. Omega-conopeptides are components of peptide toxins produced by marine snails of the genus to correct OS field.)
                                                                                                                             0;
                                                                                                                             Gaps
                                                                                                                                                                                                                                                                         Omega-conopeptide; peptide toxin; snail; calcium channel blocker; analgesia; guinea pig ileum; omega-conotoxin; pain; neuropathic.
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                                                                                                       DB 2; Length 26;
                                                                                                                         10; Indels
                                                                                                     Score 75; DB 2;
Pred. Nc. 0.23;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                 /note= "C-terminal amide"
                                                                                                                                      1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                         Analog omega-conopeptide SNX-202.
                                                                                                                                                                                                    AAW95584 standard; protein; 26
                                                                                                     46.6%;
                                                                                                                                                                                                                                        (first entry)
                                                                                                                     11; Conservative
                                                                                                            Best Local Similarity
                                                                                   Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                      29-MAR-1999
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                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                    Query Match
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                                                                                                                    Matches
                                                                                                                                                                                  RESULT 57
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Justice A, Valentino KL, Gohil KC, WPI; 1999-120002/10 Miljanich GP,

(NEUR-) NEUREX CORP

30-DEC-1991; 15-APR-1993;

96US-00675354 91US-00814759 93US-00049794 Production of analgesia in mammal - by administration of omega conopeptide(s)

Disclosure; Fig 2A-B; 59pp; English.

Sequences AAM95574-589 represent sequences of analog omega-conopeptides. Omega-conopeptides are components of peptide toxins produced by marine snails of the genus Conus, and which act as calcium channel blockers. The invention relates to a method of producing analgesia in a mammal that comprises administering an omega conopeptide having activities in (a) inhibiting electivally stimulated contraction of guinea pig ileum and (b) selectively binding to omega conopeptide WNIAA binding sites in neuronal tissue, where these activities are within the ranges of those of omega-conocoxing MVIAA and TVIA. The method is used for treating chronic pain, especially neuropathic pain

Sequence 26 AA;

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                              Gaps
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     DB 2; Length 26;
                             10; Indels
 46.6%; Score 75; DB
42.3%; Pred. No. 0.23
tive 5; Mismatches
                                             1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                           1 CKLKGQSCSRLMYDCCSGSCGRSGKC
                        Conservative
             Similarity
Query Match
Best Local Simi
Matches 11;
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AAY56496 standard; peptide; AAY56496;

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(first entry) 16-FEB-2000

Analogue omega conopeptide SNX-202.

Omega conopeptide, analgesic, nociceptive, neuropathic, pain, conotoxin, marine snail, peptide toxin, inflammation, binding, voltage-gated calcium channel, inhibition, norepinephrine, noradrenaline, anti-inflammatory.

Conus sp.

Location/Qualifiers /note= "amidated" 1. .16 8. .20 Disulfide-bond Disulfide-bond Disulfide-bond Modified-site US5994305-A. 30-NOV-1999

98US-00138439. 21-AUG-1998;

91US-00814759. 93US-00049794. 96US-00675354. 96US-00742774. 30-DEC-1991; 01-NOV-1996; .5-APR-1993; 03-JUL-1996

(ELAN-) ELAN PHARM INC

Gohil KC; Miljanich GP, Valentino KL, Justice A, Singh T, WPI; 2000-038270/03 Measuring the activity of test compounds in blocking voltage-gated calcium channels, binding to the omega conopeptide binding site and inhibiting norephrene (noradrenaline) release for treating inflammation,

Disclosure, Fig 2, 47pp, English.

A method has been developed of selecting a test compound for treating inflammation. The method comprises measuring the activity of the test compound in blocking voltage-gated calcium channels, binding to the omega compound in blocking voltage-gated calcium channels, binding to the omega compopetide binding site and inhibiting norepinephrine (noradrenaline) for treating inflammation. The method is useful for selecting compounds for treating inflammation. The selected compounds are capable of producing analgesia a mammalian subject with chronic or intractable pain. Analgesia caused by selected compounds may reduce the reliance on opioid analgesic agents of the prior art which cause dependency and tolerance, requiring potentially dangerous increases in opioid doses to achieve the analgesic effect. The present sequence represents an omega conopeptide given in the present invention AAY56496

AAY56496

AAY56496

AAY5

Sequence 26 AA;

DB 3; Length 26; 46.6%; Score 75;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is an omega-conopeptide analogue. Omega-conopeptides are components of peptide toxins produced marine snails of the genus conus. Omega-conopeptides and their derivatives act as calcium channel blockers and may be useful for producing analgesia in nociceptive and neuropathic pain. The peptides bind to omega-conopeptide binding sites, which are present mainly in neuronal tissue, and inhibit norepinephrine release from nervous tissue. Conopeptides such as WVIAA are effective as therapeutic agents for treating neurogenic conditions such as echizophrenia, tardive dyskinesia and acute dystonic reactions,
                                                                                                                                                                                                                                                        Marine snail; omega-conopeptide; calcium channel blocker; SNX-202; toxin; antidinflammatory; anticonvulsant; neuroleptic; norepinephrine release inhibitor; schizophrenia; tardive dyskinesia; acute dystonic reaction; inflammation; epilepsy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Selecting a compound for producing analgesia involves measuring activity of test compound in blocking voltage-gated calcium channels, binding to omega conopeptide binding site and inhibiting norepinephrine release.
                 Gaps
                ö
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                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Valentino KL, Miljanich GP,
                10;
Pred. No. 0.23
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "C-terminal amide"
                                          26
                                                            1 CKLKGQSCSRLMYDCCSGSCGRSGKC
                                          1 CRIXNQKCFQHLDDCCSRKCNRFNKC
                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure, Fig 2; 58pp; English
                                                                                                                                            AAB14370 standard; peptide; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91US-00814759.
93US-00049794.
96US-00675354.
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 42.3%;
                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                             Omega-conopeptide SNX-202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inflammation and epilepsy
              11; Conservative
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 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                       Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                     Disulfide-bond
Disulfide-bond
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                                                                                                                                                                                                  06-DEC-2000
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03-JUL-1996;
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                                                                                                                                                                                                                                                                                                                                Conus sp.
Synthetic.
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Best Loc
Matches
                                                                                                             RESULT 55
AAB14370
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Gaps

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10; Indels

DB 3; Length 26;

Query Match 46.6%; Score 75; DB 3; Best Local Similarity 42.3%; Pred. No. 0.23; Matches 11; Conservative 5; Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents an omega-conopeptide analogue. Omega-conopeptides are components of peptide toxins which act as voltage-gated calcium channel inhibitors. The peptides are used to enhance the analgesic effect produced by an opiate in a mammalian subject. The method comprises administering to the subject an omega-conopeptide which is able to inhibit electrically stimulated contraction of the guinea pig ileum and bind to omega-conopeptide Mulla binding sites present in neuronal tissue. Omega-conopeptides are useful for enhancing the analgesic effect produced by an opiate. Omega-conopeptides may also be used in the
                                                                                                                                                                                                                           Omega-conopeptide; voltage-gated calcium channel inhibitor; analgesic; peptide toxin; opiate; pain; neurónal damage; ischemic condition; schizophrenia; tardive dyskinesia; acute dystonic reaction; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enhancing analgesia produced by opiates by administering an omega-
conopeptide that inhibits electrically stimulated contraction of guinea
pig ilium and binds to omega-conopeptide MVIIA binding sites in neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treatment of pain, in reducing neuronal damage related to an ischemic condition in mammals, and in treating schizophrenia, tardive dyskinesia and acute dystonic reactions, inflammation and epilepsy
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                                                                                                                                                                                                Sequence of an omega-conopeptide analogue designated SNX-202.
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42.3%; Pred. No. 0.23;
ive 5; Mismatches 10; Indels
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                                                                                                                                                                                                                                                                                                                                                                                  /note= "amidated residue"
56
                 Disclosure; Col 51-52; 58pp; English.
CRIXNOKCFQHLDDCCSRKCNRFNKC
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                                                                                                         AAB19462 standard; peptide; 26
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93US-00081863.
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98US-00138439
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Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                       Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-AUG-1998
                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                            epilepsy.
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                                                                          RESULT 60
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Omega-conopeptide, analgesic, anticonvulsant; vasotropic; cardiant; neuroprotective; cerebroprotective; cardiovascular; antiinflammatory; antidipatein; antidiabetic; tranquiliser; vulnerary; antipsychotic; anxiolytic; neuroleptic; voltage gated ion channel; seizure; epilepsy; setroke; cerebrovascular accident; brain trauma; spinal chord trauma; stroke; cerebrovascular accident; brain trauma; spinal chord trauma; drowning; suffocation; perinatel asphyxia; hypoglycaemic event; pain; psychosis; anxiety; schizophrenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            omega-conopeptides useful for treating disorders associated age gated ion channels e.g. pain, inflammation, neurologic c
                                                                                                                                                                                                                                                                                                                                                                                                                              Shon K;
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   5,6
                      93
                                                                                                                                       Omega-conopeptide S6.2 toxin seguence.
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Cartier GE;
 CRIXNQKCFQHLDDCCSRKCNRFNKC
            Claim 1(a); Page 72; 195pp; English.
                                                                      ABB96887 standard; peptide; 26 AA.
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05-FEB-2001; 2001US-0265888P.
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                                                                                                                 12-JUL-2002 (first entry)
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Jones RM, Ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      voltage gated ion channel cardiovascular disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Jacobsen R,
                                                                                              ABB96887;
                                                    RESULT
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                  요
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The invention relates to isolated omega-conopeptides, nucleic acid sequences encoding them, and propeptide sequences. The activity of the peptides of the invention may be described as, analgesic, anticonvulsant, vasotropic, cardiant, neuroprotective, cerebroprotective, cardiovascular, antipsychotic, anxialytic and neuroleptic. Peptides of the invention act antipsychotic, anxialytic and neuroleptic. Peptides of the invention act by modulating the activity of voltage gated ion channels. They may be used for treating or preventing disorders, e.g. seizure (associated with epilepsy), neurotoxic injury associated with conditions of hypoxia, anoxia, ischaemia, stroke, cerebrovascular accident, brain or spinal chord trauma, drowning, suffocation, perinatal asphyxia or hypoglycaelic events; pain e.g. migraine; inflammation or cardiovascular disorders.

They may also be used for treating psychiatric disorders e.g. psychosis, anxiety or schizophrenia. The analgesic agents of the invention show sequences given in records ABB96807-ABB96805 represent omega-conopeptide

Sequence 26 AA;

Length 26; 46.0%; Score 74; DB 5;

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ô
           Gaps
           ;
0
           Indels
           10;
  Pred. No. 0.29;
5; Mismatches
                      1 CRIXNOKCFOHLDDCCSRKCNRFNKC 26
                                42.3%;
       Conservative
Similarity
         11;
Best Local S
Matches 11
                                   g
                      à
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RESULT 62 ABB9667

Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiant; neuroprotective; cerebroprotective; cardiovascular; antiinflammatory; antipiraine; antidiabetic; tranquilises; vulnerary; antipsychotic; anxiolytic; outlage gated ion channel; seizure; epilepsy; etroke; neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia; stroke; cerebrovascular accident; brain trauma; spinal chord trauma; drowning; suffocation; perinatal asphyxia; hypoglycaemic event; pain; migraine; inflammation; cardiovascular disorder; psychiatric disorder; psychosis; anxiety; schizophrenia. ABB96679 standard; peptide; 30 AA. Omega-conopeptide S6.2 propeptide. 12-JUL-2002 (first entry) ABB96679;

Conus striatus. WO200207675-A2

31-JAN-2002.

23-JUL-2001; 2001WO-US023041.

21-JUL-2000; 2000US-0219616P. 05-FEB-2001; 2001US-0265888P.

(UTAH) UNIV UTAH RES FOUND. (COGN-) COGNETIX INC

Shon K; Garrett JE, M, Watkins M, Cartier GE; Mcintosh JM, Jones RM, Olivera BM, Jacobsen R,

WPI; 2002-257318/30. N-PSDB; ABL98938. New omega-conopeptides useful for treating disorders associated with voltege gated ion channels e.g. pain, inflammation, neurologic or cardiovascular disorders.

Claim 1(c); Page 62; 195pp; English.

The invention relates to isolated omega-conopeptides, nucleic acid sequences encoding them, and propeptide sequences. The activity of the peptides of the invention may be described as, analgesic, anticonvulsant, vasotropic, cardiant, neuroprotective, cerebroprotective, cardiovascular, antiniflammatory, antimigraine, antidiabelic, tranquiliser, vulnerary, antiniflammatory, antimigraine, entidate of the invention act by modulating the activity of voltage gated ion channels rape may be ion channels such as neurological disorders, e.g. seizure (associated with epilepsy), neurotoxic injury associated with conditions of hypoxia, anoxia, ischaemia, stroke, cerebrovascular accident, brain or spinal chort reauma, drowning, suffocation, perinatal asphyxia or hypoglycaemic vents; pain e.g. migraine; inflammation or cardiovascular disorders.

They may also be used for treating psychiatric disorders e.g. psychosis, diminished side effects and toxicity, and are non-addictive. The sequences given in records ABB96695-ABB96697 represent omega-conopeptide propeptide sequences

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given in records ABB96595-ABB96697 represent omega-conopeptide
              propeptide sequences
                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
  sednences
                                                                                                                                                                                                                                                                                                                                                                                      narcotics.
                                                                                                                                                                                                                                              AAR39615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pain etc.
                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                 Best Loca
Matches
                                                                                                                                                                                          64
                                                                                                                                                                                        RESULT
                                                                                                                                                                                                       AAR3961
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ន្តដ្ត
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                                                                                                                                                                                                                     The invention relates to isolated omega-conopeptides, nucleic acid sequences encoding them, and propeptide sequences. The activity of the sequences encoding them, and propeptide sequences. The activity of the peptides of the invention may be described as, analogesic, anticonvulsant, vasocropic, cardiant, neuroprotective, creebroprotective, cardiovascular, antinspectoric, anxiolytic and neuroleptic. Peptides of the invention act by modulating the activity of voltage gated ion channels. They may be used for treating or preventing disorders associated with voltage gated ion channels such as neurological disorders, e.g. seizure (associated ion channels such as neurological disorders, e.g. seizure (associated ion channels such as neurological disorders, e.g. seizure (associated ion channels such as neurological disorders, e.g. seizure (associated ion channels pain e.g. migraine, inflammation or cardiovascular disorders. They may also be used for treating psychiatric disorders e.g. psychosis, anxiety or schizophrenia. The analgesic agents of the invention show anxiety or schizophrenia. The analgesic agents of the invention show diminished side effects and toxicity, and are non-addictive. The
                                                      ö
                                                                                                                                                                                                                                                                                  Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiant; neuroprotective; cerebroprotective; cardiovascular; antichlammatory; antimigraine; antidiabetic; tranquiliser; vulnerary; antipsychotic; anxiolytic; neuroleptic; voltage gated ion channel; seizure; epilepsy; neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia; stroke; cerebrovascular accident; brain trauma; spinal chord trauma; drowning; suffocation; perinatal asphyxia; hypoglycaemic event; pain; migraine; inflammation; cardiovascular disorder; psychiatric disorder;
                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  omega-conopeptides useful for treating disorders associated with
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shon K;
                         46.0%; Score 74; DB 5; Length 30; 42.3%; Pred. No. 0.33;
                                                      10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Garrett JE,
                                                    5; Mismatches
                                                                                               1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26

 Watkins M,
Cartier GE;

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1(c); Page 55; 195pp; English
                                                                                                                                                                                                                                                                                                                                                                                                 psychosis; anxiety; schizophrenia.
                                                                                                                                                                                                                                                             Omega-conopeptide P6.1 propeptide.
                                                                                                                                                                          ABB96666 standard; peptide; 72 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-JUL-2001; 2001WO-US023041.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-2000; 2000US-0219616P. 05-FEB-2001; 2001US-0265888P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UTAH ) UNIV UTAH RES FOUND.
(COGN-) COGNETIX INC.
                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Olivera BM, Mcintosh JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cardiovascular disorders.
                                                      11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jones RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-257318/30.
                                                                                                                                                                                                                                                                                                                                                                                                                             Conus purpurascens.
                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; ABL98925
Sequence 30 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200207675-A2
                                                                                                                                                                                                                                  12-JUL-2002
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                                                                                                                                                                                                       ABB96666;
                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    voltage
                                                      Matches
                                                                                                                                                 RESULT 63
                                                                                                                                                               ABB96666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Use of omega-cono-peptide(s) which selectively inhibit voltage-gated calcium channels - to induce analgesia, enhance opiate analgesics, treat
                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Omega conopeptide; OCT; analgesia; inhibition; voltage-gated; calcium channel; neurone; contraction; guinea pig; ileum; MVIIA; binding site; toxin; marine; snail; Conus; opiod; chronic pain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Valentino KL, Miljanich GP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 71; DB 2; Length 26; Pred. No. 0.62;
                                               Length 72;
                                                                                                       7; Indels
                                                  DB 5;
                                                                              0.86;
                                                                                                       3; Mismatches
                                                  45.3%; Score 73; 50.0%; Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                 AAR39615 standard; peptide; 26 AA.
                                                                                                                                                            1 CRIXNQKCFQHLDDCCSRKC 20
                                                                                                                                                                                          47 CKTPGRKCFPHQKDCCGRAC 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gohil K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Fig 1; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92WO-US011349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91US-00814759.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        (revised)
(first entry)
                                                                                                       10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (NEUR-) NEUREX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1993-227270/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                           Local Similarity
Sequence 72 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ą
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Disulfide-bond
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Disulfide-bond
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20-DEC-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVIB/SNX183
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Ischaemia-related neuronal damage in mammals is reduced by admin., 4-24

The after onset of ischaemia, of a cpd. (I) which binds selectively to an enega-conotoxin (OCT) MVIA site in neuronal tissue. (I) has selectivity at least 100 expressed as ratio of binding affinity for the MVIA site to the CCTS MVIA, MVIB, GVIB, GVIB, GV
                ö
                                                                                                                                                                                                                                                                                                                                                                                                        Ischaemia; neuronal; omega-conotoxin; OCT; MVIIA; MVIIC; MVIID; MVIIB; GVIA; GVIIA; RVIA; SVIA; TVIA; SVIE; SXX-207; stroke; delayed treatment; antihistamine; blood pressure; N-type voltage-gated Ca currents; N-channel mediated neurotransmitter release.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Redn. of neuronal damage caused by ischaemia - by admin. of cpds. that bind specifically to omega-conotoxin MVIIA binding sites.
              Gaps
              ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bitner RS;
         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Valentino KL,
           11;
       4; Mismatches
                                        CRIXNOKCFOHLDDCCSRKCNRFNKC 26
                                                                                      1 CKLKGOSCRKTSYDCCSGSCGRSGKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fox JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                 AAR37760 standard; peptide; 26 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure, Fig 1, 103pp; English.
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92US-00916478.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bowersox SS,
                                                                                                                                                                                                                                                                                               (revised)
(first entry)
11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1993-182487/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disulfide-bond
Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NEUR-) NEUREX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Miljanich GP,
Yamashiro DH;
                                                                                                                                                                                                                                                                                                                                                               SVIB/SNX-183
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17-JUL-1992;
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08-SEP-1993
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                                                                                                                                                                                                                                               AAR37760;
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Matches
                                                                                                                                                           RESULT 65
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AAM19544-W19553 are naturally occurring omega conopeptides (OCS) isolated from Conus sp. (cone snails). The peptides and their analogues are used as analogueis acting by blocking N-type voltage-sensitive calcium channels. The OCS can be used to treat neuropathic pain as a result of e.g. insult to the spinal cord or peripheral nerves, cancer, bone europathy, diabetic neuropathy sympathetic dystrophy, herpes zoster neuropathy, diabetic neuropathy administered in a medicament via an hyperalgesia. The OCS are preferably administered in a medicament via an hyperalgesia. The OCS are preferably administered from a medicament via an provide pain relief when administered epidurally in the absence of a permeation enhancer, at doses that are comparable to fetcitive analgesic doses using intrathecal administration. OC formulations comprising an OC and a carboxylic acid buffer anti-oxidant. They also confer stability to solutions containing them for prolonged creater and effective fails and long-term storage. (Updated on 27-AUG-2003 to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stable omega conopeptide compositions - for producing analgesia and inhibiting progression of neuropathic pain disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kristipati
                         ..
0
                                                                                                                                                                                                                                                                                          Conopeptide, cone snail; pain; analgesic; neuropathy; epidural;
N-type voltage-sensitive calcium channel; block; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                           Natural omega-conopeptide SVIB/SNX-183 used for pain relief.
                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11arity 42.3%; Pred. No. 0.62;
Conservative 4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adriaenssens PI,
                      11;
    Pred. No. 0.62;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                   /note= "optionally amidated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 2, Fig 3; 47pp; English.
                                           1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                CKLKGQSCRKTSYDCCSGSCGRSGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3, Gohil K,
Luther RR;
                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                   AAW19551 standard; peptide; 26 AA.
42.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95US-00496847.
96US-00613400.
                                                                                                                                                                                                                  (revised)
(first entry)
                 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bowersox SS,
Pettus MR, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (NEUR-) NEUREX CORP.
Best Local Similarity
Matches 11: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-100012/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                               WO9701351-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-JUN-1996;
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08-MAR-1996;
                                                                                                                                                                                                               27-AUG-2003
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Gadbois T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11;
                                                                                                                                                                                AAW19551;
                                                                                                                                                                                                                                                                                                                                       Conus.
                                                                                                                      RESULT 66
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44.18;

Query Match

26 AA;

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rheumatoid arthritis; epilepsy.
                                                                                       91US-00814759.
93US-00049794.
96US-00675354.
                                                                        96US-00742774.
                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Local 11; Conserve
                                                                                                                          CORP.
                                                                                                                                                            WPI; 1998-582596/49.
                                                                                                                                                                                                                                                                                                                                                                   Sequence 26 AA;
                                                                                                                          (NEUR-) NEUREX
                                                                                                                                            Miljanich GP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
Modified-site
                                                                       01-NOV-1996;
                                                                                                15-APR-1993;
03-JUL-1996;
                                                                                         30-DEC-1991;
                                     US5824645-A
                                                       20-0CT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW95571;
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                                                                                                                                                                                                         release
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conus genus, marine snail; cone snail; omega-conopeptide; analgesia; nociceptive pain; neuropathic pain; neuronal tissue; conotoxin; inflammation; schizophrenia; tardive dyskinesia; acute dystonic reaction;
                                                                                                                                                                                                                                                                                                                                                                The present peptide is an omega conopeptide, useful as an analgesic, especially for treating neuropathic pain. The peptide, which can be prepared by solid phase synthesis, can also be used to inhibit neuronal damage and treat schizophrenia, tardive dyskinesia, acute dystonic reactions, inflammation and epilepsy. (Updated on 25-MAR-2003 to correct
                                                                                                                                 pain; inhibition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                        cono:peptide(s) - useful as analgesics, esp. for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                 Omega conopeptide, analgesic, treatment, neuropathic pain, inh neuronal damage, schizophrenia, tardive dyskinesia, analgesia, acute dystonic reactions, inflammation, epilepsy.
                                                                                                                                                                                                                                                                                       Singh
                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Indels
                                                                                                                                                                                                                                                                                      Justice A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conus genus natural omega-conopeptide SVIB/SNX-183,
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 71; DB 2,
Pred. No. 0.62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Mismatches
                                                                                                                                                                                                                                                                                     Valentino KL,
56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Col 45-46; 58pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CRIXNOKCFOHLDDCCSRKCNRFNKC
                                                     AAW12974 standard; peptide; 26 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW72612 standard; peptide; 26 AA.
                                                                                                                                                                                                                                          91US-00814759:
                                                                                                                                                                                                                                                                                                                                                                                                                                                44.18;
42.38;
                                                                                                                                                                                                                        93US-00049794
                                                                                                                                                                                                                                                  92WO-US011349
                                                                                        (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (revised)
(first entry)
                                                                                                                 Omega conopeptide SNX-183
                                                                                                                                                                                                                                                                                     Miljanich GP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 42.3
es 11; Conservative
                                                                                                                                                                                                                                                                   (NEUR-) NEUREX CORP
                                                                                                                                                                                                                                                                                                      WPI; 1997-064830/06
                                                                                                                                                                                                                                                                                                                               neuropathic pain.
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 26 AA;
                                                                                                                                                                                                                        15-APR-1993;
                                                                                                                                                                                                                                         30-DEC-1991;
                                                                                                                                                                                                                                                   30-DEC-1992;
                                                                                       25-MAR-2003
22-APR-1997
                                                                                                                                                                                      US5587454-A.
                                                                                                                                                                                                        24-DEC-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-AUG-2003
06-JAN-1999
                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                     Gohil KC,
                                                                                                                                                                                                                                                                                                                                                                                                               field.)
                                                                      AAW12974;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW72612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                        Omega
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68
                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW7261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
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subject. The method comprises administration of an omega-conopeptide effective to: (1) block voltage-gated calcium channels; (11) bind with high affinity to an omega-conopeptide binding site, and (11) inhibit neurotransmitter release from nervous tissue. The method is used to treat inflammation and associated pain. The treatment can also be used to produce analgesia (especially in subjects experiencing neuropathic pain); and to treat schizophrenia, tardive dyskinesia and acute dystonic reactions, rheumatoid arthritis, and epilepsy. The present sequence represents a natural omega-conopeptide. Omega-conopeptides are components of peptide toxins produced by marine snails of the genus Conus, and which act as calcium channel blockers. (Updated on 27-AUG-2003 to correct OS
                                                                                                                                   Treatment of inflammation, comprises administration of omega-conopeptide - effective to block voltage-gated calcium channels, bind with high affinity to omega-conopeptide binding site, and inhibit neuro-transmitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                     A method has been developed for the treatment of inflammation in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Omega-conopeptide, peptide toxin; snail; calcium channel blocker; analgesia; guinea pig ileum; omega-conotoxin; pain; neuropathic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
Singh T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 71; DB 2; Length 26;
Pred. No. 0.62;
4; Mismatches 11; Indels
Justice A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "C-terminal amide"
Gohil KC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CKLKGÓSCRKTSYDCCSGSCGRSGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CRIXNOKCFQHLDDCCSRKCNRFNKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 1; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Omega-conopeptide SVIB/SNX-183.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW95571 standard; protein; 26
Valentino KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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Measuring the activity of test compounds in blocking voltage-gated calcium channels, binding to the omega conopeptide binding site and inhibiting norepinephrine (noradrenaline) release for treating
                                                                                         Disclosure, Fig 1; 47pp; English.
                                                                                                                                                                                                                                                                                                              11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .20
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              WPI; 2000-038270/03
                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                  Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disulfide-bond
Disulfide-bond
Disulfide-bond
Modified-site
                                                                    inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-APR-1999;
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03-JUL-1996;
01-NOV-1996;
21-AUG-1998;
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                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB14359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conus
                                                                                                                                                                                                                                                                                                                                                                                           RESULT 71
                                                                                                                                                                                                                                                                                                                                                                                                        AAB14359
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                                                                                                                                                                                                               Sequences AAM95564-573 represent primary sequences of natural omegaconopeptides. Omega-conopeptides are components of peptide toxins produced by marine snalls of the genus Conus, and which act as calcium analgesia in amemmal that comprises administering an omega conopeptide dyinea pig ileum and (b) selectively binding to omega conopeptide of guinea pig ileum and (b) selectively binding to omega conopeptide WVIIA binding sites in neuronal tissue, where these activities are within used for treating chronic pain, especially neuropathic pain used for treating chronic pain, especially neuropathic pain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Omega conopeptide, analgesic, nociceptive, neuropathic, pain, conotoxin, marine snail, peptide toxin, inflammation, binding, voltage-gated calcium channel, inhibition, norepinephrine, noradrenaline,
                                                                                                                                                         Production of analgesia in mammal - by administration of omega cono-
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   o,
                                                                                                                      Singh T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gohil KC;
                                                                                                                                                                                                                                                                                                                                                                       44.1%; Score 71; DB 2; Length 26; 42.3%; Pred. No. 0.62;
                                                                                                                                                                                                                                                                                                                                                                                                11; Indels
                                                                                                                     Justice A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Valentino KL, Miljanich GP,
                                                                                                                                                                                                                                                                                                                                                                                               4; Mismatches
                                                                                                                 Valentino KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Natural omega conopeptide SVIB/SNX-183.
                                                                                                                                                                                                                                                                                                                                                                                                                1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CKLKGOSCRKTSYDCCSGSCGRSGKC 26
                                                                                                                                                                                          Disclosure, Fig 18; 59pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY56480 standard; peptide; 26
                                    96US-00675354.
                                                         91US-00814759.
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93US-00049794.
96US-00675354.
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                                                                                                                Gohil KC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                     WPI; 1999-120002/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Singh T,
                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
les 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anti-inflammatory
                                                                                         (NEUR-) NEUREX
                                                                                                                                                                                                                                                                                                                                               Sequence 26 AA;
                                                                                                             Miljanich GP,
                                03-JUL-1996;
                                                        30-DEC-1991;
15-APR-1993;
            12-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-APR-1993;
03-JUL-1996;
01-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-FEB-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-NOV-1999
                                                                                                                                                                        peptide(s)
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                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conus sp.
                                                                                                                                                                                                                                                                                                                                                                                         Matches
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A method has been developed of selecting a test compound for treating inflammation. The method comprises measuring the activity of the test compound in blocking voltage-gated calcium channels, binding to the omega conopeptide binding site and inhibiting norepinephrine (noradrenaline) release from nervous tissue. The method is useful for selecting compounds for treating inflammation. The selected compounds are capable of producing analgesia in a mammalian subject with chronic or intractable opioid analgesia caused by selected compounds may reduce the reliance on opioid analgesic agents of the prior art which cause dependency and tolerance, requiring potentially dangerous increases in opioid doses to achieve the analgesic effect. The present sequence represents an omega conopeptide given in the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Marine snail; omega-conopeptide; calcium channel blocker; SVIB; SNX-183; toxin; analgesic; antiinflammatory; anticonvulsant; neuroleptic; norepinephrine release inhibitor; schizophrenia; tardive dyskinesia; acute dystonic reaction; inflammation; epilepsy.
                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Justice A;
                                                                                                                                                                                                                                                                               Score 71; DB 3; Length 26;
Pred. No. 0.62;
4; Mismatches 11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note≈ "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                          56
                                                                                                                                                                                                                                                                                                                                                                           1 CKLKGQSCRKTSYDCCSGSCGRSGKC 26
                                                                                                                                                                                                                                                                                                                                                    1 CRIXNOKCFOHLDDCCSRKCNRFNKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB14359 standard; peptide; 26 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Omega-conopeptide SVIB/SNX-183.
                                                                                                                                                                                                                                                                                 44.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91US-00814759.
93US-00049794.
96US-00675354.
96US-00742774.
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                                                                                           The present sequence is an omega-conopeptide from marine snails of the genus Conus. Omega-conopeptides are components of peptide toxins produced by the cone snails, and which act as calcium channel blockers. Natural omega-conopeptides and their derivatives may be useful for producing analgesia in nociceptive and neuropathic pain. The peptides bind to omega-conopeptide binding sites, which are present mainly in neuronal tissue, and inhibit norepinephrine release from nervous tissue. Conopeptides such as MVIIA and TVIA are effective as therapeutic agents for treating neurogenic conditions such as schizophrenia, tardive dyskinesia and acute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a
                       Selecting a compound for producing analgesia involves measuring activity of test compound in blocking voltage-gated calcium channels, binding to omega conopeptide binding site and inhibiting norepinephrine release.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity.
                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protection, endogenous therapeutic peptide, peptidase, conjugation, blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thibaudeau K;
                                                                                                                                                                                                                                                   Match 44.1%; Score 71; DB 3; Length 26; Local Similarity 42.3%; Pred. No. 0.62; es 11; Conservative 4; Mismatches 11; Indels
                                                                                                                                                                                                      dystonic reactions, inflammation and epilepsy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 653-654; 733pp; English.
                                                                                                                                                                                                                                                                                                     1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                  Milner PG,
                                                                       Example 4; Fig 1; 58pp; English
                                                                                                                                                                                                                                                                                                                                                                                       AAB92221 standard; peptide; 26
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99US-0153406P.
99US-0159783P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Toxin peptide SEQ ID NO:1397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-MAY-2000; 2000WO-US013576
                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ezrin AM,
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WPI; 2000-49017/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-112059/12.
                                                                                                                                                                                                                              Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200069900-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-MAY-1999;
10-SEP-1999;
15-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                     Query Match
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Matches
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peptidase stabilised therapeutic peptide composed of 3-50 amino acids.

(I) are useful for modifying therapeutic peptides e.g. hormones growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular uptake and interference with physiological processes. AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Omega-conopeptide, voltage-gated calcium channel inhibitor, analgesic, peptide toxin, opiate, pain, neuronal damage, ischemic condition, schizophrenia, tardive dyskinesia, acute dystonic reaction; inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enhancing analgesia produced by opiates by administering an omega-
conopeptide that inhibits electrically stimulated contraction of guinea
pig ilium and binds to omega-conopeptide MVIIA binding sites in neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Primary sequence of a natural omega-conopeptide SVIB/SNX-183.
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                                                                                                                                                                                                                                                                                                                                                                                               Score 71; DB 4; Length 26; Pred. No. 0.62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Miljanich GP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "amidated C-terminal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CRIXNOKCFOHLDDCCSRKCNRFNKC 26
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93US-00081863.
96US-00675354.
96US-00138439.
99US-00138439.
                                                                                                                                                                                                                                                                                                                                                                                                  44.18;
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                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 42.3
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .15
8. .19
15. .26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-030946/04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disulfide-bond
Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                    Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELAN-) ELAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US6136786-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LS-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-JUN-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   epilepsy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB19449;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB19449
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ABB96876 standard; peptide;

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The invention comprises peptides having calcium channel blocking activities which are derived from the venomous saliva of assassin bugs. The calcium channel blocking peptides of the invention are useful for treating stenceardia, hypertension, myocarditis, arrhythmia and cerebral ischaemia. The present amino acid sequence represents a cone snail wconotoxin peptide
Disclosure; Fig 1; 58pp; English.
                                                                                                          Sequence 26 AA;
                                                                                                                                                                                                                                                                                                      JP2002080499-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 26 AA;
                                                                                                                                                                                                                                 22-AUG-2002
                                                                                                                                                                                                                                                                                                                    19-MAR-2002.
                                                                                                                                                                                                                                                                           w-conotoxin
                                                                                                                                                                                                                   AA015126;
                                                                                                                                                                                                                                                                                         Conus sp.
                                                                                                                                                                                       RESULT 74
                                                                                                                                                                                              AA015126
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The present sequence represents an omega-conopeptide. Omega-conopeptides channel inhibitors. The peptides are used to enhance the analgesic effect broduced by an opiate in a mammalian subject. The method comprises administering to the subject an omega-conopeptide which is abbe to bind to omega-conopeptide MITA binding sites present in neuronal tissue. Omega-conopeptides are useful for enhancing the analgesic effect by an opiate. Omega-conopeptides may also be used in neuronal tissue. By an opiate. Omega-conopeptides may also be used in the treatment of mammals, and in treating schizophrenia, tardive dyskinesia and acute dystonic reactions, inflammation and epilepsy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cone snail; venomous saliva; calcium channel blocking activity;
stenocardia; hypertension; myocarditis; arrhythmia; cerebral ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A new peptide derived from venomous sallva of assassin bug, has calcium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 71; DB 4; Length 26;
Pred. No. 0.62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 44.1%; 5cc. 42.3%; Pred. No. c. 47.3%; A Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CRIXNOKCFQHLDDCCSRKCNRFNKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | CKLKGQSCRKTSYDCCSGSCGRSGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cone snail w-conotoxin peptide SVIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 4; 26pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAO15126 standard; peptide; 26 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-SEP-2000; 2000JP-00266187.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            channel blocking activity.
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Best Local Similarity
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Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiant; neuroprotective; cerebroprotective; cardiovascular; antinflammatory; antimigraine; antidiabetic; tranquilises; vulnerary; antipsychotic; anxiolytic; neuroleptic; voltage gated ion channel; seizure; epilepsy; stroke; cerebrovascular accident; brain trauma; spinal chord trauma; stroke; cerebrovascular accident; brain trauma; spinal chord trauma; drowning; suffocation; perinatal asphyxia; hypoglycaemic event; pain; migraine; inflammation; cardiovascular disorder; psychosis; anxiety; schizophrenia.

Omega-conopeptide P6.3 toxin sequence.

12-JUL-2002

ABB96876;

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The invention relates to isolated omega-conopeptides, nucleic acid sequences encoding them, and propeptide sequences. The activity of the peptides of the invention may be described as, analgesic, anticonvulsant, vasotropic, cardiant, neuroprotective, cerebroprotective, cardiovascular, antiniflammatory, antimigraine, antidiabelic, tranquiliser, vulnerary, antipically antionable; tranquiliser, vulnerary, by modulating the activity of voltage gated ion channels. They may be concluded to treating or preventing disorders e.g. selzure (associated with replays), neurotoxic injury associated with conditions of hypoxia, chord trauma, drowning, suffocation, perinatal asphyxia or hypozia, chord trauma, drowning, suffocation, perinatal asphyxia or hypozia, events; pain e.g. migraine; inflammation or cardiovascular disorders. They may also be used for treating psychiatric disorders e.g. psychosis, anticinal and an angesic agents of the invention show and activity of the analgesic agents of the invention show and activity of the analgesic agents of the invention show and activity of the analgesic agents of the invention show and activity of the analgesic agents and the analgesic an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Matches
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New omega-conopeptides useful for treating disorders associated with voltage gated ion channels e.g. pain, inflammation, neurologic or cardiovascular disorders.

Shon K;

Garrett JE,

Watkins M, Cartier GE;

Mcintosh JM, Jones RM, C

Olivera BM, Jacobsen R,

WPI; 2002-257318/30.

21-JUL-2000; 2000US-0219616P. 05-PEB-2001; 2001US-0265888P.

(UTAH) UNIV UTAH RES FOUND.

(COGN-) COGNETIX INC.

23-JUL-2001; 2001WO-US023041.

Conus purpurascens.

WO200207675-A2.

31-JAN-2002

1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26

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Gaps

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DB 5; Length 26; 11; Indels

Score 71; DB Pred. No. 0.62 4; Mismatches

44.18;

11; Conservative

Matches

Local Similarity

Query Match

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neuroprotective; cerebroprotective; cardiovascular; antinflammatory; antingraine; antidabetic; tranquiliser; vulnerary; antipsychotic; antidabetic; tranquiliser; vulnerary; antipsychotic; neuroleptic; voltage gated ion channel; seizure; epilepsy; neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia; stroke; cerebrovascular accident; brain trauma; spinal chord trauma; drowning; suffocation; perinatal asphyxia; hypoglycaemic event; pain; migraine; inflammation; cardiovascular disorder; psychiatric disorder; psychosis; anxiety; schizophrenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New omega-conopeptides useful for treating disorders associated with voltage gated ion channels e.g. pain, inflammation, neurologic or cardiovascular disorders.
                                                                                                                                                                                     Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiant,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shon K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Garrett JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mcintosh JM, Watkins M,
Jones RM, Cartier GE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1(c); Page 56; 195pp; English.
                                                                                                                                                           Omega-conopeptide P6.3 propeptide.
                                                                                   ABB96668 standard; peptide; 72 AA
 20
            2 CKKTGRKCFPHQKDCCGRAC 21
CRIXNOKCFQHLDDCCSRKC
                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-2000; 2000US-0219616P.
05-FEB-2001; 2001US-0265888P.
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                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-257318/30.
N-PSDB; ABL98927.
                                                                                                                                                                                                                                                                                                              Conus purpurascens.
                                                                                                                                                                                                                                                                                                                                    WO200207675-A2.
                                                                                                                                    12-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jacobsen R,
                                                                                                           ABB96668;
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                                                                       ABB96668
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The invention relates to isolated omega-conopeptides, nucleic acid sequences encoding them, and propeptide sequences. The activity of the sequences encoding them, and propeptide sequences. The activity of the peptides of the invention may be described as, analgesic, anticonvulsant, vasotropic, cardiant, neuroprotective, crebroprotective, cardiovascular, antinifisammatory, antimigraine, antidiabetic, tranquiliser, vulnerary, antipaychotic, anxiolytic and neurolegics of the invention act by modulating the activity of voltage gated ion channels. They may be used for treating or preventing disorders associated with voltage gated ion channels such as neurological disorders, e.g. seizure (associated vith epilepsy), neurotoxic injury associated with conditions of hypoxia, anoxia, ischaemia, stroke, cerebrovascular accident, brain or spinal anoxia, ischaemia, suffocation, perinatal asphyxia or hypoglycaemic events; pain e.g. migraine; inflammation or cardiovascular disorders. They may also be used for treating psychiatric disorders e.g. psychosis, diminished side effects and toxicity, and are non-addictive. The sequence given in records ABB96595-ABB96697 represent omega-conopeptide propeptide sequences

sequences encoding them, and propeptide sequences. The activity of the peptides of the invention may be described as, analgesic, anticonvulsant, vasotropic, cardiant, neuroprotective, creebroprotective, cardiant, neuroprotective, tranquiliser, vulnerary, antianglammatory, antiangraine, antidabetic, tranquiliser, vulnerary, antipsychotic, anxiolytic and neuroleptic. Peptides of the invention act by modulating the activity of voltage gated ion channels. They may be used for treating or preventing disorders associated with voltage gated ion channels such as neurological disorders, e.g. seizure (associated with epilepsy), neurotoxic injury associated with conditions of hypoxia, anoxia, ischaemia, stroke, cerebrovascular accident, brain or spinal chord trauma, drowning, suffocation, perinaral asphyxia or hypoglycaemic events; pain e.g. migraine; inflammation or cardiovascular disorders.

The invention relates to isolated omega-conopeptides, nucleic acid

Example 2; Page 62; 195pp; English.

Sequence 72 AA;

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                                                                                                                                                                                                                                Omega-conopptide; analgesic; anticonvulsant; vasotropic; cardiant; neuroprotective; cerebroprotective; cardiovascular; antiinflammatory; antimigraine; antidiabetic; tranquiliser; vulnerary; antipsychotic; anxiolytic; neuroleptic; voltage gated ion channel; seizure; epileps; neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia; stroke; cerebrovascular accident; brain trauma; spinal chord trauma; drowning; sulfocation; perinatal asphyxia; hypoglycaemic event; pain; migraine; inflammation; cardiovascular disorder; psychiatric disorder; psychosis; anxiety; schizophrenia.
                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New omega-conopeptides useful for treating disorders associated with voltage gated ion channels e.g. pain, inflammation, neurologic or cardiovascular disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Garrett JE, Shon K;
Length 72;
                        Indels
  DB 5;
                                                                                                                                                                                                           Omega-conopeptide S6.2 generic toxin sequence.
Score 71; DB 5
Pred. No. 1.4;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mcintosh JM, Watkins M,
Jones RM, Cartier GE;
                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                   ABB96786 standard; peptide; 26 AA
                                                1 CRIXNQKCFQHLDDCCSRKC 20
                                                              CKKTGRKCFPHQKDCCGRAC 66
                        3,
  44.1%; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-2000; 2000US-0219616P.
05-FEB-2001; 2001US-0265888P.
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                         Conservative
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            Local Similarity
nes 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference 13
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Jacobsen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-JAN-2002
                                                                                                                                                            ABB96786;
  Query Match
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               Best Loc
Matches
                                                                                                           RESULT 77
                                                                                                                         ABB96786
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us-10-627-685a-26.rag

Query Match Best Local S

88888888

Matches

ò g RESULT 78 ABB96790 ö

Gaps

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antipsychotic, anxiolytic and neuroleptic. Peptides of the invention act used for treating the activity of voltage gated ion channels. They may be used for treating or preventing disorders associated with voltage gated ion channels such as neurological disorders, e.g. seizure (associated with epilepsy), neurotoxic injury associated with conditions of hypoxia, chord trauma, drowning, suffocation, perinatal asphyxia or hypoxlachord trauma, drowning, suffocation, perinatal asphyxia or hypoglycaemic when may also be used for treating psychiatric disorders e.g. psychosis, anxiety or schizophrenia. The analgesic agents of the invention show a sequences given in records ABB96698-ABB96806 represent omega-conopeptide generic toxin sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Omega-conopeptide, analgesic, anticonvulsant; vasotropic; cardiant; neuroprotective; cerebroprotective; cardiovascular; antiinflammatory; antimigraine; antidiabetic; tranquiliser; vulnerary; antipsychotic; anxiolytic; neuroleptic; voltage gated ion channel; sarizure; ppilepsy; neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia; stroke, cerebrovascular accident; brain trauma; spinal chord trauma; drowning; suffocation; perinatal asphyxia; hypoglycaemic event; pain; migraine; inflammation; cardiovascular disorder; psychosis; anxiety; schizophrenia.
                                                                                                                                                                                                                                                                                                                                                                 39.8%; Score 64; DB 5; Length 26; 42.3%; Pred. No. 3.6; 1.ve 4; Mismatches 11; Indels
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/note= "OTHER is Pro or Hydroxy Pro"
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/note= "OTHER is Pro or Hydroxy Pro"
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note= "OTHER is Pro or Hydroxy Pro"
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/note= "OTHER is Pro or Hydroxy Pro"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Omega-conopeptide P6.1 generic toxin sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CKLKGOSCRKTSXDCCSGSCGRSGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB96772 standard; peptide; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-2000; 2000US-0219616P.
05-FEB-2001; 2001US-0265888P.
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Best Local Similarity 42.35
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conus purpurascens.
                                                                                                                                                                                                                                                                                                                    Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB96772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 79
ABB96772
                          8x33333333333x8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            요
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                                                                                                                                                                                                                                0;
They may also be used for treating psychiatric disorders e.g. psychosis, anxiety or schizophrenia. The analgesic agents of the invention show diminished side effects and toxicity, and are non-addictive. The sequences given in records ABB96698-ABB96806 represent omega-conopeptide generic toxin sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "OTHER is Tyr, 1251-Tyr, mono-iodo-Tyr or di-iodo-
Tyr or O-sulpho-Tyr or O-Phospho-Tyr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to isolated omega-conopeptides, nucleic acid sequences encoding them, and propeptide sequences. The activity of the peptides of the invention may be described as, analgesic, anticonvulsant, vasotropic, cardiant, neuroprotective, cerebroprotective, cardiovascular, antiinflammatory, antimigraine, antidiabetic, tranquiliser, vulnerary,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neuroprotective; cerebroprotective; cardiovascular; antinflammatory; antipigaraine; antidiabetic; tranquiliser; vulnerary; antipsychotic; anxiolytic; neuroleptic; voltage gated ion channel; serizure; epilepsy; neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia; stroke; cerebrovascular accident; brain trauma; spinal chord trauma; drowning; suffocation; perinatal asphyxia; hypoglycaemic event; pain; migraine; inflammation; cardiovascular disorder; psychiatric disorder; psychosis; anxiety; schizophrenia.
                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              opeptides useful for treating disorders associated with ion channels e.g. pain, inflammation, neurologic or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiant;
                                                                                                                                                                                                                              .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shon K;
                                                                                                                                                                                 5; Length 26;
                                                                                                                                                                                                                         10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Garrett JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Omega-conopeptide w-SVIB generic toxim sequence.
                                                                                                                                                                                 DB
                                                                                                                                                                                                                     5; Mismatches
                                                                                                                                                                             41.6%; Score 67; I 42.3%; Pred. No. 1.
                                                                                                                                                                                                                                                      1 CRIXNOKCFOHLDDCCSRKCNRFNKC 26

    Watkins M,
Cartier GE;

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                  ABB96790 standard; peptide; 26 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Page 63; 195pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New omega-conopeptides useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-JUL-2001; 2001WO-US023041.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0219616P.
2001US-0265888P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-JUL-2002 (first entry)
                                                                                                                                                                                                                11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mcintosh JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cardiovascular disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jones RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COGNETIX INC
                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-257318/30.
                                                                                                                              Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conus striatus
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voltage gated

21-JUL-2000; 05-FEB-2001;

31-JAN-2002.

(UTAH) UNIV (COGN-) COGNE

Olivera BM, Jacobsen (COGN-) COGNETIX INC.

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The invention relates to isolated omega-conopeptides, nucleic acid

sequences encoding them, and propeptide sequences. The activity of the

competides of the invention may be described as, analgesic, anticonvulsant,

vasotropic, cardiant, neuroprotective, cerebroprotective, cardiovascular,

antinflammatory, antinfgraine, antidiabetic, tranquiliser, vulnerary,

antipsychotic, anxiolytic and neuroleptic. Peptides of the invention act

by modulating the activity of voltage gated ion channels: They may be

concluded for treating or preventing disorders associated with voltage gated

concluded for treating or preventing disorders, e.g. seizure (associated

with epilepsy), neurotoxic injury associated with conditions of hypoxia,

anoxia, ischaemia, stroke, cerebrovascular accident, brain or spinal

chord trauma, drowning, suffocation, perinatal asphyxia or hypoglycaemic

chord trauma, drowning, inflammation or cardiovascular disorders.

They may also be used for treating psychiatic disorders e.g. psychosis,

anxiety or schizophrenia. The analgesic agents of the invention show

diminished side effects and toxicity, and are non-addictive. The

chord is concepted to the invention show and toxicity and are non-addictive. The
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                                                                                                  omega-conopeptides useful for treating disorders associated with age gated ion channels e.g. pain, inflammation, neurologic or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiant;
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    Garrett JE, Shon K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 5; Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39.8%; Score 64; DB 555.0%; Pred. No. 3.7; ive 2; Mismatches
      Watkins M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Omega-conopeptide P6.1 toxin sequence.
                      Cartier GE;
                                                                                                                                                                                 Example 2; Page 56; 195pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB96874 standard; peptide; 27 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CRIXNOKCFOHLDDCCSRKC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CKTXGRKCFXHQKDCCGRAC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0219616P
2001US-0265888P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-JUL-2002 (first entry)
Mcintosh'JM,
Jones RM, C
                                                                                                                                         cardiovascular disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 39.8
Best Local Similarity 55.0
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       generic toxin sequences
                                                              WPI; 2002-257318/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 27 AA;
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05-FEB-2001;
    Olivera BM,
                      Jacobsen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-JAN-2002
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equences encoding them, and properties equences. The activity of the peptides of the invention may be described as, analgesic, anticonvulsant, vasotropic, cardiant, neuroprotective, cerebroprotective, cardiavascular, antinflammatory, antimigraine, antidiabetic, tranquiliser, vulnerary, antimigraine, antidiabetic, tranquiliser, vulnerary, antipsychotic, anxiolytic and neuroleptic. Peptides of the invention act by modulating the activity of voltage gated ion channels. They may be used for treating or preventing disorders associated with voltage gated ion channels such as neurological disorders, e.g. saizure (associated with epilepsy), neurotoxic injury associated with conditions of hypoxia, anoxia, ischaemia, stroke, cerebrovascular accident, brain or spinal chord trauma, drowning, sulffocation, perinatal asphyxia or hypoglycamic events; pain e.g. migraine; inflammation or cardiovascular disorders. They may also be used for treating psychiatric disorders e.g. psychosis, anxiety or schizophrenia. The analgesic agents of the invention show diminished side effects and toxicity, and are non-addictive. The sequences given in records ABB96807-ABB96905 represent omega-conopeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiant; neuroprotective; cerebroprotective; cardiovascular; antiinflammatory; antimigraine; antidiabetic; tranquiliser; vulnerary; antipsychotic; anxiolytic; neuroleptic; voltage gated ion channel; seizure; epilepsy; neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia; stroke; cerebrovascular accident; brain trauma; spinal chord trauma; atroke; cerebrovascular accident; brain trauma; spinal chord trauma; drowning; sulfocation; perinatal asphyxia; hypoglycaemic event; pain; migraine; inflammation; cardiovascular disorder; psychiatric disorder;
                                                                                                                                     New omega-conopeptides useful for treating disorders associated with voltage gated ion channels e.g. pain, inflammation, neurologic or cardiovascular disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                      nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                        Shon K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39.8%; Score 64; DB 5; Length 27; 55.0%; Pred. No. 3.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Indels
                                                                                                                                                                                                                                                                           The invention relates to isolated omega-conopeptides,
                                     Garrett JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Omega-conopeptide Cr6.3 toxin sequence.
                                     M, Watkins M,
Cartier GE;
                                                                                                                                                                                                                                Claim 1(a); Page 72; 195pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB96842 standard; peptide; 27 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                psychosis; anxiety; schizophrenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CRIXNQKCFQHLDDCCSRKC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 CKTXGRKCFXHQKDCCGRAC 21
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05-FEB-2001; 2001US-0265888P.
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Matches 11; Conservative
                                                         Jones RM,
                                                                                                    WPI; 2002-257318/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conus circumcisus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               coxin sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200207675-A2.
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                                        Olivera BM,
Jacobsen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB96842;
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                                     Olivera
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ABB96842
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Shon K;

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23-JUL-2001; 2001WO-US023041.
                                                                                                         Conus circumcisus.
                                                       Sequence 27 AA;
                                                                                                            WO200207675-A2.
                                                                                  12-JUL-2002
                                                                               ABB96626;
                                                                          ABB96626
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The invention relates to isolated omega-conopeptides, nucleic acid
sequences encoding them, and propeptide sequences. The activity of the
peptides of the invention may be described as, analgesic, anticonvulsant,
vasotropic, cardiant, neuroprotective, cerebroprotective, cardiovascular,
antiphical anticolytic and neuroleptic. Peptides of the invention act
antipsychotic, anxiolytic and neuroleptic. Peptides of the invention act
contracting the activity of voltage gated ion channels. They may be
used for treating or preventing disorders associated with voltage gated
con channels such as neurological disorders, e.g. seizure (associated
anoxia, ischaemia, stroke, cerebrovascular acident, brain or spinal
conditions of hypoxia,
chord trauma, drowning, suffocation, perinatal asphyxia or hypoglycaemic
chord trauma, drowning, suffocation, perinatal asphyxia or hypoglycaemic
chord trauma, and so used for treating psychiatric disorders.
They may also be used for treating psychiatric disorders envisty or schizophrenia. The analgesic agents of the invention show
sequences given in records ABB96697 represent omega-conopeptide
nronnentials.
                                                                                                                                                                                                                                                                                                         New omega-conopeptides useful for treating disorders associated with voltage gated ion channels e.g. pain, inflammation, neurologic or cardiovascular disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tyrosinase inhibitor; pupae; house fly; melanin; dermal medicine; cosmetic; food preservative; insecticide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39.4%; Score 63.5; DB 5; Length 73; 37.0%; Pred. No. 9.3; 1.1ve 8; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Tyr, OTHER
/note= "OTHER = 3,4-dihydroxyphenylalanine"
                                                                                                                                                       Mcintosh JM, Watkins M, Garrett JE,
Jones RM, Cartier GE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CRIXNOKCFQHLDDCCSRKCNRFN-KC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | : : | | : : | | | | : : : | CKSKGAKCSRLMYDCCSGSCSRYSGRC 72
                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1(c); Page 36; 195pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW06589 standard; peptide; 38 AA
  21-JUL-2000; 2000US-0219616P.
05-FEB-2001; 2001US-0265888P.
                                                                           (UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tyrosinase inhibitor peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-FEB-1997 (first entry)
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Les 10; Conservative
                                                                                                      (COGN-) COGNETIX INC.
                                                                                                                                                                                                                                WPI; 2002-257318/30.
                                                                                                                                                                                                                                                      N-PSDB; ABL98885
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 73 AA;
                                                                                                                                                    Olivera BM,
Jacobsen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW06589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to isolated omega-conopeptides, nucleic acid sequences encoding them, and propeptide sequences. The activity of the peptides of the invention may be described as, analgesic, anticonvulsant, vasotropic, cardiant, neuroprotective, cerebroprotective, cardiovascular, antinflammatory, antinflammatory in the partial such as a neurological disorders, e.g. seizure (associated on channels such as neurological disorders, e.g. seizure (associated with epilepsy), neurotoxic injury associated with conditions of hypoxia, anoxia, ischaemia, stroke, cerebrovascular accident, brain or spinal chord trauma, drowning, suffocation, perinatal asphyxia or hypoglycaemic they may also be used for treating psychiatric disorders e.g. psychosis, anxiety or schizophrenia. The analgesic agents of the invention show sequences given in records ABB96807-ABB96905 represent omega-conopeptide toxin sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Omega-conopeptide, analgesic, anticonvilsant, vasotropic, cardiant, neuroprotective, cerebroprotective, cardiovascular, antiinflammatory, antimigraine, antidiabetic, tranquiliser, vulnerary, antipsychotic, antiolytic, neuroleptic, voltage gated ion channel, seizure, epilepsy, neurological disorder, neuroteoxic injury, hypoxia, anoxia, ischaemia, stroke, cerebrovascular accident, brain trauma, spinal chord trauma, drowning, suffocation, perinatal asphyxia, hypoglycaemic event; pain, migraine, inflammation, cardiovascular disorder, psychiatric disorder, psychosis, anxiety, schizophrenia.
                                                                                                                                                                                                        New omega-conopeptides useful for treating disorders associated with voltage gated ion channels e.g. pain, inflammation, neurologic or cardiovascular disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7;
                                                                                         Shon K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 39.4%; Score 63.5; DB 5; Length 27; Best Local Similarity 37.0%; Pred. No. 4.2; Matches 10; Conservative 8; Mismatches 8; Indels
                                                                                         Garrett JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CRIXNOKCFOHLDDCCSRKCNRFN-KC 26

    Watkins M,
Cartier GE;

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1(a); Page 71; 195pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Omega-conopeptide Cr6.3 propeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB96626 standard; peptide; 73 AA.
  (UTAH ) UNIV UTAH RES FOUND. (COGN-) COGNETIX INC.
                                                                           Olivera BM, Mcintosh JM,
Jacobsen R, Jones RM, Ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                       WPI; 2002-257318/30.
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ij

Gaps

1,

95JP-00038405

27-FEB-1995;

JP08231592-A. 10-SEP-1996.

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WO200202590-A2
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27-OCT-2000; 2
08-NOV-2000; 2
14-NOV-2000; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB88659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB88659
  ద
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           7
                                                                                                                                                                                                                                            This sequence represents a tyrosinase inhibitor peptide which was isolated from the pupae of house flies. The peptide has a high inhibitory activity on tyrosinase, which catalyses biological production of melanin pigment, and is stable at ambient pH. The peptide can be used for dermal medicines, cosmetics, food preservatives and insecticides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pure I-conotoxin peptides isolated from venom of cone snails, useful for
the regulation of the flow of potassium through potassium channels in the
treatment of e.g. multiple sclerosis.
                                                                                                                                            tyrosinase - useful for dermal medicines, cosmetics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conotoxin; Conus; I-conotoxin; I-superfamily conotoxin; venom; antidote; cone snail; marine gastropod; neuroprotective; antiinflammatory; ophthalmological; antibacterial; anticonvuleant; muscular; antidiabetic; antiadistrythmic; cardiant; immunosuppressive; nootropic; antiaddictive; cytostatic; crebroprotective; antiasthmatic; vasotropic; analgesic; antimigraine; relaxant; antirheumatic; antiarthritic; dermatological; tranquilliser; neuroleptic; H-ATPase stimulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conus betulinus I-superfamily conotoxin type I peptide SEQ:369.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         7
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                                                                                                                                                                                                                                                                                                                                                                                                              39.1%; Score 63; DB 2; Length 38; 39.3%; Pred. No. 6.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mcintosh JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CRIXNQKCFQHLDDCCSRKCNR-FNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | : | | : | | | | | CLANGSKCYSH-DVCCTKRCHNXAKKCV 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          potassium agonist; curare antagonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jiminez Shen GS;
                                                                                                                                                                                                        Claim 1; Page 2; 9pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB88797 standard; peptide; 36
                     95JP-00038405.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-0CT-2000; 2000US-0243410P.
08-NOV-2000; 2000US-024581P.
14-NOV-2000; 2000US-024714P.
29-JAN-2001; 2001US-0264256P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JUN-2001; 2001WO-US020796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JUN-2000; 2000US-0304166P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                           (SIYA ) SANSEI SEIYAKU KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Conservative
                                                                                                                                                                  food preservatives, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shetty R,
Jones RM,
                                                                                                                                        Peptide inhibitor of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COGNETIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-171634/22.
                                                                                                    WPI; 1996-461344/46
                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                          Sequence 38 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conus betulinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200202590-A2
                     27-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Walker CS,
Watkins M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB88797
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARBSULT 84
ABB88797
ABB877
ABB88797
ABB8879
ABB88797
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ABB88797
ABB88797
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ABB8
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of 30 -50 residues (I). (I) have neuroprotective, antinilammatory, ophthalmosoppressive, antidote, antibacterial, anticonvulsant, muscular, cardiavate, antidote, antibacterial, anticonvulsant, muscular, antidote, antibacterial, antidotein, muscular, cardiavate, antiathemic, cardiant, antidathemic, antiaddictive, immunosuppressive, cytostatic, analgesic, antimigraine, antirhummatic, antiathmatic, vasotropic, analgesic, antimigraine, antirhummatic, antiathmatic, dermatological, tranquilliser and neuroleptic activities.

(I) can be used as an H-APPase stimulator, potassium agonist and curare antagonist. (I) are useful in the treatment of multiple sclerosis, acute fulsionist. (I) are beliated encephalomyelitis, optic neuromyelitis, progressive multifocal leukoencephalomyelitis, optic neuromyelitis, metachromic contuitum toxin poisoning panencephalomyelitis, metachromic leukodystrophy, beliateus-Merzbacher disease, spinal cord injury, botulinum toxin poisoning, Huntington's chorea, compression and entrapment neuropathies, cardiovascular disease, reactive gliosis, chypersylvaemia, immunosuppression, coacine addiction, cancer, cognitive dysfunction, disease and reversal of the actions curare and other neuromainter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           blocking drugs. (I) can also be used to treat disorders associated with radical depolarisation of excitable membranes, and disorders associated with voltage gared ion channels, pain and a neuromuscular disorder. (I) are also useful for screening compounds that mimic the activity of an I-conotoxin. They are also useful for the treatment of autoimmune diseases, rheumatoid arthritis, systemic lupus erytematosus, Albraimer's and schizophrenia. Abla8662 to Abla8978 and Abb88546 to Abb88934 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cone snail; marine gastropod; neuroprotective; antiinflammatory; ophthalmological; antibacterial; anticonvulsant; muscular; antidiabetic; cardicovascular; antiarhythmic; cardiant; immunosuppressive; nootropic; antiaddictive; cytostatic; cerebroprotective; antiasthmatic; vasotropic; analgesic; antimigraine; relaxant; antirheumatic; antiarthriic; dermatcological; tranquilliser; neuroleptic; H-ATPase stimulator; potassium agonist; curare antagonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conctoxin; Conus; I-conctoxin; I-superfamily conotoxin; venom; antidote;
                                            s present invention describes substantially pure I-conotoxin peptides 30 -50 readings (T) (T) have concerned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conus betulinus I-superfamily conotoxin peptide sequence SEQ:167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Length 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 62.5;
Pred. No. 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLSLGQRCERH-SDCCGYLCCFYDKCV 27
3; Page 81; 260pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB88659 standard; peptide; 73 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0243410P.
2000US-0246581P.
2000US-0247714P.
2001US-0264256P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38.8%;
40.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Guery Match
Guery Local Similarity 40.77,
Best Local Similarity 40.77,
Best Local Similarity 40.77,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conus betulinus
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Conus purpurascens,

Olivera BM;

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The present invention describes substantially pure I-conotoxin peptides of 30 -50 residues (I). (I) have neuroprotective, antiinflammatory, cardiovascular, antidote, antibacterial, anticonvulsant, muscular, cardiovascular, antiarthythmic, cardiant, anticonvulsant, muscular, immunosuppressive, cytostatic, noctropic, cerebroprotective, relaxant, antiarthritic, dermatological, tranquilliser and neuroleptic activities.

CC antiasthmatic, dermatological, tranquilliser and neuroleptic activities antiarthritic, dermatological, tranquilliser and neuroleptic activities.

CC antiasthmatic an H-Arpase stimulator, potassium agonist and curare disseminated encephalomyelitis, optic neuromyelitis, progressive multifocal leukoencephalopathy, acremolateddystrophy, acute transverse compelities, unbacute sclerosing panencephalomyelitis, metachromic myelitis, subacute sclerosing panencephalomyelitis, metachromic compelitis, betulinum toxin poisoning, Huntington's chorea, compression and hyperglycaemia, Immunosuppression, cocaine addiction, cancer, cognitive contrapment neuropathies, cardiovascular disease, reactive gliosis, dysfunction, disorders resulting from the defects of neurotransmitter colocking drugs (I) can also be used to treat disorders associated with woltage gated ion channels, pain and aneuromuscular disorders associated with voltage gated ion channels, pain and neuromuscular disorders is neurotransmitter contoxin. They are also useful for the treatment of autoimmune diseases, are also useful for the treatment of autoimmune diseases, and schizophrenia. Abusba662 to Abla8778 and Abbs8546 to Abbs8934

C represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                    Pure I-conotoxin peptides isolated from venom of cone snails, useful for the regulation of the flow of potassium through potassium channels in the treatment of e.g. multiple sclerosis.
                                                                                                       Jiminez EC, Mcintosh JM,
Shen GS;
                                                                                                                                                                                                                                                                                                                 Claim 2; Page 54; 260pp; English.
                         (UTAH ) UNIV UTAH RES FOUND.
(COGN-) COGNETIX INC.
                                                                                                    Shetty R,
Jones RM,
                                                                                                                                                                        WPI; 2002-171634/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 73 AA;
                                                                                               Walker CS,
Watkins M,
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10; Indels 1; 5; Length 73; 38.8%; Score 62.5; DB 40.7%; Pred. No. 12; Pred. No. 12; 5; Mismatches 1 CRIXNOKCFQHLDDCCSRKCNRFNKCV 27 39 CLSLGQRCERH-SDCCGYLCCFYDKCV 64 Ouery Match
Best Local Similarity 40.7x
Best Local 11, Conservative ò

Gaps

ABB96774 standard; peptide; 27 AA. RESULT 86 ABB96774

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12-JUL-2002 (first entry)

Omega-conopeptide P6.3 generic toxin sequence.

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neuroprotective; cerebroprotective; cardiovascular; antinflammatory, antingraine; antidiabetic; tranquiliser; vulnerary; antipsychotic; anxiolytic; voltage gated ion channel; satzure; epilepsy; neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia; stroke; cerebrovascular accident; brain trauma; spinal chord trauma; drowning; suffocation; perinatal asphyxia; hypoglycaemic event; pain; migraine; inflammation; cardiovascular disorder; psychiatric disorder; psychosis; anxiety; schizophrenia. Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiant;

AAU05927 standard; peptide; 76 AA.

RESULT 87 AAU05927

24-OCT-2001 (first entry)

AAU05927;

1 CRIXNQKCFQHLDDCCSRKC 20

ò

2 CKKTGRKCFXHQKDCCGRAC

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The invention relates to isolated omega-conopeptides, nucleic acid sequences encoding them, and propeptide sequences. The activity of the sequences encoding them, and propeptide sequences. The activity of the periodic sequences. The activity of the periodic cardiant, neuroprotective, cerebroprotective, cardiovascular, antipsychotic, anxielytic and neuroleptic. Peptides of the invention act antipsychotic, anxielytic and neuroleptic. Peptides of the invention act by modulating the activity of voltage gated in channels. They may be used for treating or preventing disorders associated with voltage gated with epilepsy), neurotoxic injury associated with conditions of hypoxia, chord trauma, drowning, suffocation, perinatal asphyxia or hypoglycaemic chord trauma, drowning, suffocation, perinatal asphyxia or hypoglycaemic cents; pain e.g. migraine; inflammation or cardiovascular disorders. They may also be used for treating psychiatric disorders e.g. psychosis, anxiety or schizophrenia. The analgesic agents of the invention show sequences given in records ABB96698-ABB96806 represent omega-conopeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New omega-conopeptides useful for treating disorders associated with volteage gated ion channels e.g. pain, inflammation, neurologic or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Pred. No. 6.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7; Indels
                                                                                                                                          /label≃ OTHER
/note≃ "OTHER is Pro or Hydroxy Pro"
                                                                                                                                                                                                                                      /label= OTHER
/note= "OTHER is Pro or Hydroxy Pro"
                                                                                                                                                                                                                                                                                                                                      /label= OTHER
/note= "OTHER is Pro or Hydroxy Pro"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mcintosh JM, Watkins M, Garrett JE, Jones RM, Cartier GE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 2; Page 56; 195pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-JUL-2001; 2001WO-US023041.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-2000; 2000US-0219616P. 05-FEB-2001; 2001US-0265888P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UTAH ) UNIV UTAH RES FOUND. (COGN-) COGNETIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cardiovascular disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 50.0
les 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-257318/30.
                                                                                                                                                                                                   Misc-difference 13
                                                                                                                                                                                                                                                                                                   Misc-difference 27
                                                                                               Misc-difference 1
                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200207675-A2.
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Jacobsen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-JAN-2002.
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Cone snail; O-superfamily conotoxin; sodium channel; demyelinating disease; multiple sclerosis; Huntingdon's disease; neuropathy; carpal tunnel syndrome; cardiovascular disorder; congestive heart failure; cancer; immunosuppression; epilepsy; asthma;
                                                                                                                                                                                                                                                                    New O-superfamily polypeptides useful for treating voltage gated ion channel disorders, including demyelinating diseases i.e. multiple
        Cone snail O-superfamily conotoxin propeptide, Di6.5.
                                                                                                                                                                                                                                                                                                      Claim 15; Page 60; 277pp; English
                                                                                                                                             30-DEC-1999; 99US-0173754P.
26-UUD-2000; 2000US-0214263P.
20-UUL-2000; 2000US-0219440P.
27-OCT-2000; 2000US-024312P.
                                                                                                                            28-DEC-2000; 2000WO-US035431
                                                                                                                                                                                        UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                  Cartier GE,
                                                           ischaemia; stroke; pain.
                                                                                                                                                                                                               am, Cares RM;
                                                                                                                                                                                                 COGNETIX INC
                                                                                                                                                                                                                                          WPI; 2001-418352/44.
N-PSDB; AAS10951.
                                                                                          WO200149312-A2
                                                                          Conus distans.
                                                                                                            12-JUL-2001.
                                                                                                                                                                                                                           Layer RT,
                                                                                                                                                                                                                                                                                      sclerosis.
                                                                                                                                                                                                                 Olivera
                                                                                                                                                                                                (COGN-)
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Mcintosh JM;

Watkins M, Hillyard DR,

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The sequence is a cone snail O-superfamily conotoxin propeptide. The peptides are useful for regulating the flow of sodium through sodium channels in an individual and the treatment or prevention of disorders associated with voltage gated ion channel disorders, including demyelinating diseases i.e. multiple sclerosis, optic neuromyelitis, disseminated encephalomyelitis, adrenoleukodystrophy, acute transverse myelitis, progressive multifocal leukoencephalopathy, sub acute sclerosing panecephalomyelitis (SSPE), metachromatic leukodystrophy, celerosing panecephalomyelitis (SSPE), metachromatic leukodystrophy, celerosing panecephalomyelitis (SSPE), metachromatic leukodystrophy, celerosing huntington's, compression, entrapment neuropathies i.e. nerve palsy, and carpal tunnel syndrome, cardiovascular disorders, i.e. cardiac arrhythmias and congestive heart failure, reactive glossis, hyperglycaemia, immunosuppression, cocaine addiction, cancer, cognitive dysfunction, neurotransmitter disorders (1.e. Baton-Lambert syndrome) and reversal of curare and other neuromuscular blocking drugs. The reversal of curare and coher neuromuscular blocking drugs. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neurological disorder is a seizure, preferably one associated with epilopsy. The neurological disorder is a neurotoxic injury associated with hypoxia, anoxia or ischaemia. The neurotoxic injury is associated with stroke, cerebrovascular accident, brain or spinal cord trauma, myocardial infarct, physical trauma, drownings, suffocation, perinatal asphyxia or hypoglycaemic events. The disorder is pain i.e. migraine, acute pain, persistent pain, neuropathic pain, nociceptive pain. The disorder is inflammation or a cardiovascular disorder. A conotoxin
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peptide of is useful to alleviate pain in a mammal in pain or about to be subjected to a pain causing event, and to treat disorders associated with radical depolarisation of excitable membranes by activating a KATP
                                                                                                                                              radical depolarisation of excitable membranes by activating a KATP channel, the disorders include cardiac, ocular and cerebral ischaemia and
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Example 2; Page 42; 195pp; English.

The invention relates to isolated omega-conopeptides, nucleic acid sequences encoding them, and propeptide sequences. The activity of the peptides of the invention may be described as, analgeaic, anticonvulsant, vasocropic, cardiant, neuroprotective, cerebroprotective, cardinory antinifammatory, antimigraine, antidiabetic, tranquiliser, vulnerary, antipsychotic, anxiolytic and neuroleptic. Peptides of the invention act by modulating the activity of voltage gated ion channels. They may be used for treating or preventing disorders, associated with voltage gated ion channels such as neurological disorders, e.g. seizure (associated with epilepsy), neurotoxic injury associated with conditions of hypoxia, 7 Gaps 5 Score 62; DB 4; Length 76; Pred. No. 14; 6; Mismatches 9; Indels Query Match ' 38.5%; Best Local Similarity 39.3%; Matches 11; Conservative Sequence 76 AA;

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Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiant; neuroprotective; cerebroprotective; cardiovascular; antiinflammatory; antimigraine; antidiabetic; tranquiliser; vulnerary; antipsychotic; anxiolytic; neuroleptic; voltage gated ion channel; seizure; epilepsy; neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia; stroke; cerebrovascular accident; brain trauma; spinal chord trauma; atroke; suffocation; perinatal asphyxia; hypoglycaemic event; pain; migraine; inflammation; cardiovascular disorder; psychiatric disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               voltage gated ion channels e.g. pain, inflammation, neurologic or cardiovascular disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shon K;
                                                                                                                                                                                                                                                                                                                                                  "OTHER is Pro or Hydroxy Pro"
                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "OTHER is Pro or Hydroxy Pro"
                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= OTHER
/note= "OTHER is Pro or Hydroxy Pro"
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                                                                                                                                            Omega-conopeptide E6.2 generic toxin sequence
48 CNEAQEHCTQN-PDCCSESCNKFVGRCL 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mcintosh JM, Watkins M,
Jones RM, Cartier GE;
                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                             psychosis; anxiety; schizophrenia.
                                                                       ABB96741 standard; peptide; 27
                                                                                                                                                                                                                                                                                                                                       label= OTHER
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                                                                                                                                                                                                                                                                                                                                                                                                             label= OTHER
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05-FEB-2001; 2001US-0265888P.
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us-10-627-685a-26.rag

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anoxia, ischaemia, stroke, cerebrovascular accident, brain or spinal bord trauma, drowning, suffocation, perinatal asphyxia or hypoglycaemic events; pain e.g. migraine; inflammation or cardiovascular disorders. They may also be used for treating psychiatric disorders e.g. psychosis, anxiety or schizophrenia. The analgesic agents of the invention show sequences given in records ABB96698-ABB96806 represent omega-conopeptide generic toxin sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequences given in AAR39608-30 are omega conopeptides (OCTS) and derivatives of these, which may be used to produce analgesia in a mammal. These OCTS inhibit voltage-gated calcium channels selectively in neuronal tissue. This is shown by the peptides ability to stimulate contraction in guinea pig ileum and to bind to OCT MVIA binding sites present in marine snails of the genus Conus, and act as calcium channel blockers. These OCTS may be used to replace opiods in the treatment of chronic pain or to reduce the opiod dosage required. This helps to reduce dependence on and tolerance to opiod narcotics. (Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of omega-cono-peptide(s) which selectively inhibit voltage-gated calcium channels - to induce analgesia, enhance opiate analgesics, treat
                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Omega conopeptide; OCT; analgesia; inhibition; voltage-gated; calcium channel; neurone; contraction; guinea pig; ileum; MVIIA; binding site; toxin; marine; snail; Conus; opiod; chronic pain;
                                                                                                                                                                                                      1;
                                                                                                                                                                       Length 27;
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                                                                                                                                                                       DB 5;
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                                                                                                                                                                     Score 61.5; D
Pred. No. 6.9;
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                                                                                                                                                                                                                                                                                                                              AAR39616 standard; peptide; 26
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                                                                                                                                                                  38.2%;
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(first entry)
                                                                                                                                                               Query Match
Best Local Similarity 47.8
Matches 11; Conservative
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                                                                                                                                    Sequence 27 AA;
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Disulfide-bond
Disulfide-bond
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20-DEC-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             narcotics.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Use of omega-cono-peptide(s) which selectively inhibit voltage-gated calcium channels - to induce analgesia, enhance opiate analgesics, treat
                                                                                Gaps
                                                                                                                                                                                                                                                                                                 Omega conopeptide; OCT; analgesia; inhibition; voltage-gated; calcium channel; neurone; contraction; guinea pig; ileum; MVIIA; binding site; toxin; marine; snail; Conus; opiod; chronic pain;
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                                                                            12; Indels
                                                  Score 61; DB 2;
Pred. No. 7.6;
4; Mismatches 12
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                                                                                                1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                               Location/Qualifiers
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                                                                                                                                                                                   AAR39617 standard; peptide; 26
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                                                  37.9%;
38.5%;
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(first entry)
                                                                          Conservative
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                                                           Similarity
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                       Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                Disulfide-bond
Modified-site
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Disulfide-bond
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20-DEC-1993
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PN field.)
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                                               Query Match
Best Local 3
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Length 26;

DB 2;

37.9%; Score 61;

Sequence 26 AA;

Query Match

RESULT 9

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91US-00789913.
92US-00916478.
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38.5%;
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                               Ouery Match
Best Local Similarity 38.5.
E-thea 10; Conservative
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Disulfide-bond
Disulfide-bond
             Sequence 26 AA;
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Yamashiro DH;
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08-SEP-1993
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                                                                                                                                                                                                                                                                                                                                                                                        AAR37761;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   delayed treatment;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ischaemia, neuronal, omega-conotoxin, OCT, MVIIA, MVIIC, MVIID, MVIIB, GVIA, GVIIA, RVIA, SVIA, TVIA, SVIB, SNX-207; stroke, delayed treatmen antihistamine, blood pressure, N-type voltage-gated Ca currents,
                                    Gaps
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                                    Indels
                                    12;
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                                    4; Mismatches
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          Pred. No.
                                                                                                                   Fox JA,
                                                                                 1 CRIXNOKCFQHLDDCCSRKCNRFNKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 1; 103pp; English.
                                                                                                                                                                                                                                                           AAR37762 standard; peptide; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92WO-US009766.
38.5%;
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92US-00916478
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                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1, .16
                                                                                                                                                                                                                                                                                                                                                                 (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1993-182487/22
       Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Miljanich GP,
Yamashiro DH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9310145-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-NOV-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-JUL-1992;
                                                                                                                                                                                                                                                                                                                                                              25-MAR-2003
08-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                               AAR37762;
                                                                                                                                                                                                                                                                                                                                                                                                                                          SNX-231
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Ischaemia-related neuronal damage in mammals is reduced by admin., 4-24

CC hr after onset of ischaemia, of a cpd. (I) which binds selectively to an omega-conotoxin (oCT) WVIA site in neuronal tissue. (I) has selectivity of at least 100 expressed as ratio of binding affinity for the MVIIA site to that for the MVIIC site. (I) is one of the oCTS MVIIA, MVIIB, GVIA, GVIIA or RNA or it is the cpd. SNX-207. (I) is esp. used to reduce neuronal damage caused by stroke. By delaying admin. for some time (compare USSOS1403 where cpds. are given within 1 hr of the onset of ischaemia) a greater redn. in neuronal damage is achieved. (I) is admin. e.g. by circular (ICV) injection at 0.1-20 microg/kg, but can also contracted the creatment with antihistamines to minimise redn. in blood pressure caused by (I)). (I) is also at least as effective as the specified conotoxins for (I) selective inhibition of N-type voltage. CC gated Ca currents in neuronal tissue and (2) selective inhibition of N-type voltage. CC channel mediated neurotransmitter release in neuronal tissue. Primary comega-conopeptides are given in AAR37752-62. Several analog correct PN field.)
                                     ö
                                                                                                                                                                                                                                                                                                                                                         Ischaemia, neuronal; omega-conotoxin; OCT; MVIIA; MVIIC; MVIID; MVIIB; QVIA; GVIIA; RVIA; SVIA; TVIA; SVIB; SMX-207; stroke; delayed treatment; antihistamine; blood pressure; N-type voltage-gated Ca currents; N-channel mediated neurotransmitter release.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Redn. of neuronal damage caused by ischaemia – by admin. of cpds. that bind specifically to omega-conotoxin MVIIA binding sites.
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bitner RS;
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DB 2; Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bowersox SS, Fox JA, Valentino KL,
                                     12;
              Pred. No. 7.6;
4; Mismatches
 Score 61;
                                                                                            1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure, Fig 1, 103pp, English.
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us-10-627-685a-26.rag

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AAM19544-W19553 are naturally occurring omega conopeptides (OCs) isolated from Conus sp. (cone snails). The peptides and their analogues are used as analgesics acting by blocking N-type voltage-sensitive calcium channels. The OCs can be used to treat neuropathic pain as a result of e.g. insult to the spinal cord or peripheral nerves, cancer, bone curopathy, diabetic neuropathy, hyperesthesia, allodynia or represented to presented in a medicament via an equival route in a continuous infusion or sustained release formulation. The OCs can provide pain relief when administered diducally in the absence of a permeation enhancer, at doses that are comparable to effective analgesic doses using intrathecal administration. OC formulations comprising an OC and acroboxylic acid buffer anti-oxidant. They also confer stability to solutions containing them for prolonged corrections in the statement methods and long-term storage. (Updated on 27-AUG-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stable omega conopeptide compositions - for producing analgesia and for inhibiting progression of neuropathic pain disorders.
                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kristipati R;
                                                                                                                                                                                                                                                                                                                                                     Conopeptide; cone snail; pain; analgesic; neuropathy; epidural; N-type voltage-sensitive calcium channel; block; Conus.
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                                                                                                                                                                                                                                                                                                                    Natural omega-conopeptide MVIIC/SNX-230 used for pain relief.
                                           37.9%; Score 61; DB 2; Length 26; larity 38.5%; Pred. No. 7.6; Conservative 4; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bowersox SS, Gohil K, Adriaenssens PI,
Pettus MR, Luther RR;
                                                                                                      1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                         Disclosure; Fig 2; 47pp; English
                                                                                                                                                                                                            AAW19552 standard; peptide; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96WO-US011041
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96US-00613400,
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(first entry)
                             Ouery Match
Best Local Similarity
Thes 10; Conserve
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                Sequence 26 AA;
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08-MAR-1996;
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13-OCT-1997
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                                                                                                                                                                               RESULT 93
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Conus genus; marine snail; cone snail; omega-conopeptide; analgesia; conociceptive pain; neuropathic pain; neuropal tissue; conotoxin; inflammation; schizophrenia; tardive dyskinesia; acute dystonic reaction; rheumatoid arthritis; epilepsy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             subject. The method comprises administration of an onega-conopeptide fidefective to: (i) block voltage-gated calcium channels; (ii) bind with high affinity to an omega-conopeptide binding site; and (iii) inhibit neurotransmitter release from nervous tissue. The method is used to treat produce analgesia (sepecially in subjects experiencing neuropathic pain); produce analgesia (sepecially in subjects experiencing neuropathic pain); and to treat schizophrenia, tardive dyskinesia and acute dystonic represents a natural omega-conopeptide. Omega-conopeptides are components of peptide toxins produced by marine snails of the genus Conus, and which exit as calcium channel blockers. (Updated on 27-AUG-2003 to correct OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treatment of inflammation, comprises administration of omega-conopeptide - effective to block voltage-gated calcium channels, bind with high affinity to omega-conopeptide binding site, and inhibit neuro-transmitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A method has been developed for the treatment of inflammation in a
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Pred. No. 7.6;
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                                                                                                                                                                                          Conus genus natural omega-conopeptide MVIIC/SNX-230.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gohil KC,
1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
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                                                                                                                                                                                                                                                                                                                                                                                      96US-00742774.
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                                                                                                                                                                                                                                                                                                                                                                                                                  91US-00814759.
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                                                                                      AAW72614 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37.9%;
                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 38.5 les 10, Conservative
                                                                                                                                                 (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-582596/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (NEUR-) NEUREX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Miljanich GP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996;
                                                                                                                                                27-AUG-2003
06-JAN-1999
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03-JUL-1996;
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                                                                                                                  AAW72614;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             release.
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Matches
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ID AAW7
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1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26

AAW72613 standard; peptide; 26 AA.

ó;

Gaps

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Score 61; DB 2; Length 26; Pred. No. 7.6; 4; Mismatches 12; Indels

37.9%;

Query Match Best Local Similarity 38.5 Matches 10; Conservative

Query Match

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Conub.

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conopeptides. Omega-conopeptides are components of peptide toxins produced by marine snails of the genus Conus, and which act as calcium channel blockers. The invention relates to a method of producing analgesia in a mammal that comprises administering an omega conopeptide having activities in (a) inhibiting electrically stimulated contraction of guinea pig lleum and (b) selectively binding to omega conopeptide WVIA binding sites in neuronal tissue, where these activities are within the ranges of those of omega-conotoxins MVIA and TVIA. The method is used for treating chronic pain, especially neuropathic pain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequences AAW95564-573 represent primary sequences of natural omega-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Production of analgesia in mammal - by administration of omega cono-
                                                                                          toxin; snail; calcium channel blocker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Omega-conopeptide, peptide toxin; snail; calcium channel blocker; analgesia; guinea pig ileum; omega-conotoxin; pain; neuropathic.
                                                                                          Omega-conopeptide, peptide toxin, snail, calcium channel blocker
analgesia, guinea pig ileum, omega-conotoxin, pain, neuropathic.
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Pred. No. 7.6;
4; Mismatches 12; Indels
                                                                                                                                                                                                                                                /label= 4Hyp
/note= "4-Hydroxyproline"
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                                                                                                                                                                                                          Location/Qualifiers
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                                                      Omega-conopeptide SNX-231.
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                            Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Miljanich GP,
                                                                                                                                                                                                                                                                                     Modified-site
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                  29-MAR-1999.
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                                                                                                                                                    Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A method has been developed for the treatment of inflammation in a subject. The method comprises administration of an omega-conopeptide effective to: (i) block voltage-gated calcium channels; (ii) bind with high affinity to an omega-conopeptide binding site; and (iii) inhibit neurotransmitter release from nervous tissue. The method is used to treatmention and associated pain. The treatment can also be used to produce analgesia (sepecially in abbjects experiencing neuropathic pain); and to treat schizophrenia, tradive dyskinesia and acute dystonic reactions, rheumatoid archritis, and epilepsy. The present sequence represents a natural omega-conopeptide. Omega-conopeptides are components of peptide toxins produced by marine snails of the genus Conus, and which act, as calcium channel blockers. (Updated on 27-AUG-2003 to correct OS
                                                                                                                                                Conus genus; marine snail; cone snail; omega-conopeptide; analgesia; nostoceptive pain; neuropathic pain; neuropal tissue; conotoxin; inflammation; schizophrenia; tardive dyskinesia; acute dystonic reaction; rheumatoid arthritis; epilepsy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treatment of inflammation, comprises administration of omega-conopeptide - effective to block voltage-gated calcium channels, bind with high affinity to omega-conopeptide binding site, and inhibit neuro=transmitter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Justice A, Singh T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 61; DB 2; Length 26;
Pred. No. 7.6;
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                                                                                                              Conus genus natural omega-conopeptide SVX-231.
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                                                                                                                                                                                                                                                                                                                       /label= Hyp
/note= "hydroxyproline"
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                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               96US-00742774.
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38.5%;
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96US-00675354
                                                                        (first entry)
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                                                      (revised)
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03-JUL-1996;
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                                                    27-AUG-2003
06-JAN-1999
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                AAW72613;
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release

field.)

Matches

8 셤

Singh T;

Justice A,

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Gaps

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AAW95572 standard; protein; 26 AA

RESULT 96 AAW95572 ID AAW95 XX AC AAW95

AAW95572

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A method has been developed of selecting a test compound for treating inflammation. The method comprises measuring the activity of the test compound in blocking voltage-gated calcium channels, binding to the omega conopeptide binding site and inhibiting norepinephrine (noradrenaline) release from nervous tissue. The method is useful for selecting compounds for treating inflammation. The selected compounds are capable of producing analgesia in a mammalian subject with chronic or intractable pain. Analgesia caused by selected compounds may reduce the reliance on polioid analgesic agents of the prior art which cause dependency and tolerance, requiring potentially dangerous increases in opioid doses to achieve the analgesic effect. The present sequence represents an omega conopeptide given in the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Omega-conotoxin, venom, predatory marine snail, N-type calcium channel, neuronal damage reduction, ischemia, analgesia, opiate analgesia, schizophrenia, stimulant induced psychosis, hypertension, inflammation,
                                                                                                                                                                                         Measuring the activity of test compounds in blocking voltage-gated calcium channels, binding to the omega conopeptide binding site and inhibiting norepinephrine (noradrenaline) release for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bronchotension; neuropathic pain; voltage sensitive calcium channel
                                                                                                                         Valentino KL, Miljanich GP, Gohil KC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37.9%; Score 61; DB 3; Length 26; 38.5%; Pred. No. 7.6; tive 4; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nielsen KJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amino acid sequence of an omega-conotoxin MVIIC.
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1 CKGKGAPCRKTMYDCCSGSCGRRGKC 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CRIXNOKCFOHLDDCCSRKCNRFNKC
                                                                                                                                                                                                                                                                                    Disclosure, Fig 1; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY43715 standard; peptide; 26 AA.
             93US-00049794.
96US-00675354.
96US-00742774.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10; Conservative
                                                                                   (ELAN-) ELAN PHARM INC.
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                                                                                                                       Singh T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                           WPI; 2000-038270/03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 26 AA;
             15-APR-1993;
03-JUL-1996;
01-NOV-1996;
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                                                                                                                                                                                                                                                inflammation.
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                                                                                                                       Justice A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequences AAM95564-573 represent primary sequences of natural omegaconopeptides. Omega-conopeptides are components of peptide toxins produced by marine snalls of the genus Conus, and which act as calcium analgesia in a mammal that comprises administering an omega conopeptide baving activities in (a) inhibiting electrically stimulated contraction guinea pig ileum and (b) selectrically binding to omega conopeptide WIIA binding sites in neuronal tissue, where these activities are within used for treating chronic pain, especially neuropathic pain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Omega conopeptide; analgesic; nociceptive; neuropathic; pain; conotoxin; marine snaal; peptide toxin; inflammation; binding; voltage-gated calcium channel; inhibition; norepinephrine; noradrenaline; anti-inflammatory.
                                                                                                                                                                                                                                                                                                                                                                                          Production of analgesia in mammal - by administration of omega cono-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37.9%; Score 61; DB 2; Length 26; 38.5%; Pred. No. 7.6; iive 4; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                Justice A,
                                                                                       /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                            Valentino KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Natural omega conopeptide MVIIC/SNX-233.
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                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 1B; 59pp; English.
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                                                                                                                                                                                               96US-00675354
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93US-00049794
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                                                                                                                                                                                                                                                                                                                        Gohil KC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 38.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                    (NEUR-) NEUREX CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 26 AA;
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                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                      Miljanich GP,
                                                                                                                                                                                               03-JUL-1996;
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15-APR-1993;
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Synthetic.
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                  Conus sp.
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AAY56481;

RESULT 98 AAY56481 ID AAY

8 셤 Conus sp

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Gaps

omega conopeptide binding site and inhibiting norepinephrine release.

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                                                                          The present sequence represents an omega-conotoxin. Omega-conotoxins are isolated from women of predatory marine snails, and have a selectivity for N-type calcium channels over P/Q type channels, and so block N-type calcium channels. The omega-conotoxins of the invention can be used in any disease or disorder where blockage of N-type calcium channels is required, e.g. in the reduction of neuronal damage following ischemia, production of analgesia, or enhancement of opiate analgesia, in the treatment of schizophrania, stimulant induced psychoses, hypertension, inflammation, and diseases which cause bronchotension, and also in the inhibition of progression of neuropathic pain. They can also be used in screen to identify compounds with activity at N-type voltage sensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Selecting a compound for producing analgesia involves measuring activity of test compound in blocking voltage-gated calcium channels, binding to
 peptides used for the treatment of disorders and diseases where
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                                                                                                                                                                                                                                                                                                                    37.9%; Score 61; DB 3; Length 26; 38.5%; Pred. No. 7.6;
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Novel peptides used for the treatment of disorders a
blockage of the N-type calcium channels is required.
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                                              Disclosure; Page 12; 81pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB14377 standard; peptide; 26 AA
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93US-00049794.
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                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                         calcium channels
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Disulfide-bond
Disulfide-bond
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                                                                      The present sequence is an omega-conopeptide from marine snails of the genus Conus. Omega-conopeptides are components of peptide toxins produced by the cone snails, and which act as calculum channel blockers. Natural omega-conopeptides and their derivatives may be useful for producing analgesia in nociceptive and neuropathic pain. The peptides bind to omega-conopeptide binding sites, which are present mainly in neuronal tissue, and inhibit norepinephrine release from nervous tissue. Conopeptides such as MVIIA and TVIA are effective as therapeutic agents for treating neurogenic conditions such as schizophrenia, tardive dyskinesia and acute
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Pred. No. 7.6;
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                                      Disclosure, Fig 1; 58pp; English.
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S-09-949-016-9481
S-09-641-612-2
US-08-675-354-29
US-08-965-918-29
US-09-138-439-29
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US-09-215-9
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     \begin{array}{c} \mathsf{unu}_{\mathsf{un}} \mathsf{un}_{\mathsf{un}} \mathsf{un}_{\mathsf{un}_{\mathsf{un}} \mathsf{un}_{\mathsf{un}} \mathsf{un}_{\mathsf{un}} \mathsf{un}_{\mathsf{un}} \mathsf{un}_{\mathsf{un}} \mathsf{un}_{\mathsf{un}} \mathsf{un}_{\mathsf{un}} 
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                                                                                                                                     April 18, 2005, 20:24:17; Search time 30.5 Seconds (without alignments) 66.083 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence 19, Ar. Sequence 8, App. Sequence 167, Asp. Sequence 29, App. S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1
Sequence 1
Sequence 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jued_Patents_AA:*
/cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                      GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-619-936-1

US-07-78-91-19

US-08-496-847-19

US-08-496-847-19

US-08-72-77-19

US-08-55-918-19

US-08-965-918-19

US-09-298-017-19

US-09-298-017-19

US-09-298-017-19

US-09-298-017-19

US-08-496-847-8

US-08-496-847-8

US-08-496-847-8

US-08-496-847-8

US-08-138-491-8

US-08-138-491-8

US-08-138-49-8

US-08-613-400A-8

US-09-894-882-167
                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-742-774-29
                                                                                                                                                                                                                US-10-627-685A-26
161
1 CRIXNOKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                          513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries
                                                                                                    protein search, using sw model
                                                                                                                                                                                                                                                                                                BLOSUM62DX
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                     length: 0
length: 2000000000
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                                        Copyright
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Match
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Maximum DB seq
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62.5
62
61
61
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                                                                                                  protein -
                                                                                                                                                                                                                                                           Sequence:
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С
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No.
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LOCATION: 4
COTHER INFORMATION: /product= "4Hyp"
OTHER INFORMATION: /note= "Amino acid 4 may be 4-trans-hydroxyproline."
                                                                                                                                                                                          APPLICANT: Tetrau, Heinrich
APPLICANT: Shon, Ki-Joon
APPLICANT: Grilley, Michelle
APPLICANT: Grilley, Michelle
APPLICANT: Grilley, Michelle
APPLICANT: Glivera, Baldomero M.
TITLE OF INVENTION: Conotoxin Peptide PVIIA
NUMBER OF SEQUENCES:
ADDRESSE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Mashington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUPER: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/619,936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
100.0%; Score 161; DB 1;
Best Local Similarity 100.0%; Pred. No. 3.9e-12;
Matches 27; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24260-107574-04
ALIGNMENTS
                                                                                                                    Sequence 1, Application US/08619936
Patent No. 5672682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: SAXe, Stephen A.
REGISTRATION NUMBER: 38,609
REFERENCE/CDOCKET NUMBER: 24260
TELEFRANION NUMBER: 202-962-484
TELEFANION SOURCET NUMBER: 252600
TELEFANION: 202-962-8300
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Conus purpurascens
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1..16
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8..20
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15..26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY:
LOCATION:
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LOCATION:
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; LOCATION:
US-08-619-936-1
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GENERAL INCORMATION:
APPLICANT: Miljanich, George P.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Pox, James A.
APPLICANT: Pox, James A.
APPLICANT: Valentino, Karen L.
APPLICANT: Valentino, Karen L.
APPLICANT: Valentino, Delayed Treatment Method of Reducing TITLE OF INVENTION: Delayed Treatment Damage NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSES: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 46.6%; Score 75; DB 1; Length 26; Best Local Similarity 42.3%; Pred. No. 0.023; Matches 11; Conservative 5; Mismatches 10; Indels
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US-07-789-913-19
Sequence 19, Application US/07789913
Patent No. 5559095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-049-794-19
Sequence 19, Application US/08049794
Patent No. 5587454
GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: GOHIL, KISHOR C
APPLICANT: GOHIL, KISHOR C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: AMINO ACID
                                                                                                                                                                                                                                                                         USA
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HYPOTHETICAL:
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                                                                                                                                                                                                                                                          STATE: CA
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Gaps

Indels

1 CRIXNOKCFQHLDDCCSRKCNRFNKCV 27 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27

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APPLICANT: SINGH, TEJINDER
APPLICANT: GOHLL, KISHOR C
APPLICANT: GOHLL, KISHOR C
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA AND
TITLE OF INVENTION: BAHANCING OPIATE ANALGESIA AND
TITLE OF LOWENTON: ANANCING OPIATE ANALGESIA AND
TITLE OF INVENTION: ANANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSER: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 46.6%; Score 75; DB 1; Length 26; Best Local Similarity 42.3%; Pred. No. 0.023; Matches 11; Conservative 5; Mismatches 10; Indels
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,774
                             COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,847
FILING DATE: 27-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.31
TELEPRAN: 650-324-0980
TELEFRAX: 650-324-0980
TELEFRAX: 650-324-0960
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TURE A mino acids
TURE A mino acids
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US-08-496-847-19.
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CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: 08/675,354
FILING DATE: 03-UUL-1996.
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-APR-15
APPLICATION NUMBER: US/08/14,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 19, Application US/08742774
Patent No. 5824645
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Stratford, Carol A. REGISTRATION NUMBER: 34,444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
HVPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Pal
STATE: CA
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-742-774-19
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Sequence 19, Application US/08496847
Sequence 10: 5795864
GENERAL INFORMATION:
APPLICANT: Amstutz, Gary A.
APPLICANT: Advisenseens, Peter I.
APPLICANT: Advisenseens, Peter I.
APPLICANT: Advisenseens Peter I.
APPLICANT: Advisenseens Peter I.
APPLICANT: Advisenseens Peter I.
APPLICANT: Kristipali, Remasharma
TITLE OF INVENTION: FORMULATIONS FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
APPLICANT: VALENTINO, KAREN LA APPLICANT: MILJANICH, GEORGE POLICANT: MILJANICH, GEORGE POLICANT: MILJANICH, GEORGE POLICALE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Law Offices of Peter Dehlinger STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 46.6%; Score 75; DB 1; Length 26; Best Local Similarity 42.3%; Pred. No. 0.023; Matches 11; Conservative 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/049,794

FILING DATE: 19930415

CLASSITCATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/814,759

FILING DATE: 30-DEC-1991

ATTORNEY/AGENT INFORMATION:

NAME: Stracford, Carol A.

REGISTRATION NUMBER: 34,444

REFERENCE/DOCKET NUMBER: 5865-0009.30

TELEPHONE: (415) 324-0860

TELEPHONE: (415) 324-0860

INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Dehlinger & Associates
350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE: SNX-202, FIGURE 2
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94306-1546
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-049-794-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4
US-08-496-847-19
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us-10-627-685a-26.rai

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Gaps
                                                                                                                                                                                                                                                                                                                     APPLICANT: ABECUTA: Gary A.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Gary A.
APPLICANT: Garial Kashorchandra
APPLICANT: Golil, Kishorchandra
APPLICANT: Kristipati, Ramasharma
TITLE OF INVENTION: METHODS AND FORMILATIONS FOR PREVENTING
TITLE OF INVENTION: PROGRESSION OF NEUROPATHIC PAIN
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                  Query Match
46.6%; Score 75; DB 2; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.023;
Matches 11; Conservative 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastESEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,918
FILING DATE: 07-NOV-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Mohr, Judy M.
REGISTRATION NUMBER: 38,563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.6%; Score 75; DB 2;
42.3%; Pred. No. 0.023;
tive 5; Mismatches 1:
             INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5865-0009.34
                                                                                                                                                                1 CRIXNOKCFOHLDDCCSRKCNRFNKC 26
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                                                                                                                                                                                                                                                                     Sequence 19, Application US/08965918
Patent No. 5891849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 19, Application US/09138439; Patent No. 5994305; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 58
TELECOMMUNICATION INFORMATION
TELEPHONE: 650-324-0880
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 42.3
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94306-1546
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: 'amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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US-08-675-354-19
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US-09-138-439-19
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APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR
APPLICANT: GOHIL, KISHOR
APPLICANT: GOHIL, KISHOR
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA AND
NUMBER OF SEQUENCES: 34
CORRESPONDENCE: ADDRESS:
ADDRESSEE: Law Offices of Peter Denlinger
STREET: 350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                             ch 46.6%; Score 75; DB 2; Length 26; 
l Similarity 42.3%; Pred. No. 0.023; 
11; Conservative 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
                                                                                                                                                                                                                       ; INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
US-08-742-774-19
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEC ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                            1 CKLKGQSCSRLMYDCCSGSCGRSGKC 26
                                                                                                                                                                                                                                                                                                                                                      1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
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Sequence 19, Application US/08675354
Patent No. 5859186
                                TELEPHONE: (415) 324-0860
TELEFAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 amino acids
                                                                                                                                                                    MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                amino acid
                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 11; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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STATE: CA
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Gaps
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APPLICANT: SINGH, TELINDER
APPLICANT: SINGH, TELINDER
APPLICANT: SOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: MILLANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: BNHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
CITY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match

46.6%; Score 75; DB 3; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.023;
Matches 11; Conservative 5; Mismatches 10; Indels
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                                                                           MEDIUM TIRE: Distactive
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastESE for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/613,400A
FILING DATE: 08-MAR-1996
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTONNEY/AGENT INFORMATION:
NAME: Stratford, Carol A
REGISORATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0019
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
US-08-613-400A-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 19, Application US/09298017 Patent No. 6087091
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APPLICATION NUMBER: 08/049,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
               ZIP: 94306-1546
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               650-324-0960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94306
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COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
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                                     APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: VALENTINO, KAREN L
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA AND
NUMBER OF INVENTION: BHANCING OPIATE ANALGESIA
CORRESPONDENCE ANDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 19, Application US/08613400A
| Sequence 19, Application US/08613400A
| Patent No. 6054429
| GENERAL INFORMATION:
| APPLICANT: Bowersox, S. Scott
| APPLICANT: Gadbois, Theresa APPLICANT: Luther, Robert, R. APPLICANT: Luther, Robert, R. TITLE OF INVENTION: IMPROVED EPIDURAL
| TITLE OF INVENTION: METHOD OF PRODUCING ANALGESIA NUMBER OF SEQUENCES: 36
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Dehinger & Associates STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/138,439
                                                                                                                                                                                                            E: Law Offices of Peter Dehlinger 350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5865-0009.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-04-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009...
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CKLKGQSCSRLMYDCCSGSCGRSGKC 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415) 324-0880
TELEPAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
                    SINGH, TEJINDER
GOHIL, KISHOR C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 42.3
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                              Palo Alto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-613-400A-19
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Query Match 46.6%; Score 75; DB 3; Length 26; Best Local Similarity 42.3%; Pred. No. 0.023; Matches 11; Conservative 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: All Janich, George P. APPLICANT: Bowersox, Stephen S. APPLICANT: Bowersox, Stephen S. APPLICANT: Pox, James A. APPLICANT: Pox, James A. APPLICANT: Valentino, Karen L. APPLICANT: Valentino, Karen L. APPLICANT: Yamashiro, Donald H. TITLE OF INVENTION: Delayed Treatment Method of Reducing TITLE OF INVENTION: Ischemia-Related Neuronal Damage NUMBER OF SEQUENCES: 28
ADDRESSEE: Law Offices of Peter Dehlinger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

44.1%; Score 71; DB 1; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.065;
Matches 11; Conservative 4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/789,913
FILING DATE: 19911112
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/561,766
FILING DATE: 02-AUG-1990
PILING DATE: 22-NOV-1989
ATTORNEY/AGENT INPOMBER: US 07/440,094
FILING DATE: 22-NOV-1989
ATTORNEY/AGENT INPOMBER: US 07/440,094
FILING DATE: 22-NOV-1989
ATTORNEY/AGENT INPOMBER: 34,444
REGISTRATION NUMBER: 34,444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSE: Law Offices of Peter Dehlinger STREET: 350 Cambridge Avenue, Suite 300 Carry: Palo Alto
                                              HYPOTHETICAL: NŌ

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: SNX-202, FIGURE 2

US-09-392-979A-19
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                                                                                                                                                                                                                                                                                                     1 CRIXNOKCFOHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 34306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/07789913
Patent No. 5559095
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HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 26 amino acids
TYPE: AMINO ACID
                       MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION
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46.6%; Score 75; DB 3; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.023;
Matches 11; Conservative 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: GOHIL, KISHOR C
APPLICANT: WALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
CORRESPONDENCE ADDRESS:
ADDRESSE: LAW Offices of Peter Dehlinger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/392,979A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Law Offices of Peter Dehlinger STREET: 350 Cambridge Avenue, Suite 300 CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-04-15
APPLICATION NUMBER: US 07/814,759
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009,30
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
US-09-298-017-19
                                                                                    5865-0009.30
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Patent No. 6136786
ATTORNEY/AGENT INFORMATION:

NAME: Stratford, Carol A.

REGISTRATION UNDRER: 34,444

REFERENCE/DOCKET NUMBER: 5865-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
TELEFRX: 26 amino acids
TYPE: amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (415) 324-0880
TELEPAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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US-09-392-979A-19
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STATE:
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Gaps

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APPLICANT: Kristipati, Ramasharma
TITLE OF INVENTION: METHODS AND
TITLE OF INVENTION: FORMULATIONS FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
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44.1%; Score 71; DB 1; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.065;
Matches 11; Conservative 4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TELINDER
APPLICANT: SINGH, TELINDER
APPLICANT: VALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
ITTE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
ITTLE OF INVENTION: ENHANCING OPIATE ANALGESIA
                                                                                                                                                                             STATE:
COUNTRY: US
ZIP: 94106-1546
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPAILINE
CONTREMT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,847
FILING DATE: 27-UUN-1995
CLASSIFICATION NUMBER: 34,444
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A
REGISTRATION NUMBER: 5865-0009.31
TELECHONE: 650-324-0880
TELEPHONE: 650-324-0880
TELEPHONE: FOR SEQ ID NO: 8:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CKLKGÓSCRKTSYDCCSGSCGRSGKC 26
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Patent No. 5824645
GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: Patentin Release #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Indels
                                                                                                                                                                                                                             APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: SOUTH, KISHOR C
APPLICANT: GOHIL, KISHOR C
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: FIDEDPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 19930415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Law Offices of Peter Dehlinger STREET: 350 Cambridge Avenue, Suite 300 CITY: Palo Alto STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FLINES DATE: 1930413
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Mismatches
                               1 CKLKGQSCRKTSYDCCSGSCGRSGKC 26
1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amstutz, Gary A.
Bowersox, Stephen S.
Gohil, Kishorchandra
                                                                                                                                                          Sequence 8, Application US/08049794
Patent No. 5587454
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/08496847
Patent No. 5795864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 42.3
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: AMINO ACID
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Ametutz
APPLICANT: Bowerso:
APPLICANT: Gohil, i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                 RESULT 13
US-08-049-794-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-049-794-8
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US-08-496-847-8
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APPLICANT: Bowersox, Stephen S.
APPLICANT: Gohil, Kishorchandra
APPLICANT: Adriaenseens, Peter I.
APPLICANT: Kristipati, Ramasharma
TITLE OF INVENTION: METHODS AND FORMULATIONS FOR PREVENTING
TITLE OF INVENTION: PROGRESSION OF NEUROPATHIC PAIN
WUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
44.1%; Score 71; DB 2; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.065;
Matches 11; Conservative 4; Mismatches 11; Indels
                                                                                                                                                                                                                                  ; TOPOLOGY: linear;
; MOLECULE TYPE: protein;
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1
US-08-675-354-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,918
FILING DATE: 07-NOV-1997
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         NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5865-0009.34
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Patent No. 5891849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 07-NOV-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Mohr, Judy M.
REGISTRATION NUMBER: 38,563
REFRENCE/DOCKET NUMBER: 5866
TELECOMMUNICATION INFORNATION:
TELEPHONE: 650-324-0880
                                                                                                                                                                                                       26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      650-324-0960
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EQUENCTH: 26 ammar vog: amino acid
                                                                                                                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: US
ZIP: 94306-1546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE
                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JS-08-965-918-8
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                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Patent No. 585186

GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: GOHIL, KISHOR C
APPLICANT: GOHIL, KISHOR C
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND TITLE OF INVENTION: BNANCING OPLATE ANALGESIA AND TITLE OF SEQUENCES: 34
CORRESPONDENCE ADDRESS: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

44.1%; Score 71; DB 2; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.065;
Matches 11; Conservative 4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 94306
COMPUTER READELE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/675,354
FILING DATE: 03-UUL-1996
CLASSIFICATION: 530
PROGRAPHICATION NUMBER: US/08/049,794
FILING DATE: 1993-APR-15
APPLICATION NUMBER: US/08/049,794
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1
                                       FILING DATE:
CLASSIFICATION
PRIOR APPLICATION DATA;
APPLICATION NUMBER: 08/675,354
FILING DATE: 03-JUL-1996
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-APR-15
APPLICATION NUMBER: US 07/814,759
ATTORNEY/AGENT INFORMATION:
NAMM: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Law Offices of Peter Deklinger
350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CKLKGÓSCRKTSYDCCSGSCGRSGKC 26
TRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,774
                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: Incar
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 350 Camb
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-742-774-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-675-354-8
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ATTORNEY AGENT INFORMATION:
NAME: Stratford, Carol A
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 586
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               650-324-0960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                 COUNTRY: US
ZIP: 94306-1546
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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                                            Gaps
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APPLICANT: SINGH, TEJINDER
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
Query Match (* 44.1%; Score 71; DB 2; Length 26; Best Local Similarity 42.3%; Pred. No. 0.065; Matches 11; Conservative 4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 71; DB 2; Length 26;
Pred. No. 0.065;
4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/138,439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-04-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTONEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 565-0009.30
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                  1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                       CKLKGQSCRKTSYDCCSGSCGRSGKC 26
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                                                                                                                                                                                                     US-09-138-439-8
; Sequence 8, Application US/09138439
; Patent No. 5994305
; GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 42.3;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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US-08-613-400A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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44.1%; Score 71; DB 3; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.065;
Matches 11; Conservative 4; Mismatches 11; Indels
APPLICANT: Gadbois, Theresa APPLICANT: Gadbois, Theresa APPLICANT: Pettus, Mark, R. APPLICANT: Luther, Robert, R. TITLE OF INVENTION: IMPROVED EPIDURAL TITLE OF SEQUENCES: 36 CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: ADDRESSE: Deblinger & Associates STREET: 350 Cambridge Avenue, Suite 250 CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/09298017
; Patent No. 6087091
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: WALGENTINO, KAREN L
; APPLICANT: MILLANINO, KAREN L
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESI)
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) ORIGINAL SOURCE:
) INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1
US-08-613-400A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: 08/08/613,400A
FILING DATE: 08-MAR-1996
CLASSIFICATION: 514
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CRIXNOKCFOHLDDCCSRKCNRFNKC 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44.1%; Score 71; DB 3; Length 26; 42.3%; Pred. No. 0.065; Live 4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: University of Utah Research Foundation APPLICANT: University of Utah Research Foundation APPLICANT: Cognetix, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Shetty, Reshma APPLICANT: Jimenez, Elsie C.
APPLICANT: McIntosh, J. Michael
APPLICANT: Watkins, Maren
APPLICANT: Jones, Robert M.
                                                                                                                                                                                                                                                                                                                                                                                                 ; INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1
US-09-392-979A-8
                                                                       NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: I-Superfamily Conctoxing FILE REFERENCE: 2314-238
CURRENT APLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
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PRIOR PLING DATE: 2000-10-27
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2001-01-29
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 CLSLGQRCERH-SDCCGYLCCFYDKCV 27
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Patent No. 6767895
                                 FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A
                                                                                                                                                                                                                                                                26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 42.33
Matches 11; Conservative
                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Conus betulinus
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              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL: 1 ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-894-882-369
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APPLICANT:
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APPLICANT: SOUTH, KISHOR C
APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: MILANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: BHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 44.1%; Score 71; DB 3; Length 26; Best Local Similarity 42.3%; Pred. No. 0.065; Matches 11; Conservative 4; Mismatches 11; Indels
                                      COMPUTER: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 APPLICATION DATA: US/09/298,017 PILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA

ZIP: 94306

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatchtIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/392,979A
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INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1
                                                                                                                                                                                                                                                                                                                                                           34,444
PP: 5865-0009.30
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APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-04-15
                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/049,794
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/09392979A
Patent No. 6136786
GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 58
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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COUNTRY:
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Gaps
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                                                                                                                                                                                                               38.5%; Score 62; DB 4; Length 76; 39.3%; Pred. No. 1.7; ive 6; Mismatches 9; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTRARY APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 19930415
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 29, Application US/08049794
; Sequence 29, Application US/08049794
; Patent No. 5587454
; GENERAL INFORMATION:
APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHLL, KISHOR C
APPLICANT: GOHLL, KISHOR C
APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: BEHANGING OPPATE ANALGESIA,
UNDER OF INVENTION: BHANGING OPPATE ANALGESIA,
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      METHODS OF PRODUCING ANALGESIA ENHANCING OPIATE ANALGESIA
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REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                           1 CRIXNOKCFQHLDDCCSRKCNRF-NKCV 27
                                                                                                                                                                                                                                                                                                                                           48 CNEAQEHCTQN-PDCCSESCNKFVGRCL 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 19930415
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
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TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
PRIOR FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 409
SOFTWARE: Patentin version 3.0
SEQ ID NO 207
LENGTH: 76
                                                                                                                                                                                                                 Query Match 38.5'
Best Local Similarity 39.3'
Matches 11; Conservative
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Best Local Similarity 38.5
Matches 10; Conservative
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                     TYPE: PRT
ORGANISM: Conus distans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: AMINO ACID
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Pred. No. 1.5;
5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: Olivera, Baldomero M.
APPLICANT: Watkins, Maren
APPLICANT: Watkins, Maren
APPLICANT: Hillyard, David R.
APPLICANT: McIntosh, J. Michael
APPLICANT: McIntosh, J. Michael
APPLICANT: Jones, Richard T.
APPLICANT: Jones, Robert M.
TITLE OF INVENTION: O-Superfamily Conotoxin Peptides
                                                                                                                                                    APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Shetty, Reshma
APPLICANT: Shetty, Reshma
APPLICANT: Shetty, Reshma
APPLICANT: Michael
APPLICANT: Molivera, Baldomero M.
APPLICANT: Watkins, Maren.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: University of Utah Research Foundation
                                                                                                                                                                                                                                                                                                                                                                      AFFLICANT: Shen, Greg S.
TITLE OF INVENTION: 1-Superfamily Conotoxins
FILE REFERENCE: 2314-298:
CURRENT APPLICATION: 1-Superfamily Conotoxins
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR APPLICATION NUMBER: US 60/245,581
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-11-14
PRIOR PILING DATE: 2000-11-14
PRIOR PILING DATE: 2000-11-14
PRIOR PILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: PRICENTIN VARIENT US 60/264,256
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SEQ ID NO 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 2114-227
CURRENT APPLICATION NUMBER: US/09/749, 637A
CURRENT FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: US 60/243,412
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US60/219,440
PRIOR FILING DATE: 2000-07-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39 CLSLGQRCERH-SDCCGYLCCFYDKCV 64
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APPLICATION NUMBER: US60/219,440
FILING DATE: 2000-07-20
APPLICATION NUMBER: US 60/214,263
FILING DATE: 2000-06-26
APPLICATION NUMBER: US 60/173,754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 207, Application US/09749637A
Patent No. 6762165
                                                                                            Sequence 167, Application US/09894882
Patent No. 6767895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 40.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                            Jones, Robert M.
Shen, Greg S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Conus betulinus
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                                                                      US-09-894-882-167
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APPLICANT:
APPLICANT:
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37.9%; Score 61; DB 2; Length 26; 38.5%; Pred. No. 0.89; Live 4; Mismatches 12; Indels
                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: WILDANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGE
TITLE OF INVENTION: EMANCING OPLATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                         Peter Dehlinger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSEE: Law Offices of Peter Dehlinger
T: 350 Cambridge Avenue, Suite 300
Palo Alto
               CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehling STREET: 350 Cambridge Avenue, Suite 300 CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-230, FIGURE 1
                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNDRER:
FILING DATE: 03-JUL-1996
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-APR-15
APPLICATION NUMBER: US/08/049,794
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,44
REGISTRATION NUMBER: 34,44
REGISTRATION NUMBER: 34,644
REGISTRATION NUMBER: 34,646
TELEPHONE: (415) 324-0860
ITELEPHONE: (415) 324-0960
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
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Patent No. 5859168
GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
                                                                                                                         ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 38.5'
Matches 10; Conservative
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USA
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STREET: 35
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                                                                                                     Sequence 29, Application US/08496847
Patent No. 5795864
GENERAL INFORMATION:
APPLICANT: Ametuz, Gary A.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Golil, Kishorchandra
APPLICANT: Ariaensens, Peter I.
APPLICANT: Kristipati, Ramasharma
TITLE OF INVENTION: METHODS AND
TITLE OF INVENTION: METHODS AND
TITLE OF INVENTION: FORMULATIONS FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN
NUMBER OF SEQUENCES: 36
CORRESPONDENCE 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Deblinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         METHODS OF PRODUCING ANALGE ENHANCING OPIATE ANALGESIA
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APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOBIL, KISHOR C
APPLICANT: WALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PI
TITLE OF INVENTION: ENHANCING OP
NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 29, Application US/08742774; Patent No. 5824645
                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
2IP: 94306-1546
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 38.5%
""" Andrea 10; Conservative
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US-08-742-774-29
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ADDRESSEE: Law Offices of Peter Dehlinger STREET: 350 Cambridge Avenue, Suite 300 CITY: Palo Alto STATE: CA COUNTRY: USA
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PRIOR APPLICATION BATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-04-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEPHONE: (415) 324-0960
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
                                                                                     TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE; SNX-230, FIGURE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INDIVIDUAL ISOLATE: SNX-230, FIGURE 1
                                                                                                                                                                                                                                                                                                                                                                       1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 29, Application US/09138439
Patent No. 5994305
                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 26 amino acids
amino acid
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL: 1
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US-09-138-439-29
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Sequence 29, Application US/08965918

Settent No. 5891849

GENERAL INFORMATION:
APPLICANT: Ametuz, Gary A.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Adriaensens, Peter I.
APPLICANT: Adriaensens, Peter I.
APPLICANT: Kristipati, Ramasharma
ITILE OF INVENTION: METHODS AND FORMULATIONS FOR PREVENTING
ITILE OF INVENTION: PROGRESSION OF NEUROPATHIC PAIN
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSES: Dehlinger's Associates
STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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Pred. No. 0.89;
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       CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

APPLICATION NUMBER:

CLASSIFICATION:

APPLICATION NUMBER:

APPLICATION NUMBER:

APPLICATION NUMBER:

FILING DATE:

APPLICATION NUMBER:

AREFERENCE/DOCKET NUMBER:

TELEFONMICATION INFORMATION:

TELEFONMICATION INFORMATION:

TELEFONE:

TELEFONE:

SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:
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OFFRATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,918
FILING DATE: 07-NOV-1997
CLASSIFICATION: 514
ATONNEY/AGENT INFORMATION:
NAMME: MOAR. JUDY M.
REGISTRATION NUMBER: 38,63
REFERENCE/DOCKET NUMBER: 5865-0009.34
TELEPHONE: 650-324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
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PC-DOS/MS-DOS
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Best Local Similarity 38.5%;
Matches 10; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
HVPOTHETICAL: NO
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Palo Alto
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US-08-965-918-29
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Gaps
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Query Match

37.9%; Score 61; DB 2; Length 26;
Best Local Similarity 38.5%; Pred. No. 0.89;
Matches 10; Conservative 4; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
NUMBER OF SOUDENCES: 34
CORRESPONDENCE ADDRESS:
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MOLECULE TYPE: protein HYPOTHETICAL: NO
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Best Local Similarity
....hes 10; Conservat
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                                                                                                                                                                                                                                                                     94306
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                                                APPLICANT:
APPLICANT:
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    Score 61; DB 2; Length 26;
Pred. No. 0.89;
                                           12; Indels
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                                                                                                                                                                                                               Sequence 29, Application US/08613400A
| Patent No. 605429
| GENERAL INFORMATION:
| APPLICANT: Bowersox, S. Scott
| APPLICANT: Gadbols, Theresa
| APPLICANT: Pettus, Mark, R. |
| APPLICANT: Luther, Nobert, R. |
| TITLE OF INVENTION: IMPROVED EPIDURAL |
| TITLE OF INVENTION: METHOD OF PRODUCING ANALGESIA |
| NUMBER OF SEQUENCES: 36 |
| CORRESPONDENCES: 36 |
| CORRESPONDENCES: Dehlinger & Associates |
| ADDRESSEE: Dehlinger & Associates |
| STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASLED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/613,400A
FILING DATE: 08-MAR.1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
                                         4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             AUNKESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; INDIVIDUAL ISOLATE: SNX-230, FIGURE 1
US-08-613-400A-29
                                                                             1 CRIXNOKCFOHLDDCCSRKCNRFNKC 26
                                                                                                    1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
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REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 58
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 650-324-0500
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
TRNGTH: 26 aming acids
37.9%;
l Similarity 38.5%;
10; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 38.5°
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein HYPOTHETICAL: NO
                  Best Local Similarity
Matches 10; Conserv
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ZIP: 94306-1546
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                                                                                                                                                                                                US-08-613-400A-29
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US-09-298-017-29
Query Match
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S-09-298-017-29 ". Sequence 29, Application US/09298017 Patent No. 6087091 GENERAL INFORMATION: APPLICANT: JUSTICE, ALAN

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37.9%; Score 61; DB 3; Length 26; ilarity 38.5%; Pred. No. 0.89; Conservative 4; Mismatches 12; Indels
                                                  METHODS OF PRODUCING ANALGESIA AND ENHANCING OPIATE ANALGESIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OF PRODUCING ANALGESIA AND
                                                                                                                                                                                                                                                                                                   COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/298,017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: METHODS OF PRODUCING ANALG
TITLE OF INVENTION: ENHANCING OPLATE ANALGESIA
NUMBER OF SEQUENCES: 34
                                          TITLE OF INVENTION: METHODS OF PRODUCING ANY TITLE OF INVENTION: ENHANCING OPIATE ANALGES NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger STREET: 350 Cambridge Avenue, Suite 300 CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5865-0009.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/049,794
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-07
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
TRANGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 29, Application US/09392979A
Fatent No. 6136786
GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: OGHIL, KISHOR C
APPLICANT: VALENITNO, KAREN L
APPLICANT: MILJANICH, GEORGE P
VALENTINO, KAREN L
MILJANICH, GEORGE F
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COUNTRY:
ZIP: 943
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Gaps
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APPLICANT: Rid, Thomas
APPLICANT: Rid, Thomas
APPLICANT: Tessier-Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REFERENCE: B88-031-3
CURRENT APPLICATION NUMBER: US/09/540,245A
CURRENT PILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 60/065,544
PRIOR FILING DATE: 1997-11-14
PRIOR FILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 735
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Goodman, Corey
APPLICANT: Goodman, Corey
APPLICANT: Brose, Katja
APPLICANT: Tebsier-Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REFERENCE: B98-031-3
CURRENT APPLICATION NUMBER: US/09/191,647
CURRENT FILING DATE: 1998-11-13
EARLIER APPLICATION NUMBER: 60/065,544
EARLIER FILING DATE: 1997-11-14
EARLIER FILING DATE: 1997-11-14
SERLIER FILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Ratentin Ver. 2.0
SEQ ID NO 9
LENGTH: 735
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                                                                                                                                                                                                                          DB 1;
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Best Local Similarity 38.5%; Pred. No. 0.97;
Matches 10; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                         1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
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US-09-191-647-9
; Sequence 9, Application US/09191647
; Patent No. 6046015
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                                                                                29 amino acida
                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
            202-962-8300
                                                                                                                                              MOLECULE TYPE: protein US-08-092-215-9
                                                                                                      TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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          TELEFAX:
                                                                                LENGTH:
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Pred. No. 0.89;
4; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/08092215
Patent No. 5591821
GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M.
APPLICANT: Hillyard, David R.
APPLICANT: Imperial, Julita S.
APPLICANT: Imperial, Julita S.
APPLICANT: Monje, Virginia D.
ITILE OF INVENTION: w-Conotoxin Peptides
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue N.W., Suite 1000
CITY: Washington
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/392,979A
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ZIP: 20005
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/092,215
                                                                                                                                                        PILING DATE:
CLASSIPICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-04-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY, AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34-44
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAM: (415) 324-0960
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-107674
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INDIVIDUAL ISOLATE: SNX-230, FIGURE 1
US-09-392-979A-29
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Best Local Similarity 38.5%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 530
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US-08-092-215-9
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TYPE: PRT

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                           cn 35.7%; Score 57.5; DB 4; Length 36; 1 Similarity 37.0%; Pred. No. 2.9; 10; Conservative 6; Mismarcher
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: University of Utah Research Foundation APPLICANT: Cognetix, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Shetry, Reshma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: MAICHIB, MAIREN
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: 1-Superfamily Conctoxins
FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US 60/
FRICH APPLICATION NUMBER: US 60/243,410
FRICH APPLICATION NUMBER: US 60/245,581
FRICH APPLICATION NUMBER: US 60/246,581
FRICH APPLICATION NUMBER: US 60/247,714
FRICH FILING DATE: 2000-11-08
FRICH FILING DATE: 2000-11-14
FRICH FILING DATE: 2000-11-29
FRICH FILING DATE: 2001-11-29
FRICH FILING DATE: 2001-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27
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PRIOR FILING DATE: 2000-11-14
PRIOR PEDLICATION NUMBER: US 60/264,256
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: Patentin version 3.0
SEQ ID NO 365
LENGTH: 36
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; Sequence 368, Application US/09894882
; Patent No. 6767895
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McIntosh, J. Michael
Olivera, Baldomero M.
Watkins, Maren
Jones, Robert M.
                                                                                                                                                                                                                                                                                                                               ORGANISM: Conus betulinus
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US-09-894-882-368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity Matches 10; Conserv
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US-09-894-882-371
                                                                                                                                                                                                                                                                                        TYPE: PRT
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APPLICANT: Goodwan, Corey
APPLICANT: Goodwan, Corey
APPLICANT: Todowan, Corey
APPLICANT: Tessier-Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REFERENCE: B98-031-3
CURRENT APPLICATION NUMBER: US/09/540,153
CURRENT APPLICATION NUMBER: 09/191,647
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: 60/081,057
PRIOR FILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 735
                                                                                                                                   Query Match
36.6%; Score 59; DB 3; Length 735;
Best Local Similarity 45.0%; Pred. No. 28;
Matches 9; Conservative 4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 36.6%; Score 59; DB 3; Length 735; Best Local Similarity 45.0%; Pred. No. 28; Matches 9; Conservative 4; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Shen, Greg S.
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: 1-Superfamily Conotcxins
FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-10-27
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
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; Patent No. 6767895
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                                                                                                                                                                                                                                                                                                     8 CFQHLDDCCSRKCNRFNKCV 27
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Patent No. 6270995
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                 ; ORGANISM: Caenorhabditis elegans US-09-540-245A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-894-882-365
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APPLICANT:
APPLICANT:
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Gaps
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                                                                                Query Match
35.7%; Score 57.5; DB 4; Length 36;
Best Local Similarity 37.0%; Pred. No. 2.9;
Matches 10; Conservative 6; Mismatches 10; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: University of Utah Research Foundation
APPLICANT: Walker, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Shetty, Reshma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 164, Application US/09894882
Batent No. 6767895
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Shetty, Reshma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Galler, Robert M.
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: I. Superfamily Conotoxins FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US 009/894,882
CURRENT APPLICATION NUMBER: US 60/243,410
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/245,581
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR PILING DATE: 2000-11-14
SROR FILING DATE: 2001-11-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE PATENTIN VEYSION 3.0
SOFTWARE PATENTIN VEYSION 3.0
                                                                                                                                                                                          1 CRIXNOKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                               2 CLSLGQRCERH-SNCCGYLCCFYDKCV 27
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                                                                                                                                                                                                                                                                                                                                                                                  Sequence 155, Application US/09894882 Patent No. 6767895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jimenez, Elsie C.
McIntosh, J. Michael
Olivera, Baldomero M.
Watkins, Maren
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McIntosh, J. Michael
Olivera, Baldomero M.
Watkins, Maren
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Shen, Greg S.
; ORGANISM: Conus betulinus
US-09-894-882-372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Conus betulinus
                                                                                                                                                                                                                                                                                                                                                           US-09-894-882-155
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Pred. No. 2.9;
6; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: University of Utah Research Foundation APPLICANT: Cognetix, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Shetty, Reshma
APPLICANT: Jimenez, Elsie C.
APPLICANT: McIntosh, J. Michael
APPLICANT: McIntosh, J. Michael
APPLICANT: Watkins, Maren
                                                                                                                                                                                                        TITLE OF INVENTION: 1-Superfamily Conotoxins FILE REFERENCE: 2314-238
FILE REFERENCE: 2314-238
FILE REFERENCE: 2314-238
FILE SAPPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR PLING DATE: 2000-10-27
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR PELING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/245,714
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR PILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-16
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: PATENTIN VETSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Jones, Robert M.
APPLICANT: Jones, Robert M.
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: I-Superfamily Conotoxins
FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT APPLICATION NUMBER: US 60/29
PRIOR APPLICATION NUMBER: US 60/249, PRIOR PLING DATE: 2000-06-30
PRIOR FILING DATE: 2000-10-27
PRIOR PLILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR PLILING DATE: 2001-01-09
PRIOR PLILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 CLSLGQRCERH-SNCCGYLCCFYDKCV 27
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US-09-894-882-372
Sequence 372, Application US/09894882:
Patent No. 6767895
                                                                             McIntosh, J. Michael
Olivera, Baldomero M.
Watkins, Maren
Jones, Robert M.
Shen, Greg S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 37.0%;
Matches 10; Conservative (
                                                      Jimenez, Elsie C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Conus betulinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-894-882-371
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LENGTH: 36
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39 CLSLGQRCERH-SNCCGYLCCFYDKCV 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Cognetix, Inc.
APPLICANT: Shetty, Reshma
APPLICANT: Shetty, Reshma
APPLICANT: Mcntosh, U. Michael
APPLICANT: Olivera, Baldomero M. APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: Matkins, Maren
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FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR PELLING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR APPLICATION NUMBER: US 60/264,256
NUMBER OF SEQ ID NOS: 506
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Pred. No. 5.5;
6; Mismatches
                      FILE REFERENCE: 2314-236
CURRENT APPLICATION NUMBER: US/09/894,682
CURRENT FILING DATE: 2001-66-29
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR PILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR PLING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR PLING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR FILING DATE: 2000-11-14
PRIOR PLING DATE: 2001-11-14
PRIOR PLING DATE: 2001-11-12
NUMBER OF SEQ ID NOS: 506
SOFTHARE: Patentin version 3.0
TITLE OF INVENTION: I-Superfamily Conotoxins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27
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Patent No. 6767895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 35.7%;
Best Local Similarity 37.0%;
Matches 10; Conservative
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Shen, Greg S.

// ORGANISM: Conus betulinus
US-09-894-882-164
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Sequence 18, Application US/08185432

Sequence 18, Application US/08185432

GENERAL INFORMATION:
APPLICANT: Attavanis-Teakonas, Spyridon
APPLICANT: Busseau, Isabelle
APPLICANT: Au Grain
APPLICANT: Xu, Tian
APPLICANT: Xu, Tian
APPLICANT: Nateuno, Kenji
TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 35.7%; Score 57.5; DB 4; Length 73; Best Local Similarity 37.0%; Pred. No. 5.5; Matches 10; Conservative 6; Mismatches 10; Indels
                                                                            APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Shetky, Reshma
APPLICANT: Shetky, Reshma
APPLICANT: McIntosh, J. Michael
APPLICANT: McIntosh, J. Michael
APPLICANT: Watkins, Maren
APPLICANT: Jones, Robert M.
APPLICANT: Shen, Greg S.
                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: 1-Superfamily Conotoxins FILE REFERENCE: 2314-238
                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR PLING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR PLING DATE: 2000-11-14
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOUTHARE: PATCHTING VERSION 3.0
SEQ ID NO 176
LENGTH: 73
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1155 Avenue of the Americas
Sequence 176, Application US/09894882
Patent No. 6767895
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COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Conus betulinus
US-09-894-882-176
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NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 2523
                                                                                                                                                                                                                                                                                                                                                                               US-08-937-236-6
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Sequence 3, Application US/08899232

Sequence 3, Application US/08899232

Sequence 3, Application US/08899232

Sequence 3, Application US/08899232

GENERAL INFORMATION:

APPLICANT: 01, Hullin

TITLE OF INVERTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON

FILE REFERENCE: 7326-046

CURRENT APPLICATION NUMBER: US/08/899,232

CURRENT FILING DATE: 1997-07-23

NUMBER OF SEQ ID NOS: 4

SOFTWARE: Patentin Ver. 2.0
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US-09-121-457-3
US-09-121-457-3

US-09-121-457-3

Sequence 3, Application US/09121457

Patent No. 6692919

GENERAL INFORMATION:

APPLICANT: Artavanis-Tsakonas, S.

APPLICANT: Qi, H.

APPLICANT: Rand, M.

TITLE NEFRENCE: 7326-673

CURRENT APPLICATION NUMBER: US/09/121,457

CURRENT APPLICATION NUMBER: 08/99-032

EAALLER APPLICATION NUMBER: 08/99-232

EAALLER FILING DATE: 1997-07-23
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,432
FILING DATE: 21-JAN-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: MAGENT INFORMATION:
NAME: MAGENT NUMBER: 18,872
REGISTRATION NUMBER: 18,872
REGISTRATION NUMBER: 12,2006
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEFAX: (212) 869-8864/9741
TELEFAX: CALA PERNIE
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 57; DB 4;
Pred. No. 1.4e+02
4; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 57; DB 1; Pred. No. 1.4e+4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        249 SGONCEENIDDCPSNNCRNGGTCV 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               249 SGONCEENIDDCPSNNCRNGGTCV 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 XNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 XNQKCFQHLDDCCSRKCNRFNKCV 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 37.5%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                          2523 amino acids
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Best Local Similarity 37.5
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: protein US-08-185-432-18
                                                                                                                                                                                                                                                                                                                                                                                  unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Xenopus sp.
                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 3
LENGTH: 2523
                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-899-232-3
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GENERAL INFORMATION:

APPLICANT: MANN, BARBARA J.

APPLICANT: PETRI, WILLIAM A.

APPLICANT: PETRI, WILLIAM A.

APPLICANT: PETRI, WILLIAM A.

APPLICANT: PETRI, WILLIAM A.

APPLICANT: DODSON, JAMES M.

TITLE OF INVENTION: SUBUNIT PEPTIDES AND REAGANTS SPECIFIC FOR MEMBERS OF THE TITLE OF INVENTION: 170 KD SUBUNIT MULTIGENE FAMILY

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSE: MORRISON & FOERSTER

STREET: 2000 PENNSYLVANIA AVENUE N.W., STE. 5500
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                                                                                           Length 2523;
                                                                                                                                           11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA

ZIP: 200006-1812
COMPUTER READABLE FORM:
MEDIUW TYPE: FIDOPY disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,236
FILING DATE: 16 SEPTEMBER 1997
ATTORNEY/AGENT INFORMATION:
FILING DATE: 16 SEPTEMBER 1997
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 33,949
REFERENCE/DOCKET NUMBER: 33,949
REGISTRATION NUMBER: 33,949
REGISTRATION NUMBER: 33,949
REGISTRATION NUMBER: 30-4030
INFORMATION FOR SEQ ID NO: 6:
SEQUINCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
                                                                                           Score 57; DB 4; I
Pred. No. 1.4e+02;
4; Mismatches 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 35.1%; Score 56.5; D
Best Local Similarity 43.3%; Pred. No. 87;
Matches 13; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CRIXNOKCFQHLDDCCSRK--CNRFN-KCV 27
                                                                                                                                                                                                                    249 SGONCEENIDDCPSNNCRNGGTCV 272
                                                                                                                                                                                       4 XNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/08937236
Patent No. 6187310
                                                                                           Query Match
Best Local Similarity 37.5%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1277 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
TYPE: PRT
ORGANISM: Xenopus sp.
US-09-121-457-3
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APPLICANT: MANN, BARBARA J.
APPLICANT: PETRI, MILLIAM A.
APPLICANT: PETRI, MILLIAM A.
APPLICANT: DODSON, JAMES M.
TITLE OF INVENTION: RECOMBINANT ENTAMOEBA HISTOLYTICA LECTIN
TITLE OF INVENTION: 3UBUNIT PEPTIDES AND REAGANTS SPECIFIC FOR MEMBERS OF THE
TITLE OF INVENTION: 170 KD SUBUNIT MULTIGENE FAMILY
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVENUE N.W., STE. 5500
CITY: WASHINGTON
               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIF: 200006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DATE PLOPS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11;
                                                                                                                                                                               FILLING UMALE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06890
FILING DATE: 17-JUN-1994
ATTORNEY AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959

REFERENCE DOCKET NUMBER: 9148-0006.21
TELEPHONE: (202) 887-1500

TELEPHONE: (202) 887-1501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 56.5; D
Pred. No. 88;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CRIXNQKCFQHLDDCCSRK--CNRFN-KCV 27
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REFERENCE/DOCKET NUMBER: 291482000622
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/569,214
FILING DATE: 16 SEPTEMBER 1997
ATTORNEY/AGENT INFORMATION:
NAME: LIVNAT, SHMUEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/08937236
Patent No. 6187310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35.1%;
43.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 1292 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (202) 887-076.
TELEX: 90-4030
INFORMATION FOR ESQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1292 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 43.33
Matches 13; Conservative
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: WASH
STATE: DC
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                                                                                                      APPLICANT: MANN, BARBARA J.
APPLICANT: PETRI, WILLIAM A.
APPLICANT: PETRI, WILLIAM A.
APPLICANT: PETRI, WILLIAM A.
APPLICANT: PETRI, WILLIAM A.
TITLE OF INVENTION: SUBUNIT PETRIDES AND REAGANTS SPECIFIC FOR MEMBERS OF THE
TITLE OF INVENTION: 170 KD SUBUNIT MULTIGENE FAMILY
MUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVENUE N.W., STE. 5500
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/08569214
Patent No. 6165469
GENERAL INFORMATION:
APPLICANT: MANN, BARBARA J.
APPLICANT: PETRI, WILLIAM A.
TITLE OF INVENTION: ENCOMBINANT ENTAWORBA HISTOLYTICA LECTIN
TITLE OF INVENTION: SUBUNIT PEPTIDES AND REAGANTS SPECIFIC FOR MEMBERS OF THE
TITLE OF INVENTION: 170 KD SUBUNIT MULTIGENE FAMILY
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: MORRISON & FOERSTER
STREET: 2000-PENNSYLVANIA AVENUE N.W., STE. 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
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                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3;
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35.1%; Score 56.5; D
Best Local Similarity 43.3%; Pred. No. 88;
Matches 13; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 718 CSMGTDNIITYHDDCNSRKSQCGNFNGKCV 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06890
FILING DATE: 17-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERRACE/DOCKET NUMBER: 29,959
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CRIXNQKCFQHLDDCCSRK--CNRFN-KCV 27
                              Sequence 5, Application US/08569214 Patent No. 6165469 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1292 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: protein US-08-569-214-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 51
US-08-569-214-6
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NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 2703
                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 8; Conserva
                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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US-08-899-232-4
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| Sequence 19, Application US/08185432
| GENERAL INFORMATION: Artavanis-Teakonas, Spyridon APPLICANT: Busseau, Isabelle APPLICANT: Diederich, Robert J. APPLICANT: Xu, Tian APPLICANT: Xu, Tian APPLICANT: Matsuno, Kenji TITLE OF INVENTION: DELFEX PROTEINS, NUCLEIC ACIDS, AND TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                           3
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/09641612
Fatent No. 6703221
GENERAL INFORMATION:
FAPLICAMT: VIVIOR CHAIN et al.
TITLE OF INVENTION:
FILE REFERENCE: PPO-1602.002 / 200130.498
CURRENT FILICE DATE 2000-08-17
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5:
LENGTH: 585
                                                                                                                                                                                                                                   DB 3; Length 1292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 34.8%; Score 56; DB 4; Length 585; Best Local Similarity 37.9%; Pred. No. 50; Matches 11; Conservative 2; Mismatches 14; Indels
                                                                                                                                                                                                                                                                         11; Indels
                                                                                                                                                                                                                           35.1%; Score 56.5; Di
43.3%; Pred. No. 88;
tive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                          718 CSMGTDNIITYHDDCNSRKSQCGNFNGKCV 747
                                                                                                                                                                                                                                                                                                               1 CRIXNQKCFQHLDDCCSRK--CNRFN-KCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          377 CRAGFAGPRCEHDLDDCAGRACANAGTCV 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CR -- IXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , LUCLATION: (1)...(585)
; OTHER INFORMATION: Xaa = Any Amino Acid US-09-641-612-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: PENNIE & EDMONDS STREET: 1155 Avenue of the Americas
TELEFAX: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
LENGTH: 1292 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                           Query Match
Best Local Similarity 43.39
Matches 13, Conservative
                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-937-236-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Ne
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 54
US-08-185-432-19
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US-09-641-612-5
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APPLICANT: Artavanis-Teakonas, Spyridon
APPLICANT: O. Hullin
TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON
FILE REFERENCE: 7326-046
CURRENT APPLICATION NUMBER: US/08/899,232
CURRENT FILING DATE: 1997-07-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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APPLICANT: Artavanis-Tsakonas, S.
APPLICANT: Rand, M.
APPLICANT: Rand, M.
TITLE OF INVENTION ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON FILE REFERENCE: 7326-073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 34.8%; Score 56; DB 1; Length 2703; Best Local Similarity 33.3%; Pred. No. 1.9e+02; Matches 8; Conservative 5; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 56; DB 4; Length 2703;
Pred. No. 1.9e+02;
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,432
FILING DATE: 21-JAN-1994
CLASSIFICATION: SO
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 7326-006
TELERPHONE: (212) 790-9090
TELERPHONE: (212) 790-9090
TELERPHONE: (212) 790-9090
TELERPHONE: (212) 869-8864/9741
TELEX: (6141 PENNIE
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
FENNIEL 27073 Aminto acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/121,457
CURRENT FILING DATE: 1998-07-23
EARLIER APPLICATION NUMBER: 08/899,232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         822 TGÓKCETNIDDCVTNPCGNGGTCI 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  822 TGQKCETNIDDCVTNPCGNGGTCI 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 XNQKCFQHLDDCCSRKCNRFNKCV 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/08899232
Patent No. 6436650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-121-457-4
; Sequence 4, Application US/09121457
; Patent No. 6692919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34.8%;
Similarity 33.3%;
8; Conservative
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APPLICANT: Miljanich, George P.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Fox, James A.
APPLICANT: Fox, James A.
APPLICANT: Valentino, Karen L.
APPLICANT: Wamshiro, Donald H.
TITLE OF INVENTION: Delayed Treatment Method of Reducing TITLE OF INVENTION: Ischemia-Related Neuronal Damage CORRESSEDNUBLES 28
CORRESPONDENCES 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
34.5%; Score 55.5; DB 1; Length 25;
Best Local Similarity 38.5%; Pred. No. 3.6;
Matches 10; Conservative 4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC_DOS/MO-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CHRRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/789,913
FILING DATE: 19911112
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/561,766
FILING DATE: 02-AMG-1990
FRIUNG APPLICATION DATA:
APPLICATION NUMBER: US 07/440,094
FILING DATE: 22-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REPREBENCE/DOCKET NUMBER: 5865-0005.30
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NOPMATION:
TELEPRAK: (415) 324-0860
INFORMATION FOR SEQ ID NO: 2:
SEQUINCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CRIXNOKCFOHLDDCCSRKCNRFNKC 26
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                                                                                                                     Sequence 2, Application US/07789913
Patent No. 5559095
GENERAL INFORMATION:
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Patent No. 5587454
GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 25 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94306
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                                                                        RESULT 58
US-07-789-913-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-07-789-913-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: MVIIB Omega conotoxin.
IDENTIFICATION METHOD: Direct peptide
IDENTIFICATION METHOD: sequencing of purified Conus magus venom
                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                    Query Match
34.8$; Score 56; DB 4; Length 2703;
Best Local Similarity 33.3$; Pred. No. 1.9e+02;
Matches 8; Conservative 5; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:

APPLICANT: David Hillyard

APPLICANT: Baldomero M. Olivera

TITLE OF INVENTION: Segregated Folding Determinants

TITLE OF INVENTION: for Small Disulfide-Rich Peptides

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Thorpe, No. 5231011th & Western

STREET: 9035 South 700 East, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIRKELI: 3033 SOULLE (OU CITY: Sandy
STATE: Utah
STATE: Utah
CONTRY: USA
ZIP: 84070
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb storage
COMPUTER: Compact LTRE 286
OPERATING SYSTEM: DOS 4.01
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION NUMBER: US/07/689,693B
FILING DATE: 19910418
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: none
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
34.5%; Score 55.5; Di
Best Local Similarity 38.5%; Pred. No. 3.6;
Matches 10; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                822 TGQKCETNIDDCVTNPCGNGGTCI 845
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                                                                                                                                                                                                                                                                                                                  4 XNOKCFQHLDDCCSRKCNRFNKCV 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Western, M. Wayne
REGISTRATION NUMBER: 22,788
REFRENCE/DOCKET NUMBER: 9925
TELECOMMUNICATION INFORMATION:
TELEPAX: (801) 566-653
TELEPAX: (801) 566-0750
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
EARLIER FILING DATE: 1997-07-23
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 2703
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 25 amino acids
TYPE: AMINO ACIDS
TOPOLOGY: linear
                                                                                                                       ) TYPE: PRT
; ORGANISM: Drosophila sp.
US-09-121-457-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 57
US-07-689-693B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-07-689-693B-2
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APPLICANT: SINGH, TEJINDER
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHLL, KISHOR C
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: SHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,774
                                                                                OURENTER: 150 COMPACTER: 150 COMPACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE: INDIVIDUAL ISOLATE: MVIIB/SNX-159, FIGURE 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/675,354
FILING DATE: 03-JUL-1996
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-APR-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CRIXNOKCFOHLDDCCSRKCNRFNKC 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08742774
Patent No. 5824645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stratford, Carol A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 amino acids
                              Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                  MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08496847

Patent No. 5795864

GENERAL INFORMATION:
APPLICANT: Amstutz, Gary A.
APPLICANT: Gohil, Kiehorchandra
APPLICANT: Adriaensens, Peter I.
APPLICANT: Aristipati, Ramasharma
TITLE OF INVENTION: METHODS AND
TITLE OF INVENTION: PORMULATIONS FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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APPLICANT: GOHÍL, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OFTWARE: PATENTING SYSTEM: VC-UOS/MS-LUOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 19930415
CLASSIFICATION: 514
RHIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAK: (415) 324-0960
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE: MVIIB/SNX-159, FIGURE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94306-1546
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 60
US-08-496-847-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-049-794-2
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Query Match 34.5%; Score 55.5; DB 2; Length 25; Best Local Similarity 38.5%; Pred. No. 3.6; Matches 10; Conservative 4; Mismatches 11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Anstutz, Gary A. APPLICANT: Bowersox, Stephen S. APPLICANT: Gohil, Kishorchandra APPLICANT: Gohil, Kishorchandra APPLICANT: ACTIOENS SENS PREED I TITLE OF INVENTION: METHODS AND FORMULATIONS FOR PREVEITIE OF INVENTION: PROGRESSION OF NEUROPATHIC PAIN NUMBER OF SEQUENCES: 36 CORRESPENDENCE ADDRESS: ADDRESSE: Dehlinger & Associates STREET: 350 Cambridge Avenue, Suite 250 CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34.5%; Score 55.5; DB 2; 38.5%; Pred. No. 3.6;
                   ; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: MVIIB/SNX-159, FIGURE 1
US-08-675-354-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Comparible
OPERATING SYSTEM: DOS
SOFTWARE: FastESQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,918
FILING DATE: 07-10V-1997
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: MVIIB/SNX-159, FIGURE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Mismatches
                                                                                                                                                                                                    1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08965918
Patent No. 5891849
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Mohr, Judy M.
REGISTRATION NUMBER: 38,563
REFERENCE/DOCKET NUMBER: 5865
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 64
US-009-103-168-2
'Sequence 2, Application US/09039168
'Patent No. 5965534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 38.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               650-324-0960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: Tinear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: US
ZIP: 94306-1546
                                                                                                                                                                                                                                                                                                                                       US-08-965-918-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-965-918-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                               Query Match 34.5%; Score 55.5; DB 2; Length 25; Best Local Similarity 38.5%; Pred. No. 3.6; Matches 10; Conservative 4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO; GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSES: LAW OFF:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURENT APPLICATION DATA: "C-UOS/MS-LUCS
CURRENT APPLICATION DATA: "C-UOS/MS-LUCS
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/675,354
FLING DATE: 03-JUL-1996
CLASSIPICATION: 530
PRICA APPLICATION NUMBER: US/08/049,794
FILING APPLICATION NUMBER: US/08/049,794
FILING DATE: 30-DEC-1991
APPLICATION NUMBER: US/08/049,759
FILING DATE: 30-DEC-1991
APPLICATION NUMBER: SEC-1991
ATORNEY AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: $865-0009.30
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                 HYPOTHETICAL: NO ORIGITAL SOURCE:
INDIVIDUAL ISOLATE: MVIIB/SNX-159, FIGURE 1 US-08-74-2-774-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEE: Law Offices of Peter Dehlinger
: 350 Cambridge Avenue, Suite 300
Palo Alto
                REFERENCE/DOCKET NUMBER: 5865-0009.30
TELEPOMMUNICATION INFORMATION:
TELEPOMMUNE: (415) 324-0880
TELEFAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CKGKGASCHRISYDCCTGSCNR-GKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CRIXNOKCFQHLDDCCSRKCNRFNKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
REGISTRATION NUMBER: 34,444
                                                                                                                                                             25 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                         MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 25 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: protein
                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 62
US-08-675-354-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPOLOGY:
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Length 25
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APPLICANT: Bowersox, S. Scott
APPLICANT: Gadbois, Theresa
APPLICANT: Gadbois, Theresa
APPLICANT: Gadbois, Theresa
APPLICANT: Luther, Robert, R.
TITLE OF INVENTION: IMPROVED EPIDURAL
TITLE OF INVENTION: METHOD OF PRODUCING ANALGESIA
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSE: Deblinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/138,439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11;
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ZIF: 94306-1546
ZIF: 94306-1546
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FeatSRQ for windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/613,400A
...TNG DATE: 08-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

34.5%; Score 55.5; DB 2;
Best Local Similarity 38.5%; Pred. No. 3.6;
Matches 10; Conservative 4; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: MVIIB/SNX-159, FIGURE 1
                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-04-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 0-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION: NEORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CKGKGASCHRTSYDCCTGSCNR-GKC 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08613400A
Patent No. 6054429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-138-439-2
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                                                             TITLE OF INVENTION: The Use of w-Conotoxin Analogs For TITLE OF INVENTION: Treating Retinal and Optic Nerve Head Damage NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS: ALCON Laboratories, Inc. STREET: 6201 South Freeway, Patent Legal CITY: Fort Worth CITY: Fort Worth STATE: 76.34-2099
COUNTRY: USA ZIP: 76.34-2099
COUNTRY: USA ZIP: 76.34-2099
COUNTRY: Compag Deskpro XE 560
CORPUTER: Compag Deskpro XE 560
CORPUTER: Compag Deskpro XE 560
CORPUTER: Compag Deskpro XE 560
CORRATING SYSTEM: Wicrosoft Windows for Workgroups, OPERATING SYSTEM: Version 3.11
SOCTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/039,168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34.5%; Score 55.5; DB 2; Length 25; 38.5%; Pred, No. 3.6; Live 4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: VALENTINO, KAREN L
APPLICANT: VALENTINO, ENCHORE P
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
     Pang, Iok-Hou; Kapin, Michael and Hellberg,
Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/562,142
APPLING DATE: NO. 5965314ember 22, 1995
FILING DATE: NO. 5965314ember 22, 1995
ATTORNEY/AGENT INFORMATION:
NAME: MAYO, MICHAEL C.
REGISTRATION NUMBER: 38,545
REFERENCE/DOCKET NUMBER: 1462
TELECOMMUNICATION INFORMATION:
TELEFAN: (817) 551-4610
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
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US-09-138-439-2
, Sequence 2, Application US/09138439
, Patent No. 5994305
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Best Local Similarity 38.5'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: JUSTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Palo Alto
GENERAL INFORMATIÖN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ANTI-SENSE: NO US-09-039-168-2
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                                                                                                       Query Match 34.5%; Score 55.5; DB 3; Length 25; Best Local Similarity 38.5%; Pred. No. 3.6; Matches 10; Conservative 4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: JUNCKALIUE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: GOHIL, KISHOR C
APPLICANT: GOHIL, KISHOR C
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/392,979A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.5%; Score 55.5; DB 3; 38.5%; Pred. No. 3.6; tive 4; Mismatches 11;
                  ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: MVIIB/SNX-159, FIGURE 1
US-09-298-017-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INDIVIDUAL ISOLATE: MVIIB/SNX-159, FIGURE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELEFPONE: (415) 324-0880
                                                                                                                                                                                          1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                      1 CKGKGASCHRTSYDCCTGSCNR-GKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-04-15
APPLICATION NUMBER: US 07/814,759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                ; Sequence 2, Application US/09392979A
; Patent No. 6136786
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 38.59
Matches 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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                                                                                                                                                                                                                                                                                                    RESULT 68
US-09-392-979A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-392-979A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHL, KISHOR C
APPLICANT: MILJANICH, GORDER
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                          Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Indels
                ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/298,017
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
34.5%; Score 55.5; DB 3;
Best Local Similarity 38.5%; Pred. No. 3.6;
Matches 10; Conservative 4; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION DATA:
APPLICATION NUMBER: 08/049,794
FILING DATE:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELEPHONE: (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CRIXNOKCFOHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CKGKGASCHRISYDCCTGSCNR-GKC 2.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09298017
Patent No. 6087091
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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US-09-298-017-2
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FILING DATE: 22-NOV-1989
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5189020-2
;Patent No. 5189020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 74
5424218-2
;Patent No. 5424218
                                                                                                                                                                                                                                                                                                                                5189020
               SEQ ID NO:2:
LENGTH: 25
                                                                                                                                                                                                                                                                                     RESULT 72
5189020-1
;Patent No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO:1:
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                                                       5424218-2
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5424218-2
Patent NO. 5424218
PAPLICANT: MILJANICH, GEORGE P.; BITNER, ROBERT S.; BOWERSOX,
STEPHEN S.; FOX, JAMES A.; VALENTINO, KAREN L.; YAMASHIRO, DONALD H.
TITLE OF INVENTION: SCREENING METHOD FOR NEUROPROTECTIVE COMPOUNDS
                                           Stephen S.;Fox, James A.;Valentino, Karen L.;Yamashiro, Donald
;H.;Tsubokawa, Makoto
;H.;Tsubokawa, Makoto
;TITLE OF INVENTION: METHOD OF REDUCING NEURONAL DAMAGE USING
;OMEGA COMOTONIN EPTIDES
; MARBER OF SEQUENCES: 29
; CURRENT APPLICATION DATA:
; FILING DATE: 02-AUG-1990
; PRIOR APPLICATION DATA:
; FILING DATE: 22-NOV-1989
; SEQ ID NO:1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   H. Teubokawa, Makoto
TITLE OF INVENTION: METHOD OF REDUCING NEURONAL DAMAGE USING
OMEGA CONOTOXIN PEPTIDES
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/561,766
FILING DATE: 02-AUG-1990
PRIOR APPLICATION NUMBER: 440,094
FILING DATE: 22-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 5189020; APPLICANT: Milijanich, George P.;Bitner, Robert S.;Bowersox, Stephen S.;Fox, James A.;Valentino, Karen L.;Yamashiro, Donald
                                                                                                                                                                                                                                                                                                                                                                                                             34.5%; Score 55.5; DB 6; Length 25; 38.5%; Pred. No. 3.6;
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34.5%; Score 55.5; DB 6;
Best Local Similarity 38.5%; Pred. No. 3.6;
Matches 10; Conservative 4; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 21
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/147,714
FILING DATE: 04-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 855,269
FILING DATE: 23-MR-1992
APPLICATION NUMBER: 561,766
FILING DATE: 02-ANG-1990
APPLICATION NUMBER: 561,766
FILING DATE: 02-ANG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
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Best Local Similarity 38.5%
.....hes 10; Conservative
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5189020-2
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H.;Tsubokawa, Makoto
H.;Tsubokawa, Makoto
MUNENION: METHOD OF REDUCING NEURONAL DAWAGE USING SOMEGA CONOTOXIN PEPTIDES
NUMBER OF SEQUENCES: 29
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/561,766
FILING DATE: 02-AUG-1990
PRIOR APPLICATION DATE: 440,094
FILING DATE: 22-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Miljanich, George P.;Bitner, Robert S.;Bowersox, Stephen S.;Fox, James A.;Valentino, Karen L.;Yamashiro, Donald H.;Fsubokawa, Makoto
TITLE OF INVENTION: METHOD OF REDUCING NEURONAL DAMAGE USING SOMEGA CONOTOXIN PEPTIDES
NUMBER OF SEQUENCES: 29
CURRENT APPLICATION DATA:
PELLING DATE: 02-AUG-1990
PRIOR APPLICATION NUMBER: 440,094
FILING DATE: 22-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 55.5; DB 6; Length 25;
Pred. No. 3.6;
4; Mismatches 11; Indels
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                                                Indels
                                                11;
                                                4; Mismatches
                                                                                                                            1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
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Query Match
Best Local Similarity 38.5%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 38.5%;
Matches 10; Conservative
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US-07-689-693B-1
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                                                                                                                                                                                                                                                                                              RESULT 76
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APPLICANT: MILJANICH, GEORGE P., BITNER, ROBERT S., BOWERSOX, STEPHEN S., FOX, JAMES A., VALENTINO, KAKEN L., YAMASHIRO, DONALD H. TITLE OF INVENTION: SCREENING METHOD FOR NEUROPROTECTIVE COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                      Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: David Hillyard
APPLICANT: Baldomero M. Olivera
TITLE OF INVENTION: Segregated Folding Determinants
TITLE OF INVENTION: for Small Disulfide-Rich Peptides
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSE: Thorpe, No. 5231011th & Western
STREET: 9035 South 700 Bast, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb storage COMPUTER: Compag LTE/286
COMPUTER: DOS 4.01
SOFTWARE: Word Perfect 5.1
SOFTWARE: Word Perfect 5.1
SOFTWARE: 19910418
FILING DATE: 19910418
CLASSIFICATION: 5.30
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: none
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Prepropeptide sequence for four-loop
NAME/KEY: MVIIB Omega conotoxin from Conus magus.
IDENTIFICATION METHOD: Libraries were created
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
34.5%; Score 55.5; D
Best Local Similarity 38.5%; Pred. No. 3.6;
Matches 10; Conservative 4; Mismatches
                                                               NUMBER OF SEQUENCES: 21
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/147,714
FILING DATE: 04-NOV-1993
PRIOR APPLICATION NUMBER: 855,269
FILING DATE: 23-MAR-1992
APPLICATION NUMBER: 561,766
FILING DATE: 22-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CKGKGASCHRTSYDCCTGSCNR-GKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/07689693B Patent No. 5231011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PILING DATE: na
ATTORNEY/AGENT INFORMATION:
NAME: WESTERT, M. Wayne
REGISTRATION NUMBER: 22,788
REFERENCE/DOCKET NUMBER: 9925
TELECOMUNICATION INFORMATION:
TELEPHONE: (801) 566-6633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (801) 566-0750
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 71 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECUIE TYPE: , peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Utah
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                           LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 75
US-07-689-693B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY:
STATE:
                                                                                                                                                                                                                                                                                                                   SEQ ID NO:2
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SUBUNIT PEPTIDES AND REAGANTS SPECIFIC FOR MEMBERS OF THE 170 KD SUBUNIT MULTIGENE FAMILY
                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                               RECOMBINANT ENTAMOEBA HISTOLYTICA LECTIN
IDENTIFICATION METHOD: using oligo-dT primed pUC13 vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1276;
                                                                      Length 71;
                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVENUE N.W., STE. 5500
CITY: WASHINGTON
                                                                                                               11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: BPRICATION NUMBER: US/08/937,236 FILING DATE:
                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 55.5; DB 3;
Pred. No. 1.1e+02;
4; Mismatches 11;
                                                                                                           4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34.5%; Score 55.5; ilarity 38.5%; Pred. No. 9; Conservative 4; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CRIXNOKCFQHLDDCCSRK--CNRFN-KCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: LIVNAT, SHMUEL
REGISTRATION NUMBER: 33,949
REFERENCE,DOCKET NUMBER: 291482000622
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                         46 CKGKGASCHRTSYDCCTGSCNR-GKC 70
                                                                                                                                               1 CRIXNOKCFOHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: DC
COUNTRY: USA
ZIP: 200006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
"WAUTER: IBM PC compatible
"WATEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                  Sequence 3, Application US/08937236
Patent No. 6187310
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/569,214
FILING DATE: 16 SEPTEMBER 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/08569214
Patent No. 6165469
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                          APPLICANT: MANN, BARBARA J.
APPLICANT: PETRI, WILLIAM A.
APPLICANT: PETRI, WILLIAM A.
TITLE OF INVENTION: RECOMBINAN
TITLE OF INVENTION: SUBUNIT PE
TITLE OF INVENTION: 170 KD SUB
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (202) 887-1500
TELERAX: (202) 887-0763
TELES: 90-4030
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 40.0%;
Matches 12; Conservative
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                                                          Query Match
Best Local Similarity
Matches 10; Conserva
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STRANDEDNESS: sir
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GENERAL INFORMATION:
APPLICANT: MAIN, BARBARA J.
APPLICANT: PETRI, WILLIAM A.
TITLE OF INVENTION: RECOMBINANT ENTAMOEBA HISTOLYTICA LECTIN
TITLE OF INVENTION: SUBUNIT PEPTIDES AND REAGANTS SPECIFIC FOR MEMBERS OF THE
TITLE OF INVENTION: 1.70 KD SUBUNIT MULTIGENE FAMILY
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.5%; Score 55.5; DB 3; Length 1291;
40.0%; Pred. No. 1.1e+02;
tive 4; Mismatches 11; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,214
FILING DATE:
CLASSIFICATION 424
PRIOR APPLICATION DATE:
APPLICATION NUMBER: PCT/US94/06890
FILING DATE: 17-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVENUE N.W., STE. 5500
CITY: WASHINGTON
  SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,236
                                                                                              TILING CALLS
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/569,214
FILLING DATE: 16 SEPTEMBER 1997
ATTORNEY/AGENT INFORMATION:
NAME: LIVNAT, SHMUEL
REGISTRATION NUMBER: 33,949
REFERENCE/DOCKET NUMBER: 291482000622
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          717 CSMGTDNIITYHDDCNSRKSQCGNFNGKCI 746
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ZIP: 200006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08569214
Patent No. 6165469
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TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (202) 887-0763
TELEK: 90-4030
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1291 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 40.0
Matches 12; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino
TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-569-214-2
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APPLICANT: MANN, BARBARA J.

APPLICANT: PETRI, WILLIAM A.

TITLE OF INVENTION: RECOMBINANT ENTAMOEBA HISTOLYTICA LECTIN

TITLE OF INVENTION: SUBUNIT PEPTIDES AND REAGANTS SPECIFIC FOR MEMBERS OF THE

TITLE OF INVENTION: 170 KD SUBUNIT MULTIGENE FAMILY

NUMBER OF SEQUENCES: 10

CORRESSORDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 2000 PENNSYLVANIA AVENUE N.W., STE. 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RECOMBINANT ENTAMOEBA HISTOLYTICA LECTIN
SUBUNIT PEPTIDES AND REAGANTS SPECIFIC FOR MEMBERS OF THE
170 KD SUBUNIT MULTIGENE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11; Indels
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                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.5%; Score 55.5; DB 3; 40.0%; Pred. No. 1.1e+02;
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FLIANG LARE:
FLIANG LARE:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06890
FILING DATE: 17-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: WURASHIGE, KATE H.
REGISTRATION NUMBER: 9148-0006.21
FELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-0763
TELEFAX: 90-4030
TELEEX: 90-4030
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   717 CSMGTDNIITYHDDCNSRKSQCGNFNGKCI 746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CRIXNQKCFQHLDDCCSRK--CNRFN-KCV 27
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ZIP: 200006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08937236
Patent No. 6187310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: MANN, BARBARA J.
APPLICANT: PETRI, WILLIAM A.
APPLICANT: DODSON, JAMES M.
TITLE OF INVENTION: RECOMBINANT
TITLE OF INVENTION: 170 KD SUBINIT PER
TITLE OF INVENTION: 170 KD SUBINIT PER
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1291 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 40.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear US-08-569-214-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 78
US-08-937-236-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 7
OTHER INFORMATION: /note= "where X is hydroxyproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDJUGE

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NOTA:
APPLICATION NOTA:
APPLICATION: 514
ATTOMNSY/AGENT INFORMATION:
NAME: Stratford, Carol A
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.31
TELEPHONE: 650-324-0880
TELEPAX: 650-324-0980
TELEPAX: 650-324-0980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INDIVIDUAL ISOLATE: SNX-231, FIGURE 2
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Patent No. 5824645
GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
                   8 CFQHLDDCCSRKCNRFNKC 26
                                         8 CRKTMYDCCSGSCGRRGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 CFOHLDDCCSRKCNRFNKC 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 47.41
Best Local Similarity 47.41
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL: DORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                      S
                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-496-847-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-742-774-21
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                                                                                                              Score 55.5; DB 3; Length 1295;
Pred. No. 1.1e+02;
4; Mismatches 11; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                   Sequence 21, Application US/08049794

Fatent No. 5587454

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: SINGH, TEJINDER

APPLICANT: GOHIL, KISHOR C

APPLICANT: VALENTINO, KAREN L

APPLICANT: WILJANICH, GEORGE P

TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND

TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : LOCATION: 7
; OTHER INFORMATION: /note= "where X is hydroxyproline"
US-08-049-794-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 350 Camming CITY: Palo Alto
STATE: 400
STATE: 400
STATE: 400
STATE: 400
ZIP: 94306
COMPUTER: 180 FC Compatible
COMPUTER: 180 FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: 19930415
CLASSIFICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1931
ATTORNEY/AGENT INFORMATION:
NAME: STRATEORY 34,444
REFERENCE/DOCKET NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 34,080
TELEPHONE: (415) 324-0860
TELEPHONE: (415) 324-0860
TELEPHONE: (415) 324-0860
TELEPHONE: (415) 324-0860
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TUDENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124.2%; Score 55; DB 1; ity 47.4%; Pred. No. 4.3; Servative 2; Mismatches
                                                                                                                                                                                                       ADDRESSEE: Law Offices of Peter Dellinger
STREET: 350 Cambridge Avenue, Suite 300
                                                                                                                                                                             1 CRIXNOKCFQHLDDCCSRK--CNRFN-KCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INDIVIDUAL ISOLATE: SNX-231, FIGURE 2
                                                                                                            Query Match
34.5%;
Best Local Similarity 40.0%;
Matches 12; Conservative
 1295 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Modified-site

// TYPE: amino acid
// TOPOLOGY: linear
// MOLECULE TYPE: protein
US-08-569-214-2

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Best Local Similarity 47.4
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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LENGTH:
                                                                                                          Query Match
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Sequence 21, Application US/08965918
Patent No. 5891849
GENERAL INFORMATION:
APPLICANT: Ametutz, Gary A.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Gohil, Kishorchandra
APPLICANT: Adriaensens, Peter I.
APPLICANT: Kristipati, Ramasharma
APPLICANT: Kristipati, Ramasharma
TITLE OF INVENTION: PROGRESSION OF NEUROPATHIC PAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 34.2%; Score 55; DB 2; Length 26; Best Local Similarity 47.4%; Pred. No. 4.3; Matches 9; Conservative 2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 7
OTHER INFORMATION: /note= "where X is hydroxyproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: FIDPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/675,354
FILING DATE: 03-JUL-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-ARR-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTONENTY/AGENT INPORMATION:
ANAME: CENSIFENCY CAPALICALIDA
ANAME: CENSIFENCY CAPALICA
                                                                                                                                                                                           3: Law Offices of Peter Dehlinger
350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 34,444
REGISTRATION NUMBER: 34,444
RECISTRATION NUMBER: 34,444
TELEPHONE: (415) 324-0860
RECIPERAX: (415) 324-0860
RECI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INDIVIDUAL ISOLATE: SNX-231, FIGURE 2
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94306
COMPUTER READABLE FORM:
                                                                                                                                                                                           ADDRESSEE: Law C
STREET: 350 Camb
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                  USA
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APPLICANT: VALENTINO, KAREN L
APPLICANT: MILANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCE: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.2%; Score 55; DB 2; Length 26; 47.4%; Pred. No. 4.3;
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; OTHER INFORMATION: /note= "where X is hydroxyproline"
05-08-742-774-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: SINGH, TEJINDER
APPLICANT: GOHLL, KISHOR C
APPLICANT: GOHLL, KISHOR C
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: SHANCING OPIATE ANALGESIA
NUMBER OF SQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/675,354
FILING DATE: 03-JUL-1996
APPLICATION NUMBER: 05/08/049,794
FILING DATE: 1993-ARR-15
FILING DATE: 1993-ARR-15
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: SCRAELOAG, CAROL A.
REGISTRATION NUMBER: 34,44
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELEPHONE: (415) 324-0860
TELEPHONE: (415) 324-0860
TELEPHONE: (415) 324-0860
TELEPHONE: (415) 324-0860
TELEPHONE: CARACTERISTICS:
LENGTH: 26 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 CFOHLDDCCSRKCNRFNKC 26
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Best Local Similarity 47.4'
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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APPLICANT:
APPLICANT:
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US-08-675-354-21
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Gaps

us-10-627-685a-26.rai

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Length 26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bowersox, S. Scott
APPLICANT: Gadbois, Theresa
APPLICANT: Gadbois, Theresa
APPLICANT: Duther, Robert, R.
TITLE OF INVENTION: IMPROVED EPIDURAL
TITLE OF INVENTION: METHOD OF PRODUCING ANALGESIA
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: BALO ALLO
STATE: CA
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OMPRATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/613,400A
FILING DATE: 08-MAR-1996
CLASSIFICATION: 514
PRIOR APPLICATION S14
PRIOR APPLICATION S14
PRIOR APPLICATION S14
PRIOR APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

34.2%; Score 55; DB

Best Local Similarity 47.4%; Pred. No. 4.3;

Matches 9; Conservative 2; Mismatches
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Patent No. 6054429
                                                              NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFRENCE/DOCKET NUMBER: 5865-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
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NAME: Stratford, Carol A
REGISTRATION NUMBER: 34,444
REFRENCE/DOCKET NUMBER: 586
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SN
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94306-1546
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TOPOLOGY: linear
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Patent No. 5994305
GENERAL INFORMATION:
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: GOHIL, KISHOR C
APPLICANT: MILDANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: BUHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

34.2%; Score 55: DB 2; Length 26;
Best Local Similarity 47.4%; Pred. No. 4.3;
Matches 9; Conservative 2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: /note= "where X is hydroxyproline" US-08-965-918-21
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFERATING SYSTEM: DOS
SOFERATION SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,918
FILING DATE: 07-N0v-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MAD. JUMPER: 38,563
REFERENCE/DOCKET NUMBER: 5865-0009.34
TELEPHONE: 650-324-0880
TELEPHONE: 650-324-0880
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-231, FIGURE 2
FFREATHER: AND STEATHER: S
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ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSE: Law Offices of Peter Dehlinger STREET: 350 Cambridge Avenue, Suite 300 CITY: Palo Alto STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-04-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
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DB 3; Length 26;

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11arity 47.4%; Score 55; DB 3 ilarity 47.4%; Pred. No. 4.3; Conservative 2; Mismatches
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Patent No. 6136786
                                                                                 8 CFQHLDDCCSRKCNRFNKC 26
                                                                                                                     8 CRKTMYDCCSGSCGRRGKC 26
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INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INDIVIDUAL ISOLATE:
  Query Match
Best Local Similarity
Matches 9; Conserve
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Best Local Similarity
Matches 9; Conserva
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APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C.
APPLICANT: VALENTINO, KAREN L.
APPLICANT: WILJANICH, GEORGE P.
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA AND TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Off:
                                                                                                                                                                                                       Length 26;
                                                                                                                     ; LOCATION: 7
; OTHER INFORMATION: /note= "where X is hydroxyproline"
US-08-613-400A-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ), OTHER INFORMATION: /note= "where X is hydroxyproline"
US-09-298-017-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/298,017
                                                                                                                                                                                                   Score 55; DB 3;
Pred. No. 4.3;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Law Offices of Peter Dehlinger STREET: 350 Cambridge Avenue, Suite 300 CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/049,794
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,44
RECISTRATION NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 21:
LENGTH: 26 amino acids
                  HYPOTHETICAL: NO ORIGINAL SOURCE: SNX-231, FIGURE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-231, FIGURE 2
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 21, Application US/09298017
Patent No. 6087091
GENERAL INFORMATION: APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
                                                                                                                                                                                                                                                                                                            CRKTMYDCCSGSCGRRGKC 26
                                                                                                                                                                                                                                                                                     8 CFOHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                     Query Match
Best Local Similarity 47.4%;
Matches 9; Conservative ;
                                                                                                NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
MOLECULE TYPE: 'protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                    RESULT 87
US-09-298-017-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                               FEATURE:
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APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: MILANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 55; DB 3; Length 26; Pred. No. 4.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 7
OTHER INFORMATION: /note= "where X is hydroxyproline"
                                                                                                                                                                                                                                                                                                                                                        ZIP: 94306

COMPUTER READABLE FORM:
MEDIUM TYPES Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/09/392,979A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-04-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 0-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34 44 44
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 CRKTMYDCCSGSCGRRGKC 26
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GENERAL INFORMATION:
APPLICANT: Miljanich, George P.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Valentino, Karen L.
APPLICANT: Valentino, Karen L.
APPLICANT: Yamashiro, Donald H.
TITLE OF INVENTION: Delayed Treatment Method of Reducing TITLE OF INVENTION: Ischemia-Related Neuronal Damage CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlings
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
33.9%; Score 54.5; DB 1; Length 25;
Best Local Similarity 38.5%; Pred. No. 4.7;
Matches 10; Conservative 5; Mismatches 10; Indels
          Delayed Treatment Method of Reducing
Ischemia-Related Neuronal Damage
28
                                                                                                                                                                                                                                                                                                                                                                                                                   CUPTOLISM: LIMP VC COMPACIDATE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/789,913

FILING DATE: 1991112

CLIASSIFICATION DATA:

APPLICATION NUMBER: US 07/561,766

FILING DATE: 02-AUG-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/440,094

FILING DATE: 22-NOV-1989

ATTORNEY/AGENT INPORMATION:

NAME: SLEAT GOOCET NUMBER: 34,444

REGISTRATION NUMBER: 34,444

REJERPAN: (415) 324-0960

INPORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LUMPTHAND AND COIDS

                                                                                AND MESSEE: Law Offices of Peter Dehlinger STREET: 350 Cambridge Avenue, Suite 300 CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Law Offices of Peter Dehlinger
350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
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US-007-789-913-9
'Sequence 9, Application US/07789913
'Patent No. 5559095
                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IDM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: Patentin Release #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-111
TITLE OF INVENTION: Del.
TITLE OF INVENTION: 18C)
WOMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 350 TITY: Palo Alto
                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                    94306
                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: C. COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-07-789-913-1
                                                                  Sequence 3481, Application US/09949016
Factor No. 681239
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: 06/241,755
FILE REFERENCE: 2000-04-11,755
PRIOR FILING DATE: 2000-10-20
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOUTHAND APPLICATION NUMBER: 60/231,498
NUMBER OF SEQ ID NOS: 207012
SOUTHAND APPLICATION NUMBER: 60/231,498
NUMBER OF SEQ ID NOS: 207012
SOUTHAND APPLICATION NUMBER: 06/231,498
NUMBER OF SEQ ID NOS: 207012
SOUTHAND APPLICATION NUMBER: 06/231,498
NUMBER OF SEQ ID NOS: 207012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 2, Application US/09641612; Patent No. 6703221; Patent No. 6703221; GENERAL INFORMATION:
; APPLICANT: Vivien Chan et al.; TITLE OF INVENTION: NOTCH RECEPTOR LIGANDS AND USES THEREOF; FILE REFERRING PO-1602.002 / 200130.458; CURRENT APPLICATION NUMBER: US/09/641,612; CURRENT FILING DATE: 2000-08-17; NUMBER OF SEQ ID NOS: 10; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 2.
; LENGTH: 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 473;
54;
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34.2%; Score 55; DB 4; Length 583;
Best Local Similarity 37.9%; Pred. No. 65;
Matches 11; Conservative 2; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.2%; Score 55; DB 44.0%; Pred. No. 54; tive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  375 CRAGFAGPRCEHDLDDCAGRACANGGTCV 403
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Valentino, Karen L.
Bitner, Robert S.
Yamashiro, Donald H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 91
US-07-789-913-1
; Sequence 1, Application US/07789913
; Patent No. 5559095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Miljanich, George P.
Bowersox, Stephen S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-641-612-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 11; Conserva
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APPLICANT: Miljani,
APPLICANT: Bowcros
APPLICANT: Fox, Jan
APPLICANT: Valenti,
APPLICANT: Pitner,
APPLICANT: Yamashi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9481
                                         -09-949-016-9481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-641-612-2
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APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C.
APPLICANT: MILJANINO, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA AND
TITLE OF ENVENTION: METHODS OF PRODUCING ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 33.9%; Score 54.5; DB 1; Length 25; Best Local Similarity 38.5%; Pred. No. 4.7; Matches 10; Conservative 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: ISM PC compatible

COMPUTER: BEAFOLD disk

SOFTWARE: Patentin Release #1.0, Version #1.25

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA: 19930415

FILING DATE: 19930415

CLASSIFICATION: 514

PRIOR APPLICATION NUMBER: US 07/814,759

FILING DATE: 30-DEC-1991

ATTORNEY/AGENT INFORMATION:

NAME: Stratford, Carol A.

REFERENCE/DOCKET NUMBER: 5865-0009.30

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFRAK: (415) 324-0880

TELEFRAK: (415) 324-0800

INFORMATION FOR SEQ ID NO: 9:

SEQUINCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         INDIVIDUAL ISOLATE: MVIIA/SNX-111, FIGURE 1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,44
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 anino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9, Application US/08049794
Patent No. 5587454
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 350 Camb
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-049-794-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-049-794-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       uery Match
33.9%; Score 54.5; DB 1; Length 25;
Best Local Similarity 38.5%; Pred. No. 4.7;
Matches 10; Conservative 5; Mismatches 10. 10. 10.1
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US-08-049-794-1

i Sequence 1, Application US/08049794

j Sequence 1, Application US/08049794

i GENERAL INFORMATION:

APPLICANT: JUSTICE, ALAN

APPLICANT: GOHIL, KISHOR C

APPLICANT: MILANICH, GEORGE P

TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND

TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:

ADDRESSEE: Law Offices of Peter Dehlinger
               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
SOFTWARE PATENTIN DATA:
APPLICATION NUMBER: US/07/789,913
FLING DATE: 1991112
CLASSIFICATION NUMBER: US 07/561,766
FILING DATE: 02-AUG-1990
FILING DATE: 02-AUG-1990
FILING DATE: 02-AUG-1990
FILING DATE: 02-AUG-1990
ATPORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0005.30
TELECOMMUNICATION NUMBER: 5865-0005.30
TELECOMMUNICATION NUMBER: 5865-0005.30
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COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYBE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 19930415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Law Offices of Peter Dehlinger STREET: 350 Cambridge Avenue, Suite 300 CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
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TELEFAX: (415) 324-0960
INPORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide
NO
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HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE:
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Sequence 9, Application US/08496847

Patent No. 5795864

GENERAL INFORMATION

APPLICANT: Ametutz, Gary A.

APPLICANT: Gonil, Kishorchandra

APPLICANT: Aprlicant: Aprlicant: Applicant: App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Patent No. 582445

GENERAL INFORMATION:
APPLICANT: 3UNCH TEJINDER
APPLICANT: GOHLL, KISHOR C
APPLICANT: WILLIANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OFIATE ANALGESIA
NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:
ADDRESSE: Law Offices of Peter Dehlinger
STERET: 350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: US
ZIP: 94306-1546
ZIP: 94306-1546
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: PRESENT DOS
SOFTWARE: FREESEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,847
FILING DATE: 27-UN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: STREAFOR CARO, CATO, A
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5665-0009.31
TELEPHONE: G50-324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; INDIVIDUAL ISOLATE: SNX-190, FIGURE 2
US-08-496-847-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-742-774-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Amsturz, Gary A.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Goall, Kishorchandra
APPLICANT: Goall, Kishorchandra
APPLICANT: Adriaensens, Peter I.
APPLICANT: Kristipati, Ramasharna
TITLE OF INVENTION: METHODS AND
TITLE OF INVENTION: FORMULATIONS FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSE: Dealinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ι;
                                                                                                                                                                                                                                          Length 25;
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                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                 Query Match
33.9%; Score 54.5; DB 1;
Best Local Similarity 38.5%; Pred. No. 4.7;
Matches 10; Conservative 5; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: DESCRIPTION
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,847
FILING DATE: 27-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.31
TELEPHONE: 650-324-0880
TELEPHONE: 650-324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
33.9%; Score 54.5; DB 1;
Best Local Similarity 38.5%; Pred. No. 4.7;
Matches 10; Conservative 5; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INDIVIDUAL ISOLATE: MVIIA/SNX-111, FIGURE 1
                                                       HYPOTHETICAL: NO ORIGINAL SOURCE: ; INDIVIDUAL ISOLATE: SNX-190, FIGURE 2 US-08-049-794-9
                                                                                                                                                                                                                                                                                                                                                        1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                      1 CKGAGAKCSRLMYDCCTGSC-RSGKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. CKGKGAKCSRLMYDCCTGSC-RSGKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08496847
Patent No. 5795864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 650-324-000 INPORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: T.ENGTH: 25 amino acids
                    MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein HYPOTHETICAL: NO
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              us
TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: E
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Palo Alto

STATE:

RESULT 96

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Indels
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APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KIGHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: MILJANICH, GENGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: ParentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Law Offices of Peter Dehlinger STREET: 350 Cambridge Avenue, Suite 300 CITY: Palo Alto
                                                 FILING DATE: 03-JUL-1996
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-APR-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ 1D NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 33.9%; Score 54.5; Best Local Similarity 38.5%; Pred. No. 4. Matches 10; Conservative 5; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-190, FIGURE 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 5865-0009.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/675,354
FILING DATE: 03-JUL-1996
CLASSIPICATION: 530
BRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-APR.15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08675354
Patent No. 5859186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34,444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
PRIOR APPLICATION DATA APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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Patent No. 5824645

GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: WALENTINO, KAREN L
APPLICANT: MILLANIO, KAREN L
APPLICANT: MILLANIO, RAREN L
APPLICANT: MILLANIO, REPROBUCING ANALGESI
TITLE OF INVENTION: BNHANCING OPIATE ANALGESIA
INTERPROPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   мылим туре: Floppy disk
CCMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,774
FILING DATE:
                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,774
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 54.5; DB 2;
Pred. No. 4.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: MVIIA/SNX-111, FIGURE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3: Law Offices of Peter Dehlinger
350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER:
FILING DATE: 03-JUL-1996
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-APR-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTOMBEY ABOUT INFORMATION:
NAME: Stratford, Carol A. REGISTRATION NUMBER: 34,444
REGISTRATION NUMBER: 34,444
REGISTRATION NUMBER: 34,444
REGISTRATION NUMBER: 34,444
REGISTRATION FOR SEQ 1D NO: 1:
TELEPOMMUNICATION INFORMATION:
TELEPAX: (415) 324-0860
INFORMATION FOR SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:
LEGGHING ASSOCIATION OCIDES
TELEPAX: ASSOCIATION OCIDES

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                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
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38.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
ZIP: 94306
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 10; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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                                                          MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-742-774-9
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Gaps
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APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHLL, KISHOR C
APPLICANT: WALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: BURANCING OPLATE ANALGESIA AND
TITLE OF INVENTION: ENTANCING OPLATE ANALGESIA
NUMBER OF SEQUENCES:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                 Length 25;
                                                                                                                                                                                                                                                                                                                                                                             10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CUMUTRY: USA

CUMUTRY: USA

CUMUTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: ISM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

FILING DATE: 03-UJL-1996

CLASSITCATION: 530

PRIOR APPLICATION NUMBER: US/08/049,794

FILING DATE: 1993-ARR-15

APPLICATION NUMBER: US/08/049,794

FILING DATE: 1993-ARR-15

ATTORNEY/AGBNT INFORMATION:

NAMME: Stratford, Carol A

REGISTRATION NUMBER: 34,444

REGISTRATION NUMBER: 34,444

FILING DATE: 415) 324-0960

INFORMETION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 25 amino acids

TUPER EMBRISHICS:

LENGTH: 25 amino acids

TOPPOLACY: 11-24
                                                                                                                                                                                                                                                                                                                     Ouery Match . 33.9%; Score 54.5; DB 2; Best Local Similarity 38.5%; Pred. No. 4.7; Matches 10; Conservative 5; Mismatches 10;
                                                                                                                                                                                                                                     ; INDIVIDUAL ISOLATE: MVIIA/SNX-111, FIGURE 1 US-08-675-354-1
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INDIVIDUAL ISOLATE: SNX-190, FIGURE 2
                                                                                                                                                                                                                                                                                                                                                                                                                 1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                              | CKGKGAKCSRLMYDCCTGSC-RSGKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/08675354
Patent No. 5859186
TELECOMMUNICATION INFORMATION
                               LEBERA: (415) 324-0880
INFORMATION FOR SEQ ID NO: 1.
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acida
TYPE: amino acida
TYPE: amino acid
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLAGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
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Search completed: April 18, 2005, 20:39:52 Job time : 31.5 secs

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Title: Perfect score:

Sequence:

OM protein -

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Run

Scoring table:

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Sequence 217, App Sequence 384, App Sequence 384, App Sequence 223, App Sequence 223, App Sequence 228, App Sequence 288, App Sequence 288, App Sequence 382, App Sequence 382, App Sequence 369, App Sequence 369, App Sequence 224, App Sequence 234, App Sequence 234, App Sequence 234, App Sequence 359, App Sequence 5, Appli Sequence 5, 
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US.10-352-254-10
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      April 18, 2005, 20:29:42; Search time 91.5 Seconds (without alignments) 98.077 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/NCNO PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT NEW PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/NCNO NEW PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/NSO NEW PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/NSO NEW PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/NSO NEW PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/NSOB_NEW PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/NSOB_NEW PUB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/NSOB_NEW PUB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/NSOB_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/NSOB_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/NSOB_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/NSOB_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/NSOB_PUBCOMB.pep:*

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19: /cgn2_6/ptodata/1/pubpaa/NSOB_PUBCOMB.pep:*

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Compugen Ltd.
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US-10-627-685-24
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US-10-352-254-19
US-10-352-254-18
US-10-627-685-9
US-10-627-685-18
US-10-627-685-18
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US-10-352-254-23
US-10-627-685-13
US-10-627-685-23
US-10-352-254-4
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                                                                                                                                                                                                                                     US-10-627-685A-26
161
1 CRIXNOKCFQHLDDCCSRKCNRFNKCV 27
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                        GenCore version (c) 1993 - 2005
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Match 100%
first 100 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Score

Result No.

161 158 158 158 158 158 158 157 157 157 157

Appliant App

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APPLICANT: Jones, Robert M. APPLICANT: Jones, Robert M. APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: McIntoch, J. Michael
APPLICANT: Olivera, Baldomero M. TITLE OF INVENTION: Kappa PVIIA-Related Conotoxins as Organ Protectants
FILE REFERENCE: 2314-254
CURRENT APPLICATION NUMBER: US/10/352,254
CURRENT APPLICATION NUMBER: US 60/352,219
PRIOR FILING DATE: 2002-01-29
PRIOR FILING DATE: 2002-01-29
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
                                                                                                                                                                                                                                                                                  Gaps
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APPLICANT: University of Utah Research Foundation

APPLICANT: Pemberton-Goodman, Karen

APPLICANT: Pemberton-Goodman, Karen

APPLICANT: Temple, Davis

APPLICANT: Temple, Davis

APPLICANT: McIntosh, J. Michael

APPLICANT: Olivera, Baldomero M.

TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants

FILE REFERENCE: 2314-254
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                                                                                                                                                                                                                                       ; Score 161; DB 15;
Pred. No. 1.2e-12;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cognetix, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: Pemberton-Goodman, Karen
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                                                                                                                                                                                                                                                                                                             1 CRIXNOKCFQHLDDCCSRKCNRFNKCV 27
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                                         60/155,135
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US-10-352-254-12
Sequence 12, Application US/10352254
Publication No. US20030224343A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9, Application US/10352254
Publication No. US20030224343Al
GENERAL INFORMATION:
            PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: US 60,
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 24
LENGTH: 27
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96.3%; P
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COTHER INFORMATION: Xaa is Hyp
US-10-352-254-9
                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Conus purpurascens
US-10-627-685-24
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Matches 26, Conservative
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Best Local Similarity 96.3
Matches 26; Conservative
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NAME/KEY: PEPTIDE
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Sequence 392, 7
Sequence 391, 7
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GENERAL INFORMATION:
APPLICANT: Cognetix, Inc.
APPLICANT: Cognetix, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: Demberton-Goodman, Karen
APPLICANT: Pemberton-Goodman, Karen
APPLICANT: Morple, Davis
APPLICANT: Olivera, Baldomero M.
FILLE REFERENCE: 2314-254
CURRENT APPLICATION NUMBER: US/10/352,254
PRIOR ADDITORATION NUMBER: US/10/352,254
PRIOR ADDITORATION: ADDITORATION NUMBER: US/10/352,254
                              Sequence 236,
Sequence 390,
Sequence 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 24, Application US/10627685

Sequence 24, Application US/10627685

Publication No. USZO040092447A1

SEMERAL INFORMATION:
APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Gones, R. Tyler
APPLICANT: Jones, Robert M.
APPLICANT: Cognetix, Inc.
ITTLE OF INFORTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
CURRENT APPLICATION NUMBER: US/10/627,685
    US-09-910-082A-390
US-10-765-926-236
US-10-765-926-390
US-09-910-082A-235
US-10-765-926-235
US-10-26999
US-10-289-776-9
US-09-910-082A-391
US-09-910-082A-391
US-09-910-082A-392
US-10-765-926-392
US-10-765-926-392
US-10-765-926-392
US-09-910-082A-238
US-09-910-082A-238
US-09-910-082A-238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 2003-01-28
PRIOR PLING DATE: 2003-01-29
PRIOR FILING DATE: 2002-01-29
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 24
LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US/09/666,837
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 60/219,438
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Best Local Similarity
Matches 26; Conserv
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APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Pemberton, Karen E.
APPLICANT: Tayer, Sichard T.
APPLICANT: Layer, Richard T.
APPLICANT: Layer, Richard T.
APPLICANT: McCabe, R. Tyler
APPLICANT: Cognetix, Inc.
TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
CURRENT COGNETIX, Inc.
TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: 2000-07-28
RICH APPLICATION NUMBER: US/9/666,837
PRIOR PLIING DATE: 2000-09-21
PRIOR PPLICATION NUMBER: US 60/154,135
PRIOR PLIING DATE: 2000-07-20
PRIOR PLIING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOCTWARE: PACENTIN VET. 2.0
SEQ ID NO. 12
TANDEL DATE: TANDEL DATE: US 60/155,135
                                                    APPLICANI: COGNES, ACCORDED.

TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
CURRENT APPLICATION NUMBER: US/10/627,685
CURRENT FILING DATE: 2003-07-28
PRIOR APPLICATION NUMBER: US/09/666,837
PRIOR PLING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-22
PRIOR PILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTI VET. 2.0
SEQ ID NO SEQ ID NOS: 25
LENGTH: 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 158; DB 15;
Pred. No. 2.8e-12;
1; Mismatches 0;
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Publication No. US20040092447A1
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LOCATION: (1)..(27)
CTHER INFORMATION: Xaa is Hyp
US-10-627-685-9
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; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-12
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Best Local Similarity 96.3%;
Matches 26; Conservative
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ORGANISM: Conus purpurascens
FEATURE:
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Best Local Similarity 96.33
Matches 26; Conservative
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APPLICANT: University of Utah Research Foundation
APPLICANT: University of Utah Research Foundation
APPLICANT: Demberton-Goodman, Karen
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: McIntosh, Jo Michael
APPLICANT: McIntosh, Jo Michael
APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
CURRENT APPLICATION NUMBER: US/10/352,254
CURRENT FILING DATE: 2003-01-28
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 98.1%; Score 158; DB 15; Length 27; Best Local Similarity 96.3%; Pred. No. 2.8e-12; Matches 26; Conservative 1; Mismatches 0; Indels
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CURRENT APPLICATION NUMBER: US/10/352,254
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US 60/352,219
PRIOR FILING DATE: 2002-01-29
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PATENTIN Ver: 2.0
SEQ ID NO 12
LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 18, Application US/10352254; Publication No. US20030224343A1; GENERAL INFORMATION:
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Publication No. US20040092447A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; CTHER INFORMATION: Xaa is Hyp
US-10-352-254-18
                                                                                                                                                                                                                                                                                                                           LOCATION: (1)..(27)
CTHER INFORMATION: Xaa is Hypus-10-352-254-12
                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Conus purpurascens
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ORGANISM: Conus purpurascens
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Best Local Similarity 96.3<sup>3</sup>
Matches 26; Conservative
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NAME/KEY: PEPTIDE
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LENGTH: 27
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APPLICANT: Aciticsh, J. Michael
APPLICANT: McIntosh, J. Michael
APPLICANT: McIntosh, J. Michael
APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: Rappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REFERENCE: 2314-254
CURRENT APPLICATION NUMBER: US/10/352,254
CURRENT APPLICATION NUMBER: US 60/352,219
PRIOR FILING DATE: 2002-01-29
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 23
LENGTH: 27
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APPLICANT: CORDELL'Bell, Ann H.
APPLICANT: CORDELL'Bell, Ann H.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: Layer, Richard T.
APPLICANT: McCabe, R. Tyler
APPLICANT: Cognetix, Inc.
TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
CURRENT APLICATION WMBER: US/09/666,837
PRIOR APPLICATION NUMBER: US/09/666,837
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-20
                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Cognetix, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: Pemberton-Goodman, Karen
APPLICANT: Jones, Robert M.
APPLICANT: Temple, Davis
                                                                                                                    Query Match
97.5%; Score 157; DB 15;
Best Local Similarity 96.3%; Pred. No. 3.7e-12;
Matches 26; Conservative 1; Mismatches 0;
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Publication No. US20040092447A1
GENERAL INFORMATION:
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; ORGANISM: Conus purpurascens
; FRATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-23
                     ; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-13
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Best Local S:
Matches 26
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APPLICANT: Temple, Davis
APPLICANT: McIntosh, J. Michael
APPLICANT: McIntosh, J. Michael
APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
CURRENT APPLICATION NUMBER: US,10/352,254
CURRENT PILING DATE: 2003-01-28
PRIOR PEPLIORING DATE: 2002-01-28
PRIOR FILING DATE: 2002-01-29
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                              APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: McCabe, R. Tyler
APPLICANT: Jones, Robert M.
APPLICANT: Cognetix, Inc.
TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Cognetix, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: Pemberton-Goodman, Karen
APPLICANT: Jones, Robert M.
1 CRIXNQKCYQHLDDCCSRKCNRFNKCV 27
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PRIOR APPLICATION NUMBER: US/09/666,837
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-07-20
PRIOR FILING DATE: 2000-07-20
PRIOR FILING DATE: 199-09-22
NUMBER OF SEQ ID NOS: 25
SSOFTWARE: PATCHTIN VET: 2.0
LENGTH: 27
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CURRENT FILING DATE: 2003-07-28
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Sequence 18, Application US/10627685
Publication No. US20040092447A1
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Publication No. US20030224343A1
GENERAL INFORMATION:
                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Pemberton, Karen E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: PEPTIDE
LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Conus purpurascens
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ORGANISM: Conus purpurascens
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LENGTH: 27
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...rulCANT: Jones, Robert M.
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REFERENCE: 2314-254
CURRENT APPLICATION NUMBER: US/10/352,254
CURRENT FILING DATE: 2003-01-28
PRIOR FILING DATE: 2002-01-29
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 27
TYPE.
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APPLICANT: Jones, Robert M...
APPLICANT: Temple, Davis
APPLICANT: McIntosh, J. Michael
APPLICANT: McIntosh, J. Michael
APPLICANT: Olivera, Baldomero M.
TILLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REFERENCE: 2314-235
CURRENT APPLICATION NUMBER: US/10/352,254
CURRENT FILING DATE: 2002-01-29
PRIOR APPLICATION NUMBER: US 60/352,219
PRIOR APPLICATION NUMBER: US 60/352,219
PRIOR PILING DATE: 2002-01-29
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.0
LENGTH: 27
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APPLICANT: University of Utah Research Foundation
APPLICANT: Pemberton-Goodman, Karen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 96.9%; Score 156; DB 15; Best Local Similarity 96.3%; Pred. No. 4.9e-12; Matches 26; Conservative 0; Mismatches 1;
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US-10-627-685-4
; Sequence 4, Application US/10627685
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LOCATION: (1)..(27)
OTHER INFORMATION: Xaa is Hyp
US-10-352-254-20
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CTHER INFORMATION: Xaa is Hyp
US-10-352-254-4
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Best Local Similarity 96.3%;
Matches 26; Conservative
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ORCANISM: Conus purpurascens
FEATURE:
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Pred. No. 3.7e-12;
1; Mismatches 0; Indels
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; Publication No. US20040092447A1
; GENERAL INFORMATION:
; APPLICANT: Cornell-Bell, Ann H.
; APPLICANT: Temple Jr., Davis L.
; APPLICANT: Layer, Richard T.
; APPLICANT: Layer, Richard T.
; APPLICANT: Jones, Robert M.
; APPLICANT: Jones, Robert M.
; APPLICANT: Gonetix, Inc.;
; TITLE OF INVENTION: USes of Kappa-Conotoxin PVIIA
; FILE REFERENCE: Kappa-PVIIA
; CURRENT APPLICATION NUMBER: US/10/627,685
; CURRENT FILING DATE: 2003-07-28
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Publication No. US20030224343A1
GENERAL INFORMATION:
APPLICANT: Cognetix, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: Pemberton-Goodman, Karen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 2003-07-28
PRIOR FILING DATE: 2000-07-28
PRIOR FILING DATE: 2000-09-21
PRIOR PLILOR DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/219,438
PRIOR FILING DATE: 2000-07-20
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                          97.5%;
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; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-13
                                                                                                                                      PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13
LENGTH: 27
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US-10-627-685-23
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ORGANISM: Conus purpurascens
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ORGANISM: Conus purpurascens
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Best Local Similarity 96.33
Warches 26; Conservative
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Best Local Similarity 100.
Matches 26; Conservative
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US-10-627-685-23
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Gaps

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APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: Temple, J. Michael
APPLICANT: Colivera, J. Michael
APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: Kappa-PVIA-Related Conotoxins as Organ Protectants
TITLE OF INVENTION: 2314-234
CURRENT APPLICATION NUMBER: US/10/352,254
CURRENT FILING DATE: 2003-01-28
PRIOR PAPLICATION NUMBER: US 60/352,219
PRIOR FILING DATE: 2002-01-29
NUMBER: OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cognetix, Inc.
APPLICANT: Cognetix, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: Demberton-Goodman, Karen
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: Morincosh, J. Michael
APPLICANT: Morincosh, J. Michael
APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REPERBURG: 2314-254
CURRENT FILING DATE: 2003-01-28
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                                           Query Match 96.9%; Score 156; DB 15; Best Local Similarity 96.3%; Pred. No. 4.9e-12; Matches 26; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Cognetix, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: Pemberton-Goodman, Karen
APPLICANT: Jones, Robert M.
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Pred. No. 6.5e-12;
0; Mismatches 1;
                                                                                                                                              1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27
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PRICA APPLICATION NUMBER: US 60/352,219
PRIOR FILING DATE: 2002-01-29
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.0
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Publication No. US20030224343Al
GENERAL INFORMATION:
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Publication No. US20030224343A1
GENERAL INFORMATION:
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GRANISM: Conus purpurascens
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(27)
CTHER INFORMATION: Xaa is Hyp
US-10-352-254-2
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Best Local Similarity 96.3
Matches 26; Conservative
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                                           APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Pemberton, Karen E.
APPLICANT: Layer, Bavis L.
APPLICANT: McCabe, R. Tyler
APPLICANT: Mocabe, R. Tyler
APPLICANT: Cognetix, Inc.
TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
CURRENT APPLICATION NUMBER: US/10/627,685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Temple Jr., Davis L.
APPLICANT: McCabe, R. Tyler
APPLICANT: Jones, Robert M.
APPLICANT: Jones, Robert M.
APPLICANT: Cognetix, Inc.
TILLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
CURRENT APPLICATION NUMBER: US/10/627,685
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Pred. No. 4.9e-12;
0; Mismatches 1;
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PRIOR PLICATION NUMBER: US/09/666,837
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/219,438
PRIOR PLICATION NUMBER: US 60/159,135
PRIOR PLING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VOY: 2.0
| INNOR OF ILINOS: 25
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PRIOR FILING DATE: 2000-09-21
PRIOR PELING DATE: 2000-09-21
PRIOR PELING DATE: 2000-07-20
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
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Publication No. US20040092447A1
GENERAL INFORMATION:
Publication No. US20040092447A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-4
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Best Local Similarity 96.3%;
Matches 26; Conservative
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COTHER INFORMATION: Xaa is Hyp
US-10-627-685-20
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NAME/KEY: PEPTIDE
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ORGANISM: Conus purpurascens

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Publication No. US20030224343A1
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
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96.3%;
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CTHER INFORMATION: Xaa is Hyp
US-10-352-254-6
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; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-8
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ORGANISM: Conus purpurascens
FEATURE:
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Best Local Similarity 96.3#
Matches 26; Conservative
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APPLICANT: University of Utah Research Foundation
APPLICANT: University of Utah Research Foundation
APPLICANT: Pembertoon-Goodman, Karen
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: Mointooh, J. Michael
APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REFERENCE: 2314-254
CURRENT APPLICATION NUMBER: US/10/352,254
CURRENT FILING DATE: 2003-01-28
FRIOR APPLICATION NUMBER: US 60/352,219
PRIOR FILING DATE: 2002-01-29
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.0
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APPLICANT: University of Utah Research Foundation
APPLICANT: University of Utah Research Foundation
APPLICANT: Demberton-Goodman, Karen
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: McIntosh, J. Michael
CURRENT APPLICANTON: Kappa-PVIIA-Related Conotoxins as Organ Protectants
CURRENT APPLICATION NUMBER: US/10/352,254
CURRENT FILING DATE: 2002-01-28
PRIOR PELICATION NUMBER: US 60/352,219
PRIOR FILING DATE: 2002-01-29
NUMBER OF SEQ ID NOS: 28
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Pred. No. 6.5e-12;
0; Mismatches 1; Indels
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Pred. No. 6.5e-12;
0; Mismatches 1; Indels
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                                                                                                                                                  96.3%;
96.3%;
                                               ; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-3
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1 Similarity 96.3%;
26; Conservative (
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; OTHER INFORMATION: Xaa is Hyp. US-10-352-254-5
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Matches 26; Conservative
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Best Local Similarity
Matches 26; Conserva
                         NAME/KEY: PEPTIDE
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LENGTH: 27
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APPLICANT: Cognetix, Inc.
APPLICANT: Cognetix, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: University of Utah Research Foundation
APPLICANT: Jones, Robert M.
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: McIntosh, J. Michael
APPLICANT: Mappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REFERENCE: 2314-254
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US 60/352,219
PRIOR APPLICATION NUMBER: US 60/352,219
PRIOR PLING DATE: 2002-01-29
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENTH: 27
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APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REFERENCE: 2314-254
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APPLICANT: University of Utah Research Foundation
APPLICANT: Pemberton-Goodman, Karen
Score 155; DB 15;
Pred. No. 6.5e-12;
0; Mismatches 1;
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Pred. No. 6.5e-12;
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Best Local Similarity 96.3%; Pred. No. 6.5«
Matches 26; Conservative 0; Mismatches
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APPLICANT: Cognetix, Inc.

APPLICANT: Cognetix, Inc.

APPLICANT: Cognetix, Inc.

APPLICANT: University of Utah Research Foundation

APPLICANT: Demberton-Goodman, Karen

APPLICANT: Pemberton-Goodman, Karen

APPLICANT: Temple, Davis

APPLICANT: Temple, Davis

APPLICANT: McIntosh, J. Michael

APPLICANT: Oliveza, Baldomero M.

TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants

FILE REFERENCE: 2314-254

CURRENT APPLICATION NUMBER: US/10/352,254

CURRENT FILING DATE: 2003-01-28

PRIOR FILING DATE: 2002-01-29

PRIOR FILING DATE: 2002-01-29

SOFTWARE: PACENTIN VET: 2.0

SEQ ID NO 22

LENGTH: 27
                                                  APPLICANT: MCINICA, J. Michael
APPLICANT: MCINICA, J. Michael
APPLICANT: MCINICA, J. Michael
APPLICANT: Olivera, Baldomero M
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REFERENCE: 2314-254
CURRENT APPLICATION NUMBER: US/10/352,254
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US 60/352,219
PRIOR PILING DATE: 2002-01-29
SOFTWARE: PATENT OF SEQ ID NOS: 28
SOFTWARE: PATENT OF SEQ ID NOS: 28
TENGTH: 27
TYPE: PRT
CORGANISM: Conus purpurascens
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96.3%; Score 155; DB 15;
Best Local Similarity 96.3%; Pred. No. 6.5e-12;
Matches 26; Conservative 0; Mismatches 1;
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96.3%; Score 155; DB 15;
Best Local Similarity 96.3%; Pred. No. 6.5e-12;
Matches 26; Conservative 0; Mismatches 1;
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Publication No. US20030224343A1
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; Publication No. US20040092447A1
                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (1)..(27)
OTHER INFORMATION: Xaa is Hyp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Conus purpurascens
                                      Temple, Davis
                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: PEPTIDE LOCATION: (1)..(2'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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US-10-627-685-2
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APPLICANT: Cognetix, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: University of Utah Research Foundation
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
CURRENT APPLICATION NUMBER: US/10/352,254
CURRENT FILING DATE: 2003-01-28
PRIOR PPLICATION NUMBER: US 60/352,219
PRIOR FILING DATE: 2002-01-29
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                           Query Match 96.3%; Score 155; DB 15; Length 27; Best Local Similarity 96.3%; Pred. No. 6.5e-12; Matches 26; Conservative 0; Mismatches 1; Indels
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Ouer Matches Similarity 96.3%; Pred. No. 6.5e-12;
Matches 26; Conservative 0; Mismatches 1;
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CURRENT APPLICATION NUMBER: US/10/352,254
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US 60/352,219
PRIOR FILING DATE: 2002-01-29
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 27
TYPE: PRT
ORGANISM: CONUS PUTPULASCENS
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Publication No. US20030224343A1
GENERAL INFORMATION:
APPLICANT: Cognetix, Inc.
APPLICANT: University of Utah Research APPLICANT: Pemberton-Goodman, Karer APPLICANT: Jones, Robert M.
                                                                                                                                                                                                                                                                                     , OTHER INFORMATION: Xaa is Hyp
US-10-352-254-10
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; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-11
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ORGANISM: Conus purpurascens
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NAME/KEY: PEPTIDE
LOCATION: (1)..(27
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US-10-352-254-16
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        Length 27;
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APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: Layer, Richard T.
APPLICANT: Jones, Robert M.
APPLICANT: Cognetix, Inc.
ITILE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
CURRENT FILING DATE: 2003-07-28
PRIOR APPLICATION NUMBER: US/09/666,837
PRIOR PLING DATE: 2000-09-21
PRIOR PLING DATE: 2000-09-21
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEOFTWARE: Patentin Ver. 2.0
SEOFTWARE: APPLICATION NUMBER: US/09-22
NUMBER OF SEQ ID NOS: 25
LUMBER OF SEQ ID NOS: 25
LUMBER OF SEQ ID NOS: 25
LUMBER OF SEQ ID NOS: 25
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APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: Layer, Richard T.
APPLICANT: Layer, Richard T.
APPLICANT: Layer, Robert M.
APPLICANT: Jones, Robert M.
FILE REFERENCE: Kappa-PVIIA
FILE REFERENCE: Kappa-PVIIA
FILE REFERENCE: Rappa-PVIIA
FILE REFILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR PLING DATE: 2000-07-20
PRIOR PPLICATION NUMBER: US 60/219,438
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: US 60/219,438
  Score 155; DB 15;
Pred. No. 6.5e-12;
0; Mismatches 1;
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Pred. No. 6.5e-12;
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                                                                                                            1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27
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Publication No. US20040092447A1
GENERAL INFORMATION:
96.3%;
Local Similarity 96.3%;
les 26; Conservative 0
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CTHER INFORMATION: Xaa ie Hyp
US-10-627-685-5
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        Query Match
                                                         Matches
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Pred. No. 6.5e-12;
0; Mismatches 1; Indels
                                                                         APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: McCabe, R. Tyler
APPLICANT: McCabe, R. Tyler
APPLICANT: Gornetax, Inc.
TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
CURRENT APPLICATION NUMBER: US/10/627,685
CURRENT APPLICATION NUMBER: US/09/666,837
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-07-20
PRIOR PLILING DATE: 1999-09-22
PRIOR FILING DATE: 1999-09-22
PRIOR FILING DATE: 1999-09-22
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VET. 2.0
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APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Temple Jr. Chard T.
APPLICANT: Layer, Richard T.
APPLICANT: McCabe, R. Tyler
APPLICANT: Jones, Robert M.
APPLICANT: Cognetix, Inc.
APPLICANT: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
CURRENT FILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-20
PRIOR PILING DATE: 2000-09-20
PRIOR PILING DATE: 1999-09-22
NUMBER OF EEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
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Publication No. US20040092447A1
GENERAL INFORMATION:
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Best Local Similarity 96.3%;
Matches 26; Conservative
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OTHER INFORMATION: Xaa is Hyp
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LENGTH: 27
TYPE: PRT
ORGANISM: Conus purpurascens
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ORGANISM: Conus purpurascens
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PRIOR FILING DATE: 1999-09-22

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96.3%; Score 155; DB 15; Length 27; 96.3%; Pred. No. 6.5e-12; tive 0; Mismatches 1; Indels
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                                                        AFFLICANT: COUNTED, NUMBER: CONDUCTOR, TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA FILE REPERENCE: Kappa-PVIIA CURRENT APPLICATION NUMBER: US/10/627,685 CURRENT APPLICATION NUMBER: US/09/666,837 PRIOR APPLICATION NUMBER: US/09/666,837 PRIOR APPLICATION NUMBER: US 60/219,438 PRIOR APPLICATION NUMBER: US 60/219,438 PRIOR APPLICATION NUMBER: US 60/215,135 PRIOR APPLICATION NUMBER: US 60/155,135 PRIOR FILING DATE: 1999-09-22 NUMBER OF SEQ ID NOS: 25 SQ ID NOS: 25 SQ ID NO 10 SERVING DATE: DPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Pemberton, Karen E.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: Layer, Richard T.
APPLICANT: Cagnetix, Inc.
TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
CURRENT APPLICATION NUMBER: US/09/666,837
FILOR APPLICATION NUMBER: US/09/666,837
PRIOR PILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
LENGTH: 27
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Publication No. US20040092447A1
                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Conus purpurascens;
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(27)
OTHER INFORMATION: Xaa is Hyp
US-10-627-685-10
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; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-11
                           McCabe, R. Tyler
Jones, Robert M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Conus purpurascens
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Best Local Similarity 96.3
Matches 26; Conservative
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Publication No. US20040092447A1

Sebelication No. US20040092447A1

APPLICANT: Cornell-Bell, Ann H.

APPLICANT: Temple Jr., Davis L.

APPLICANT: Layer. Riched T.

APPLICANT: Layer. Riched T.

APPLICANT: Cognetix, Inc.

APPLICANT: Cognetix, Inc.

TITLE OF INVENTION: Usee Of Kappa-Conotoxin PVIIA

FILE REFERENCE: Kappa-PVIIA

CURRENT APPLICATION UNMER: US/10/627,685

CURRENT FILING DATE: 2003-07-28

PRIOR PPLICATION NUMBER: US 60/219,438

PRIOR FILING DATE: 2000-09-21

PRIOR FILING DATE: 1099-09-22

NUMBER OF SEQ ID NOS: 25

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 8

LENGTH: 27

LENGTH: 27
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6.5e-12;
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96.3%; Score 155; DB
Best Local Similarity 96.3%; Pred. No. 6.5e
Matches 26; Conservative 0; Mismatches
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Publication No. US20040092447A1
GENERAL INFORMATION:
                                                                                                                                                             NAME/KEY: PEPTIDE
LOCATION: (1)..(27)
// OTHER INFORMATION: Xaa is Hyp
US-10-627-685-6
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                                         SEQ ID NO 6
LENGTH: 27
TYPE: PRT
ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Conus purpurascens
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                               FEATURE:
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Sequence 7, Application US/10352254

Sequence 7, Application US/10352254

Publication No. US20030224343A1

GENERAL INFORMATION:

APPLICANT: Cognetix, Inc.

APPLICANT: University of Utah Research Foundation

APPLICANT: University of Utah Research Foundation

APPLICANT: Office Nobert M.

APPLICANT: Temple, Davis

APPLICANT: Temple, Davis

APPLICANT: McIntosh, J. Michael

APPLICANT: Olivera, Baldomero M.

TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants

FILE REFERENCE: 2314-254

CURRENT APPLICATION NUMBER: US/10/352,254

CURRENT FILING DATE: 2002-01-28

PRIOR FILING DATE: 2002-01-29

NUMBER OF SEQ ID NOS: 28

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 7

LENGTH: 27
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APPLICANT: Ollyvera, Baldomero M.
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REFERENCE: 2314-254
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Publication No. US20030224343A1
GENERAL INFORMATION:
APPLICANT: Cognetix, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: Jones, Robert M.
APPLICANT: Jones, Robert M.
APPLICANT: Temple, Davis
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95.0%; Score 153; DB 15;
Best Local Similarity 96.3%; Pred. No. 1.1e-11;
Matches 26; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                               Query Match 96.3%; Score 155; DB 15; Best Local Similarity 96.3%; Pred. No. 6.5e-12; Matches 26; Conservative 0; Mismatches 1;
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CURRENT FILING DATE: 2003-01-28
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                                                                                                                  FEATURE:

NAME/KEY: PEPTIDE

LOCATION: (1)..(27)

OTHER INFORMATION: Xaa is Hyp
US-10-627-685-22
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NAME/KEY: PEPTIDE

LOCATION: (1)..(27)

OTHER INFORMATION: Xaa is Hyp
US-10-352-254-7
                                      TYPE: PRT ORGANISM: Conus purpurascens
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ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-352-254-15
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                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Pemberton, Karen E.
APPLICANT: Pemberton, Karen E.
APPLICANT: Pemple Jr., Davis L.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: McCabe, R. Tyler
APPLICANT: Cognes, Robert M.
APPLICANTON NUMBER: US/09/666,837
PRIOR APPLICATION NUMBER: US 60/19,438
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: US 60/19,438
PRIOR APPLICATION NUMBER: US 60/155,135
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APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: Mores, Robert M.
APPLICANT: Cognetix, Inc.
TITLE OF INVENTION: Ubes of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
CURRENT FILING DATE: 2003-07-28
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 1050-07-20
PRIOR FILING DATE: 1050-07-20
PRIOR FILING DATE: 2000-07-20
PRIOR FILING DATE: 
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6.5e-12;
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CRIKNQKCFQHLDDCCSRKCNRFNKCV 27
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                                                                       CRIXNOKCMOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                          Sequence 16, Application US/10627685; Publication No. US20040092447A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 22, Application US/10627685; Publication No. US20040092447A1
GENERAL INFORMATION:
APPLICANT: Cornell.Bell, Ann H.
APPLICANT: Pemberton, Karen E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-16
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                                                                                                                                                                                                  RESULT 33
US-10-627-685-16
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US-10-627-685-22
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## APPLICANT: Olivera, Baldomero M.

TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REFERENCE: 2314-254

CURRENT APPLICATION NUMBER: US/10/352,254

PRIOR APPLICATION NUMBER: US 60/352,219

PRIOR PILING DATE: 2002-01-29

NUMBER OF SEQ ID NOS: 28

SOFTWARE: Patentin Ver. 2.0

LENGTH: 27

TYPE: PAT

ORGANISM: Conus purpurascens

FRATURE:

NAMBKEX: PEPTIDE

NORGANISM: (1). (27)

OTHER INFORMATION: Xaa is Hyp

US-10-352-254-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | GENERAL INFORMATION: US.00.243434A1 |
| GENERAL INFORMATION: D.2.00.30.24343A1 |
| APPLICANT: Cognetix, Inc. |
| APPLICANT: University of Utah Research Foundation |
| APPLICANT: Pember Goodman, Karen |
| APPLICANT: Temple, Davis |
| APPLICANT: Temple, Davis |
| APPLICANT: McIntosh, J. Michael |
| TILLE OF INTENTION: Kappa-PVIIA-Related Conctoxins as Organ Protectants |
| TILLE OF INTENTION: Kappa-PVIIA-Related Conctoxins as Organ Protectants |
| TILLE OF INTENTION: Kappa-PVIIA-Related Conctoxins as Organ Protectants |
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| TILLE OF INTENTION: Kappa-PVIIA-Related Conctoxins as Organ Protectants |
| TILLE OF INTENTION: Kappa-PVIIA-Related Conctoxins as Organ PVIIA-Related Conctoxins |
| TILLE OF INTENTION: Kappa-PVIIA-Related Conctoxins |
| TILLE OF INTENTION: Kappa-PVIIA-Re
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Best Local Similarity 96.3%; Pred. No. 1.1e-11;
Matches 26; Conservative 0; Mismatches 1;
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Best Local Similarity 96.3%; Pred. No. 1.1e-11;
Matches 26; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CRIXNOKCFQHLDDCCSRKCNRFNKCV 27
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Publication No. US20030224343A1
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Publication No. US20030224343A1
GENERAL INFORMATION: APPLICANT: Cognetix, Inc.
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ORGANISM: Conus purpurascens
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NAME/KEY: PEPTIDE
LOCATION: (1)..(2
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US-10-352-254-21
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APPLICANT: University of Utah Research Foundation
APPLICANT: Pemberton-Goodman, Karen
APPLICANT: Pember on Goodman, Karen
APPLICANT: Jones, Robert M.
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: On Trough, J. Michael
APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REPERENCE: 234-254
CURRENT APPLICATION NUMBER: US/10/352,254
CURRENT FILING DATE: 2002-01-29
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PATENTIN VENER: 2002-01-29
SOFTWARE: PATENTIN VENER: 2002-01-29
SEQ ID NO 17
LENGTH: ...
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Publication No. US20030224343A1
APREAT INFORMATION:
APPLICANT: Cognetix, Inc.
APPLICANT: University.of Utah Research Foundation
APPLICANT: Pemberton-Goodman, Karen
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: McIntosh, J. Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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PRIOR FILING DATE: 2002-01-29
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.0
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US-10-352-254-17
Sequence 17, Application US/10352254
Publication No. US20030224343A1
GENERAL INFORMATION:
APPLICANT: Cognetix, Inc.
                                                                                                                                                                                                                                                                                                   COTION: (1)...(27)
COTHER INFORMATION: Xaa is Hyp
US-10-352-254-15
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McIntosh, J. Michael
                                                                                                               SEO ID NO 15
LENGTH: 27
TYPE: PRT
ORGANISM: Conus purpurascens
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; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-17
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ORGANISM: Conus purpurascens
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Matches 26; Conservative
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1 CRIXNQKCAQHLDDCCSRKCNRFNKCV 27
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                                                                            APPLICANT: MCINICOSh, J. Michael
APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILLE REPERENCE: 2114-254
CURRENT APPLICATION NUMBER: US/10/352,254
CURRENT APPLICATION NUMBER: US/03-01-28
PRIOR APPLICATION NUMBER: US/03-01-29
PRIOR FILING DATE: 2002-01-29
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APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: Layer, Richard T.
APPLICANT: McCabe, R. Tyler
APPLICANT: McCabe, R. Tyler
APPLICANT: Cognetix, Inc.
TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
CURRENT APPLICATION NUMBER: US/09/666,837
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATCHTIN VET. 2.0
University of Utah Research Foundation
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                                                                                                                                                                                                                                                                                                                                                                                                                                             , LUCATION: (1)...(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-25
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OTHER INFORMATION: Xaa is Hyp
                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Conus purpurascens
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ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 25
LENGTH: 27
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Best Local Similarity 96.3
Matches 26; Conservative
                                                                     Temple, Davis
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LENGTH: 27
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1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27

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Gaps
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                                                                                                                          APPLICANT: Temple Jr., Davis L.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: Layer, Richard T.
APPLICANT: Jones, Robert M.
APPLICANT: Jones, Robert M.
TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
CURRENT APPLICATION NUMBER: US/10/627,685
CURRENT FILING DATE: 2003-07-28
PRIOR APPLICATION NUMBER: US/09/666,837
PRIOR APPLICATION NUMBER: US 60/219,438
PRIOR FILING DATE: 2000-09-21
PRIOR PLING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SEQ ID NO 15
LENGTH: 27
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APPLICANT: Temple Jr., Davis L.
APPLICANT: Temple Jr., Davis L.
APPLICANT: McCabe, R. Tyler
APPLICANT: Gones, Robert M.
APPLICANT: Cognetix, Inc.
TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
CURRENT APPLICATION NUMBER: US/10/666,837
PRIOR APPLICATION NUMBER: US/09/666,837
PRIOR APPLICATION NUMBER: US 60/219,438
PRIOR FILING DATE: 2000-07-20
PRIOR FILING DATE: 2000-07-20
PRIOR FILING DATE: 2000-07-20
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PALENTIN VEY: 2.0
SEQ ID NO 17
LENGTH: 27
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95.0%; Score 153; DB 15;
Best Local Similarity 96.3%; Pred. No. 1.1e-11;
Matches 26; Conservative 0; Mismatches 1;
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Sequence 15, Application US/10627685 Publication No. US20040092447A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(27)
OTHER INFORMATION: Xaa is Hyp
US-10-627-685-15
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ORGANISM: Conus purpurascens
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Gaps
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APPLICANT: Corneal-Beall, Ann H.
APPLICANT: Pemberton, Karen E.
APPLICANT: Pemberton, Karen E.
APPLICANT: Pemple Jr., Davis L.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: Gones, R. Tyler
APPLICANT: Ognesix, Inc.
TILLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
CURRENT PLILNG DATE: 2003-07-28
FRIOR APPLICATION NUMBER: US 60/219,438
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/155,135
PRIOR FILING DATE: 2000-07-20
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
TENNARE: Patentin Ver. 2.0
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                    CURRENT APPLICATION NUMBER: US/10/627,685
CURRENT FILING DATE: 2003-07-28
PRIOR APPLICATION NUMBER: US/9/666,837
PRIOR FILING DATE: 2000-09-21
PRIOR PLING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/219,438
PRIOR FILING DATE: 2000-07-20
PRIOR PILING DATE: 1990-09-22
NUMBER OF SEQ ID NOS: 25
SEQ ID NO 21
LENGTH: 27
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Publication No. US20040092447A1
GENERAL INFORMATION:
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; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-21.
                                                                                                                                                                                                                                                                                                                                   ORGANISM: Conus purpurascens FEATURE:
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; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-25
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ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: PEPTIDE LOCATION: (1)..(27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:

APPLICANT: COTNEIL-Bell, Ann H.

APPLICANT: Demberton, Karen E.

APPLICANT: Temple Jr., Davis L.

APPLICANT: Temple Jr., Davis L.

APPLICANT: Temple Jr., Davis L.

APPLICANT: McCabe, R. Tyler

APPLICANT: McCabe, R. Tyler

APPLICANT: Cognetix, Inc.

TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA

FILE REFERENCE: Kappa-PVIIA

CURRENT FILING DATE: 2003-07-28

PRIOR PLING DATE: 2000-07-20

PRIOR PLING DATE: 2000-07-20

PRIOR APPLICATION NUMBER: US 60/15,135

PRIOR FILING DATE: 1999-09-22

PRIOR FILING DATE: 1999-09-22

NUMBER OF SEQ ID NOS: 25

SOFTWARE: PATENTING UNING DATE: 1999-09-22

NUMBER OF SEQ ID NOS: 25

SSOFTWARE: PATENTING UNING DATE: 1999-09-22
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APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: Layer, Richard T.
APPLICANT: Jones, R. Tyler
APPLICANT: Cognetx, Inc.
TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
                                                                                                                                                                                                                                                                  1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27
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Publication No. US20040092447A1
GENERAL INFORMATION:
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Publication No. US20040092447A1
GENERAL INFORMATION:
                                                  NAME/KEY: PEPTIDE
LOCATION: (1)..(27)
JOHER INFORMATION: Xaa is Hyp
US-10-627-685-17
ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (1)...(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-19
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TITLE OF INVENTION: Uses of
FILE REFERENCE: Kappa-PVIIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 26; Conserva'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: PEPTIDE
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US-10-627-685-21
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; Score 78.5; DB
; Pred. No. 0.011
6; Mismatches
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CURRENT APPLICATION NUMBER: US/09/910,082A
CURRENT APPLICATION NUMBER: US/09/910,082A
CURRENT APPLICATION NUMBER: US 60/219,616
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: Patentin version 3.0
SEQ ID NO 354
     96.3%; Pred. No. 2e-1
:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIncosh, J. Michael
APPLICANT: Markins, Maren
APPLICANT: Garrett, James E.
APPLICANT: Garrett, James E.
APPLICANT: Jacobsen, Ki-Joon
APPLICANT: Jacobsen, Richard
APPLICANT: Cartier, G. Edward
TITLE OF INVENTION: Omes
                                                                              1 CRIXNOKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                               1 CRIXNOKCFOALDDCCSRKCNRFNKCV 27
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CURRENT APPLICATION NUMBER: US/10/765,926
CURRENT FILING DATE: 2004-01-29
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PPLICANT: Jacobsen, Richard
PPLICANT: Jones, Robert M.
PPLICANT: Cartier, G. Edward
ITLE OF INVENTION: Omega-Conopeptides
                                                                                                                                                                                                                                                    Sequence 354, Application US/09910082A Publication No. US20030119731A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 354, Application US/10765926 Publication No. US20040132663A1 GENERAL INFORMATION:
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Watkins, Maren
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Best Local Similarity 46.2%;
Matches 12; Conservative
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     Best Local Similarity 96.3
Matches 26; Conservative
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                                                                                             APPLICANT: Cognetix, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: University of Utah Research Foundation
APPLICANT: University of Utah Research Foundation
APPLICANT: Jones, Robert M.
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: Meintosh, J. Michael
APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REFERENCE: 2314-254
CURRENT APPLICATION NUMBER: US/10/352,254
CURRENT FILING DATE: 2003-01-28
FRIOR APPLICATION NUMBER: US 60/352,219
FRIOR APPLICATION NUMBER: US 60/352,219
NUMBER OF SEQ ID NOS: 28
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.0
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TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
CURRENT APPLICATION NUMBER: US/10/627,685
CURRENT FILING DATE: 2003-07-28
PRIOR PLING DATE: 2000-09-21
PRIOR PLING DATE: 2000-09-21
PRIOR PLING DATE: 2000-07-20
PRIOR PLING DATE: 2000-07-20
PRIOR PLING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VET: 2000-07-20
SOFTWARE: PATENTIN VET: 2000-07-20
SOFTWARE: PATENTIN VET: 2000-07-20
SOFTWARE: PATENTIN VET: 2000-07-20
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Pred. No. 2e-11;
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US-10-352-254-14,
Sequence 14, Application US/10352254;
Publication No. US20030224343A1
GENERAL INFORMATION:
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Publication No. US20040092447A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Pemberton, Karen E.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: MCCAbe, R. Tyler
APPLICANT: Jones, R. Pyler
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96.3%;
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; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Conus purpurascens
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Best Local Similarity 96.3
Matches 26; Conservative
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LENGTH: 27
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93.8%; Score 151; DB 15; Length 27;

Query Match

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Gaps
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0.011;
ches 7;
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APPLICANT: University of Utah Research Foundation
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PRIOR PEPLICATION NUMBER: US 09/910,082
PRIOR FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: US 60/265,888
PRIOR FILING DATE: 2001-02-05
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ch 46.0%; Score 74; DB 10; Length 26; 
l Similarity 42.3%; Pred. No. 0.037; 
11; Conservative 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
48.8%; Score 78.5; DB 16;
Best Local Similarity 46.2%; Pred. No. 0.025;
Matches 12; Conservative 6; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: University of Utah Research Foundation
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US-10-765-926-395
Sequence 395, Application US/10765926
Publication No. US20040132663A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
                                  CURRENT APPLICATION NUMBER: US/10/765,926
CURRENT FILING DATE: 2004-01-29
PRIOR APPLICATION NUMBER: US 09/910,082
PRIOR FILING DATE: 2001-07-23
PRIOR FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR PILING DATE: 2000-07-21
PRIOR PILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SEQ ID NO 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Garrett, James B.
APPLICANT: Shon, Ki. Joon
APPLICANT: Shon, Ki. Joon
APPLICANT: Jacobsen, Richard
APPLICANT: Jones, Robert M.
APPLICANT: Garrier, G. Edward
ITLE APPLICANT: Carrier, G. Edward
FILE REFERENCE: 2314-241
CURRENT APPLICATION WUMBER: US/09/910,082A
CURRENT FILING DATE: 2001-07-23
PRIOR PILING DATE: 2000-07-21
PRIOR PILING DATE: 2000-07-21
PRIOR PILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SEQ ID NO 395
SEQ ID NO 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
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Olivera, Baldomero M.
McIntosh, J. Michael
Watkins, Maren
                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Conus ermineus
US-10-765-926-130
                      FILE REFERENCE: 2314-241
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Best Local Similarity
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US-09-910-082A-395
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; ORGANISM: Conu
US-09-910-082A-395
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Pred. No. 0.025;
6; Mismatches 7; Indels
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0.011;
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APPLICANT: Olivera, Baldomero M.
APPLICANT: Molitosh, J. Michael
APPLICANT: Warkins, Maren
APPLICANT: Garrett, James B.
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                                                                                                                                                                      Query Match

48.8%; Score 78.5; D
Best Local Similarity 46.2%; Pred. No. 0.01
Matches 12; Conservative 6; Mismatches
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TITLE OF INVENTION: Cmega-Conopeptides
FILE REFERENCE: 2314-241
CURRENT APPLICATION NUMBER: US/09/910,082A
FRIOR APPLICATION NUMBER: US 60/219,616
FRIOR APPLICATION NUMBER: US 60/219,616
FRIOR FILING DATE: 2000-07-21
FRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: PATENTIN VERSION 3.0
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                                                                                                                                                                                                                                                                                   2 CKPKGRKCFPHQKDCCNKTCTR-SKC 26
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47 CKPKGRKCFPHQKDCCNKTCTR-SKC 71
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TITLE OF INVENTION: Omega-Conopeptides
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Olivera, Baldomero M.
McIntosh, J. Michael
Watkins, Maren
NUMBER OF SEQ ID NOS: 413
SOFTWARE: Patentin version 3.0
SEQ ID NO 354
LENGTH: 27
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Jacobsen, Richard
Jones, Robert M.
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Jacobsen, Richard
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Best Local Similarity 46.2
Matches 12; Conservative
                                                                                      ; TYPE: PRT
; ORGANISM: Conus ermineus
US-10-765-926-354
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US-09-910-082A-130
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Gaps

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Application US/10765926
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Olivera, Baldomero M.
McIntosh, J. Michael
Watkins, Maren
Garrett, James E.
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Pred. No. 0.042;
5; Mismatches
                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/765,926
CURRENT FILING DATE: 2004-01-29
PRIOR APPLICATION NUMBER: US 09/910,082
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR APPLICATION NUMBER: US 60/265,888
PRIOR FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: US 60/265,888
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/910,082A CURRENT FILING DATE: 2001-07-23
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PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: US 60/265,888
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: Patentin version 3.0
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TITLE OF INVENTION: Omega-Conopeptides
FILE REFERENCE: 2314-241
                                                                                                                                                    CANT: Cartier, G. Edward
OF INVENTION: Omega-Conopeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 257, Application US/09910082A
; Publication No. US20030119731A1
; GENERAL INFORMATION:
Olivera, Baldomero M.
McIntosh, J. Michael
Watkins, Maren
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Best Local Similarity 42.3%;
Matches 11; Conservative
                                                                                        Shon, Ki-Joon
Jacobsen, Richard
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Jacobsen, Richard
Jones, Robert M.
                                                                   Јатев Е.
                                                                                                                                      Jones, Robert M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Conus striatus
US-10-765-926-395
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; ORGANISM: Conus striatus
US-09-910-082A-257
                                                                                                                                                                                                   REFERENCE: 2314-241
                                                                     Garrett
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Ouery Match 46.0%; Score 74; DB 16; Length 30; Best Local Similarity 42.3%; Pred. No. 0.042; Matches 11; Conservative 5; Mismatches 10; Indels
APPLICANT: University of Utah Research Foundation
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Olivers Baldomero M.
APPLICANT: Watkins, Maren
APPLICANT: Watkins, Maren
APPLICANT: Show, Ki-Joon
APPLICANT: Jacobsen, Richard
APPLICANT: Jones, Robert M.
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CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: PatentIn version 3.0
SEQ ID NO 217
LENGTH: 72
                                                                                                                                                                                                                                                                                                                                                                         CURRENT FILING DATE: 2004-01-29
PRIOR APPLICATION NUMBER: US 09/910,082
PRIOR FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR FILING DATE: 2000-07-21
PRIOR PELING DATE: 2000-07-21
PRIOR FILING DATE: 2000-07-81
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
                                                                                                                                                                                                                                                        APPLICANT: Carrier, G. Edward
TITLE OF INVENTION: Omega-Conopeptides
FILE REFERENCE: 2314-241
FILE REFERENCE: 2314-241
CURRENT APPLICATION NUMBER: US/10/765,926
CURRENT FILING DATE: 2004-01-29
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PPLICANT: Cartier, G. Edward
ITLE OF INVENTION: Omega-Conopeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 217, Application US/09910082A Publication No. US20030119731A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cognetix, Inc.
Olivera, Baldomero M.
McIntosh, J. Michael
Watkins, Maren
Garrett, James E.
Shon, Ki-Joon
Jacobsen, Richard
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Gaps

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Tue Apr 19 09:12:34 2005

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Score 71; DB 10; Length 27;
Pred. No. 0.087;
3; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: University of Utah Research Foundation APPLICANT: Cognetix, Inc.
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Publication No. US20030119731A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cartier, G. Edward
TITLE OF INVENTION: Omega-Conopeptides
FILE REPERENCE: 2314-241
CURRENT APPLICATION NUMBER: US/10/765,926
CURRENT FILING DATE: 2004-01-29
PRIOR APPLICATION NUMBER: US 09/910,082
PRIOR FILING DATE: 2001-07-23
PRIOR PRILING DATE: 2000-07-21
PRIOR PILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR APPLICATION NUMBER: US 60/265,888
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: PATENT VERSION 3.0
SSOFTWARE: PATENT VERSION 3.0
                                                60/265,888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 384, Application US/10765926
Publication No. US20040132663A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      1 CRIXNOKCFQHLDDCCSRKC 20
                                                                                                                                                                                                                                                                                                                                                                                  2 CKKTGRKCFPHQKDCCGRAC 21
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McIntosh, J. Michael
Warkins, Maren
Garrett, James E.
Shon, Ki-Joon
Jacobsen, Richard
Jones, Robert M.
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Olivera, Baldomero M.
McIntosh, J. Michael
Watkins, Maren
Garrett, James E.
                  PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2000-02-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: Patentin version 3.0
LENGTH: 27
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1 Similarity 50.0%;
10; Conservative
                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Conus purpurascens
US-09-910-082A-384
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Best Local Similarity 50.0%;
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 10; Conserv
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                                                                                                        Gaps
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                                            Query Match 45.3%; Score 73; DB 10; Length 72; Best Local Similarity 50.0%; Pred. No. 0.12; Matches 10; Conservative 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 16; Length 72;
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                                                                                                                                                                                                                                                                                                                                                      APPLICANT: University of Utah Research Foundation APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M. APPLICANT: Michael APPLICANT: Watkins, Maxen APPLICANT: Garrett, James E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: University of Utah Research Foundation
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Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Shon, Ki-Joon
APPLICANT: Shon, Ki-Joon
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Cartier, G. Edward
ITILE OF INVENTION: Omega-Conopeptides
FILE REFERENCE: 2314-241
CURRENT APPLICATION NUMBER: US/10/765,926
CURRENT FILING DATE: 2004-01-29
PRIOR APPLICATION NUMBER: US 09/910,082
PRIOR PELING DATE: 2001-07-23
PRIOR PELING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR PELING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: US 60/265,888
PRIOR PELING DATE: 2001-02-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: Markins, Maren
APPLICANT: Garrett, James E.
APPLICANT: Shon, Ki-Joon
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Gartier, G. Edward
TITLE OF INVENTION: Omega-Conopeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 60/219,616
                                                                                                                                                                                                                                                                                          Sequence 217, Application US/10765926
Publication No. US20040132663A1
GENERAL INFORMATION:
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                                                                                                                                  1 CRIXNOKCFOHLDDCCSRKC 20
                                                                                                                                                                1 CRIXNOKCFQHLDDCCSRKC 20
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SOFTWARE: PatentIn version 3.0
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1 Similarity 50.0%;
10; Conservative
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; ORGANISM: Conus purpurascens
US-10-765-926-217
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Matches 10; Conserva
US-09-910-082A-217
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LENGTH: 72
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Gaps

7; Indels

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US-10-765-926-258
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                                                 APPLICANT: Jones, Robert M.
APPLICANT: Cartier, G. Edward
TITLE OF INVENTION: Omega-Conopeptides
FILE REFERENCE: 2314-241
CURRENT APPLICATION NUMBER: US/09/910,082A
CURRENT APPLICATION NUMBER: US 60/219,616
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2000-055
NUMBER OF SEQ ID NOS: 413
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
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APPLICANT: Olivera, Baldomero M.
APPLICANT: Marchins, Marcen
APPLICANT: Warkins, Marcen
APPLICANT: Warkins, Marcen
APPLICANT: Shon, Ki-Joon
APPLICANT: Jacobsen, Richard
FILE REFERENCE: 2314-241
CURRENT PILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 60/205, 888
PRIOR FILING DATE: 2001-07-21
PRIOR APPLICATION NUMBER: US 60/205, 888
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
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Best Local Similarity 50.0%;
Matches 10; Conservative
Shon, Ki-Joon
Jacobsen, Richard
                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GRGANISM: Conus purpurascens US-10-765-926-223
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Matches 10; Conservative
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LENGTH: 72
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RESULT 63 US-09-910-082A-258

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FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(26)
OTHER INFORMATION: Xaa at residue 13 is Tyr, 1251-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O
OTHER INFORMATION: -sulpho-Tyr or O-phospho-Tyr
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41.6%; Score 67; DB 10; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.26;
Matches 11; Conservative 5; Mismatches 10; Indels
                                                                   APPLICANT: University of Utah Research Foundation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: University of Utah Research Foundation APPLICANT: University Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: Watkins, Maren
                                                                                                                                                                                                                                            APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Jones, Robert M.
APPLICANT: Jones, Robert M.
APPLICANT: Jones, Robert M.
TITLE OF INVENTION: Omega-Conopeptides
FILE REFERENCE: 2314-241
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR FILING DATE: 2000-07-21
PRIOR PILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: PatentIn Version 3.0
SEQ ID NO 258
LENGTH: 26
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PRIOR APPLICATION NUMBER: US 09/910,082
PRIOR FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR APPLICATION NUMBER: US 60/265,888
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/765,926 CURRENT FILING DATE: 2004-01-29
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APPLICANT: Shon, Ki-Joon
APPLICANT: Jacobsen, Richard
APPLICANT: Jones, Robert M.
APPLICANT: Carrier, G. Edward
TITLE OF INVENTION: Omega-Conopeptides
Application US/09910082A
... US20030119731A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 258, Application US/10765926
Publication No. US20040132663A1
                                                                                                       Cognetix, Inc.
Olivera, Baldomero M.
McIntosh, J. Michael
Matkins, Maren
Garrett, James E.
Shon, Ki-Joon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Conus striatus
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GENERAL INFORMATION:
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Gaps
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OTHER INFORMATION: Xaa at residue 13 is Tyr, 1251-Tyr, mono-iodo-Tyr,
OTHER INFORMATION: di-iodo-Tyr, 0 -sulpho-Tyr or O-phospho-Tyr
US-10-765-926-268
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; OTHER INFORMATION: Xaa at residue 1, 5, 11 and 27 is Pro or Hyp US-09-910-082A-218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

39.8%; Score 64; DB 16; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.59;
Matches 11; Conservative 4; Mismatches 11; Indels
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                                            APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Cartier, G. Edward
TITLE OF INVENTION: Omega-Conopeptides
FILE REFERENCE: 2314-241
CURRENT APPLICATION NUMBER: US/10/765,926
CURRENT FILING DATE: 2004-01-29
PRIOR APPLICATION NUMBER: US 09/910,082
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR PILING DATE: 2000-07-21
PRIOR PILING DATE: 2000-07-21
PRIOR PILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: Patentin Version 3.0
SENGTH: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: COGNETIX, INC.
APPLICANT: COGNETIX, INC.
APPLICANT: COGNETIX, INC.
APPLICANT: MCINTON, J. Michael
APPLICANT: MATLAIS, MARCH
APPLICANT: WATKINS, MARCH
APPLICANT: GATTEL, James E.
APPLICANT: Shon, Ki-Joon
APPLICANT: Shon, Ki-Joon
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Robert M.
APPLICANT: Jacobsen, Robert M.
APPLICANT: Gattler, G. Edward
TITLE OF INVENTION: Omega-Conopeptides
FILE REFERENCE: 2314-241
CURRENT FILING DATE: 2001-07-23
PRIOR PILING DATE: 2001-07-21
PRIOR PILING DATE: 2001-02-05
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SOCTUMEN: PARCHIN VERSION 3.0
SEQ ID NO 2.18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CKLKGQSCRKTSXDCCSGSCGRSGKC 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Conus striatus
FEATURE:
NAME/KER: PEPTIDE
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Best Local Similarity
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OTHER INFORMATION: Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
OTHER INFORMATION: -sulpho-Tyr or O-phospho-Tyr
                                                                                                                                                                                                                                                                     ö
                                                            ; LOCATION: (1)..(26); OTHER INFORMATION: Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, CTHER INFORMATION: di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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41.6%; Score 67; DB 16; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.26;
Matches 11; Conservative 5; Mismatches 10; Indels
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39.8%; Score 64; DB 10; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.59;
Matches 11; Conservative 4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 65
US-09-910-082A-268
; Sequence 268, Application US/09910082A
; Publication No. US20030119731A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Coquetix, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 268, Application US/10765926
Publication No. US20040132663A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cógnetix. Inc.
APPLICANT: Olivera, Baldomero M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 2314-241
CURRENT APPLICATION NUMBER: US/09/910,082A
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/265,888
PRIOR FILING DATE: 2001-02-05
SQFTWARE: Patentin version 3.0
SGFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                 1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
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APPLICANT: Cartier, G. Edward
TITLE OF INVENTION: Omega-Conopeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Olivera, Baldomero M. McIntosh, J. Michael Watkins, Maren Garrett, James E.
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Olivera, Baldomero M.
McIntosh, J. Michael
Watkins, Maren
Garrett, James B.
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: Jacobsen, Richard
ORGANISM: Conus striatus
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ORGANISM: Conus striatus
                                                  NAME/KEY: PEPTIDE LOCATION: (1) . (2)
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COTHER INFORMATION: Xaa at residue 1, 5, 11 and 27 is Pro or Hyp
US-10-765-926-218
                                                                                                                                                                                                                                                                                                      Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 16; Length 27;
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                                                                                                                                                                                                                                                                                                                                                  7:
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                                                                                                                                                                                                                                                                                                        Score 64; DB 16
Pred. No. 0.61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION UNMBER: US 0/10/765,926

PRIOR APPLICATION NUMBER: US 09/910,082

PRIOR PILING DATE: 2001-07-23

PRIOR APPLICATION NUMBER: US 60/219,616

PRIOR FILING DATE: 2000-07-21

PRIOR APPLICATION NUMBER: US 60/265,888

PRIOR APPLICATION NUMBER: US 60/265,888

PRIOR FILING DATE: 2001-02-05

NUMBER OF SEQ ID NOS: 413

SOFTWARE: PATCHILING PATE: 201-20-6

SEQ ID NO 382

LENGTH: 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cognetix, Inc.
APPLICANT: Coloretix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: Matkins, Maren
APPLICANT: Garrett, James E.
APPLICANT: Shon, Ki-Joon
APPLICANT: Jacobsen, Richard
APPLICANT: Onces, Robert M.
APPLICANT: Onces, Robert M.
APPLICANT: Cartier, G. Edward
TITLE OF INVENTION: Omega-Conopeptides
FILE REFERENCE: 2314-241
CURRENT APPLICATION NUMBER: US/10/765,926
CURRENT FILING DATE: 2004-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 64;
Pred. No.
                         60/265,888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 71
US-09-910-082A-350
; Sequence 350, Application US/09910082A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 382, Application US/10765926 Publication No. US20040132663A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                          1 CRIXNOKCFOHLDDCCSRKC 20
                                                                                                                                                                                                                                                                                                                                                                                                                   2 CKTXGRKCFXHQKDCCGRAC 21
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PRIOR FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: US 60/2
PRACOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: Patentin version 3.0
SEQ ID NO 218
LENGTH: 27
TYPE: PRT
ORGANISM: Conus purpurascens
FEATURE:
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COTHER INFORMATION: Xaa is Hyp
US-10-765-926-382
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55.0%;
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Best Local Similarity 55.0%;
Matches 11; Conservative
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Best Local Similarity 55.0.
Then 11; Conservative
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        7; Indels
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APPLICANT: Olivers, Baldomero M.
APPLICANT: McIncosh, J. Michael
APPLICANT: Watkins, Maren
                                                                                                                                                                                                                                           APPLICANT: University of Utah Research Foundation
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TITLE OF INVENTION: Omega-Conopeptides
FILE REFERENCE: 2314-241
CURRENT APPLICATION NUMBER: US/09/910,082A
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR APPLICATION NUMBER: US 60/25,888
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: PALENTIN Version 3.0
SEQ ID NO 382
      2; Mismatches
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CURRENT APPLICATION NUMBER: US/10/765,926
CURRENT FILING DATE: 2004-01-29
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APPLICATION NUMBER: US 09/910,082
FILING DATE: 2001-07-23
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APPLICANT: Cartier, G. Edward
IITLE OF INVENTION: Omega-Conopeptides
                                                                                                                                                                          Sequence 382, Application US/09910082A Publication No. US20030119731A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 218, Application US/10765926; Publication No. US20040132663A1; GENERAL INFORMATION:
                                            1 CRIXNQKCFQHLDDCCSRKC 20
                                                                   1 CRIXNOKCFOHLDDCCSRKC 20
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Olivera, Baldomero M.
McIntosh, J. Michael
Watkins, Maren
Garrett, James E.
Shon, Ki-Joon
Jacobsen, Richard
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OTHER INFORMATION: Xaa is Hyp
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Shon, Ki-Joon
Jacobsen, Richard
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ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                             Jones, Robert M.
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hes 11; Conservative
    11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-910-082A-382
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APPLICANT:
APPLICANT:
APPLICANT:
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Matches
    Matches
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Publication No. US20030119731A1

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39.4%; Score 63.5; DB 10; Length 73;
Best Local Similarity 37.0%; Pred. No. 1.7;
Matches 10; Conservative 8; Mismatches 8; Indels :
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Sequence 94, Application US/10765926

Publication No. US20040132663A1

GENERAL INFORMATION:

APPLICANT: University of Utah Research Foundation

APPLICANT: Oggnetix, Inc.

APPLICANT: Olivera, Baldomero M.

APPLICANT: Olivera, Baldomero M.

APPLICANT: McIntosh, J. Michael

APPLICANT: Garkful, Maren

APPLICANT: Garkful, James E.

APPLICANT: Shon, Ki-Joon

APPLICANT: Accobes, Richard
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                                                                                                                                                                                                                                                                                                                   APPLICANT: Cognetix, To Coult Research Founda APPLICANT: Cognetix, To Coult Research Founda APPLICANT: Marins, Marchael APPLICANT: Marins, Marchael APPLICANT: Watkins, Marchael APPLICANT: Watkins, Marchael APPLICANT: Shon, Ki-Joon APPLICANT: Jacobsen, Richard APPLICANT: Jacobsen, Richard APPLICANT: Jones, Robert M. APPLICANT: Cartier, G. Edward APPLICANT: Cartier, G. Edward APPLICANT: Cartier, G. Edward APPLICANT: Dones, Robert M. CURRENT APPLICATION NUMBER: US 60/219,616 PRIOR FILING DATE: 2001-07-23 PRIOR PRLING DATE: 2000-07-21 PRIOR FILING DATE: 2000-07-21 PRIOR FILING DATE: 2001-02-05 NUMBER OF SEQ ID NOS: 413 SOFTWARE PATENTION NUMBER: US 60/265,888 SOFTWARE: Patentin version 3.0
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APPLICANT: CARTIER, G. Edward
TITLE OF INVENTION: Omega-Conopeptides
FILE REFERENCE: 2314-24
CURRENT APPLICATION NUMBER: US/10/765,926
PRIOR APPLICATION NUMBER: US/910,082
PRIOR FILING DATE: 2001-07-23
PRIOR FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR FILING DATE: 2001-07-21
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR FILING DATE: 2001-07-21
PRIOR FILING DATE: 2001-07-21
PRIOR FILING DATE: 2001-07-21
NUMBER: OF SEQ. ID NOS: 413
      1 CRIXNOKCFQHLDDCCSRKCNRFN-KC 26
                                          1 CRIXNOKCFQHLDDCCSRKCNRFN-KC 26
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; ORGANISM: Conus circumcisus
US-09-910-082A-94
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39.4%; Score 63.5; DB 10; Length 27;
Best Local Similarity 37.0%; Pred. No. 0.7;
Matches 10; Conservative 8; Mismatches 8; Indels
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APPLICANT: University of Utah Research Foundation
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: Marinesh, J. Michael
APPLICANT: Watkins, Maren
APPLICANT: Shon, Ki-Joon
APPLICANT: Shon, Ki-Joon
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Jones, Robert M.
APPLICANT: Ornes, Robert M.
APPLICANT: Onega-Conopeptides
CURRENT FILING DATE: 2001-07-21
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2001-07-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: PatentIn version 3.0
SEQ ID NO 350
LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: University of Utah Research Foundation
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix Inc.
APPLICANT: Cognetix Inc.
APPLICANT: McIntcosh, J. Michael
APPLICANT: Matkins, Maren
APPLICANT: Garrett, James E.
APPLICANT: Shon, Ki. Joon
APPLICANT: Shon, Ki. Joon
APPLICANT: Jacobsen, Richard
APPLICANT: Cartier, G. Schard
TITLE OF INVENTION: Omega-Conopeptides
FILE REFERENCE: 2314-241
CURRENT APPLICATION NUMBER: US 09/910,082
FRIOR APPLICATION NUMBER: US 09/910,082
FRIOR PELING DATE: 2001-07-23
FRIOR PELING DATE: 2000-07-21
FRIOR PELING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: PARCHING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: PERMET ON SEQ ID NOS: 413
SEQ ID NO 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CRIXNOKCFQHLDDCCSRKCNRFN-KC 26
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| CKSKGAKCSRLMYDCCSGSCSRYSGRC 27
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; Publication No. US20040132663A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Conus circumcisus
US-09-910-082A-350
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Best Local Similarity
Matches 10; Conserva
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; ORGANISM: Conu
US-10-765-926-350
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; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa at residue 1, 11 and 27 is Pro or Hyp
US-09-910-082A-224
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Sequence 224, Application US/09910082A
Publication No. US20030119731A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Genetix, Inc.
APPLICANT: Matchis, March
APPLICANT: Watkins, March
APPLICANT: Grarett, James E.
APPLICANT: Garrett, James E.
APPLICANT: Garrett, Genes E.
APPLICANT: Garrett, Genes E.
APPLICANT: Garrier, G. Edward
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Robert M.
APPLICANT: Jacobsen, Robert M.
APPLICANT: Jones, Robert M.
APPLICANT: Jones, Robert M.
APPLICANT: Geriter, G. Edward
TITLE OF INVENTION: Omega-Conopeptides
FILE REFERENCE: 2314-241
CURRENT FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: US 60/265,888
PRIOR FILING DATE: 2001-07-26
PRIOR FILING DATE: 2001-07-26
PRIOR PAPLICATION NUMBER: US 60/265,888
PRIOR FILING DATE: 2001-02-05
SEQ ID NO SEQ ID NOS: 413
LENGTH: 27
LENGTH: 27
                    APPLICANT: Marching, Walten, APPLICANT: Shen, Greg S.
TITLE OF INVENTION: 1.2 Superfamily Conotoxins FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: PATCHIN VERSION 3.0
SEQ ID NO 167
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38.8%; Score 62.5; D
Best Local Similarity 40.7%; Pred. No. 2.2;
Matches 11; Conservative 5; Mismatches
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ORGANISM: Conus purpurascens
PEATURE:
LOCATION: (1)..(27)
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US-09-894-882-167
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                                                                                                                                                                   Query Match 39.4%; Score 63.5; DB 16; Length 73; Best Local Similarity 37.0%; Pred. No. 1.7; Matches 10; Conservative 8; Mismatches 8; Indels 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 369, Application US/09894882
Patent No. US20020102607A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Shetty, Reshma
APPLICANT: Shetty, Reshma
APPLICANT: Jimenez, Elsie C.
APPLICANT: Offivera, Baldomero M.
APPLICANT: Olivera, Maichael
APPLICANT: Matkins, Maren
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Cognetix, Inc.
Walker, Craig S.
Shetry, Resha
Jimenez, Elsie C.
McIncosh, J. Michael
Olivera, Baldomero M.
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APPLICANT: Shen, Greg S.
TITLE OF INVENTION: I-Superfamily Conotoxins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILLING DATE: 2001-00-629
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR PILING DATE: 2000-11-08
PRIOR PILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-14
PRIOR PILING DATE: 2001-01-29
PRIOR FILING DATE: 2001-01-29
PRIOR FILING DATE: 2001-01-29
PRIOR FILING DATE: 2001-01-29
PRIOR FILING DATE: 2001-01-29
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CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
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Patent No. US20020102607A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research
APPLICANT: Cognetix, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Shetty, Rebhna
                                                     TYPE: PRT; Conus circumcisus
ORGANISM: Conus circumcisus
US-10-765-926-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Conus betulinus
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US-09-894-882-167
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SOFTWARE: Pate
SEQ ID NO 369
SEQ ID NO 94
LENGTH: 73
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NAME/KEY: PEPTIDE

LOCATION: (1)..(27)

COTHER INFORMATION: Xaa at residue 1, 4, 11 and 27 is Pro or Hyp
US-09-910-082A-131
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38.2%; Score 61.5; DB 10; Length 27;
Best Local Similarity 47.8%; Pred. No. 1.2;
Matches 11; Conservative 5; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                        9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 131, Application US/09910082A
Publication No. US20030119731A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 131, Application US/10765926
Publication No. US20040132663A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
                                                                                                                                                                                                                                                                                       Score 62; DB
Pred. No. 2.6;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: McIntosh, J. Michael
APPLICANT: Garrett, James E.
APPLICANT: Garrett, James E.
APPLICANT: Shon, Ki-Joon
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Cartier, G. Edward
TITLE OF INVENTION: Omega-Conopeptides
TITLE OF INVENTION: Omega-Conopeptides
TITLE OF INVENTION NUMBER: US/09/910,082A
CURRENT FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR APPLICATION NUMBER: US 60/265,888
PRIOR FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: US 60/265,888
NUMBER OF SEQ ID NOS: 413
SOFTWARE: PatentIn version 3.0
SEROID NO 131
                                                                                                                                                                                                                                                                                                                                                                       1 CRIXNQKCFQHLDDCCSRKCNRF-NKCV 27
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PRIOR FILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: US 60/173,754
PRIOR FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 409
SOFTWARE: Patentin version 3.0
SEQ ID NO 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S KGRKCFXHQKDCCNKTCTR-SKC 26
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                                                                                                                                                                                                                                                                                Query Match 38.5%;
Best Local Similarity 39.3%;
Matches 11; Conservative (
                                                                                                                                                                                          TYPE: PRT
ORGANISM: Conus distans
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ORGANISM: Conus ermineus
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; OTHER INFORMATION: Xaa at residue 1, 11 and 27 is Pro or Hyp
US-10-765-926-224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 38.5%; Score 62; DB 16; Length 27; Best Local Similarity 50.0%; Pred. No. 1.1; Matches 10; Conservative 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Only versity of Utah Research Foundation APPLICANT: Only vers, Baldomero M. APPLICANT: Hilly and David R. APPLICANT: Hilly and David R. APPLICANT: Hilly and David R. APPLICANT: Layer, Richard T. APPLICANT: Layer, Richard T. APPLICANT: Jones, Robert M. TITLE OF INVENTION: O-Superfamily Conotoxin Peptides FILE REFERENCE: 2314-227
CURRENT APPLICATION NUMBER: US 60/243,412
PRIOR APPLICATION NUMBER: US 60/243,412
                                                                                                                                                Sequence 224, Application US/10765926
Publication No. US20040132663A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
                                                                                                                                                                                                                         Sequence 207, Application US/09749637A Patent No. US20020173449A1 GENERAL INFORMATION:
CRIXNOKCFOHLDDCCSRKC 20
                          2 CKKTGRKCFXHQKDCCGRAC 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: PEPTIDE LOCATION: (1)..(27
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8; Conservative
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ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-910-082A-5
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                Matches
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; OTHER INFORMATION: Xaa at residue 1, 4, 11 and 27 is Pro or Hyp US-10-765-926-131
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APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: Watchins, Maren
APPLICANT: Garrett, James E.
APPLICANT: Garrett, James E.
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Jones, Robert M.
APPLICANT: Jones, Robert M.
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Jones, Robert M.
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, 
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38.2%; Score 61.5; I
Best Local Similarity 47.8%; Pred. No. 1.2;
Matches 11; Conservative 5; Mismatches
                                                                                                                                                                                             APPLICANT: Jones, Robert M.
APPLICANT: Cartier, G. Edward
TITLE OF INVENTION: Onega-Conopeptides
FILE REPERENCE: 214-241
CURRENT APPLICATION NUMBER: US/10/765,926
CURRENT FILING DATE: 2004-01-29
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR FILING DATE: 2001-07-21
SRIOR FILING DATE: 2001-07-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 359, Application US/09910082A Publication No. US20030119731A1 GENERAL INFORMATION:
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J. Michael
                                                                                                                                                                     Jacobsen, Richard
                                             Watkins, Maren
Garrett, James E.
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ORGANISM: Conus ermineus
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Best Local Similarity
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ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-910-082A-359
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SEQ ID NO 359
LENGTH: 27
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CH 2 CKPORKCIANRON 22

SEQUENCE 339, ADDICATION NO. US200401286331

SEQUENCE 330, ADDICATION NO. US200401286331

SEQUENCE 314, ADDICATION NO. US200401280

SEQUENCE 314, ADDICATION NO. USBR. US 50,710,822

CURRENT FILING DATE: 2014-31

SEQUENCE 314, ADDICATION NO. USBR. US 50,710,822

CURRENT FILING DATE: 2014-01.29

SEQUENCE 314, ADDICATION NO. USBR. US 50,710,822

SEQUENCE 314, ADDICATION NO. USBR. USBR.
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Watkins, Maren
Garrett, James E.
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; ORGANISM: Conus rattus
US-09-910-082A-236
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ORGANISM: Conus rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-910-082A-390
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US-10-765-926-236
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37.9%; Score 61; DB 10; Length 74;
Best Local Similarity 38.1%; Pred. No. 3.4;
Matches 8; Conservative 6; Mismatches 7; Indels
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37.9%; Score 61; DB 16; Length 74;
Best Local Similarity 38.1%; Pred. No. 3.4;
Matches 8; Conservative 6; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: University of Utah Research Foundation APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M. APPLICANT: Minnosh, J. Michael APPLICANT: Watkins, Maren APPLICANT: Garrett, James E.
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WS-09-910.082A-236
Sequence 236, Application US/09910082A
Publication No. US20030119731A1
GENERAL INFORMATION: ..
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J. Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US/10/765,926

PRIOR APPLICATION NUMBER: US 09/910,082

PRIOR FILING DATE: 2001-07-23

PRIOR PLILING DATE: 2000-07-21

PRIOR PELICATION NUMBER: US 60/219,616

PRIOR PELICATION NUMBER: US 60/265,888

PRIOR PILING DATE: 2000-07-21

PRIOR PELING DATE: 2001-02-05

NUMBER OF SEQ ID NOS: 413

SOFTWARE: PATENTIN VERSION 3.0

SEQ ID NO 5

LENGTH: 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Shon, Ki-Joon
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Cartier, G. Edward
ITLE OF INVENTION: Omega-Conopeptides
FILE REFERENCE: 2314-241
CURRENT APPLICATION NUMBER: US/10/765,926
CURRENT FILING DATE: 2004-01-29
                                                                                                                                                                                       ; OTHER INFORMATION: unknown Conus species US-09-910-082A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) OTHER INFORMATION: unknown Conus species US-10-765-926-5
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                                                                                                                                                                                                                                                                                                                                                                                     47 CKPPGRKCLNRKNECCSKFCN 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47 CKPPGRKCLNRKNECCSKFCN 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/10765926; Publication No. US20040132663A1; GENERAL INFORMATION:
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: Patentin version 3.0
SEQ ID NO 5
LENGTH: 74
                                                                                                                TYPE: PRT
ORGANISM: Unknown
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ORGANISM: Unknown
                                                                                                                                                                      FEATURE:
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  Length 27;
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5.1;
                                                     Indels
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APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Markins, Maren
APPLICANT: Matkins, Maren
APPLICANT: Sans E.
APPLICANT: Shon, Ki-Joon
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Cartier, G. Edward
TITLE OP INVENTION: Omega-Conopeptides
Query Match 37.0%; Score 59.5; DB 16; Best Local Similarity 45.5%; Pred. No. 2.1; Matches 10; Conservative 2; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: University of Utah Research Foundation APPLICANT: University of Utah Research Foundation APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M. APPLICANT: McInael APPLICANT: Watkins, Maren APPLICANT: Garrett, James E.
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CURRENT APPLICATION NUMBER: US/09/910,082A
CURRENT APPLICATION NUMBER: US 60/219,616
PRIOR PELLING DATE: 2001-07-21
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SEQ ID NO 235
LENGTH: 74
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37.0%; Score 59.5; D
Best Local Similarity 45.5%; Pred. No. 5.1;
Matches 10; Conservative 2; Mismatches
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APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, G. Bdward
TITLE OF INVENTION: Omega-Conopeptides
FILE REFERENCE: 2314-241
CURRENT APPLICATION NUMBER: US/10/75,926
CURRENT APPLICATION NUMBER: US 09/910,082
PRIOR FILING DATE: 2001-07-23
PRIOR FILING DATE: 2000-07-21
PRIOR PLING DATE: 2000-07-21
PRIOR PLING DATE: 2000-07-21
                                                                                                                                                                                                                                                                         Sequence 235, Application US/09910082A Publication No. US20030119731A1 GENERAL INFORMATION:
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Publication No. US20040132663A1
GENERAL INFORMATION:
                                                                                                                                       1 CNARNDGCSQH-SQCCSGSCNK 21
                                                                                                       1 CRIXNOKCFOHLDDCCSRKCNR 22
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ORGANISM: Conus rattus
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                                                             APPLICANT: University of Utah Research Foundation APPLICANT: Cognetix, Inc.
APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: Watkins, Maren
APPLICANT: Garrett, James E.
APPLICANT: Shon, Ki-Joon
APPLICANT: Jacobsen, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: University of Utah Research Foundation
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Marchis, Maren
APPLICANT: Watkins, Maren
APPLICANT: Garrett, James E.
APPLICANT: Garcett, James E.
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US/910,082
PRIOR PELING DATE: 2004-01-29
PRIOR PILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR PILING DATE: 2000-07-21
PRIOR PELING DATE: 2000-02-15
PRIOR PELING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SEQ ID NO 236
LENGTH: 27
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PRIOR APPLICATION NUMBER: US 09/910,082

PRIOR PILING DATE: 2001-07-23

PRIOR APPLICATION NUMBER: US 60/219,616

PRIOR PELING DATE: 2000-07-21

PRIOR APPLICATION NUMBER: US 60/265,888

PRIOR PILING DATE: 2001-02-05

NUMBER OF SEQ ID NOS: 413

SEQ ID NO 390

LENGTH: 27
                                                                                                                                                                                                                                                                               APPLICANT: Jones, Robert M.
APPLICANT: Cartier, G. Edward
TITLE OF INVENTION: Omega-Conopeptides
FILE REFERENCE: 2314-241
CURRENT APPLICATION NUMBER: US/10/765,926
CURRENT FILING DATE: 2004-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cartier, G. Edward
TITLE OF INVENTION: Omega-Conopeptides
TILE REFERENCE: 2314-24
CURRENT APPLICATION NUMBER: US/10/765,926
CURRENT FILING DATE: 2004-01-29
Application US/10765926
o. US20040132663A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 390, Application US/10765926 Publication No. US20040132663A1 GENERAL INFORMATION:
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Best Local Similarity 45.5
Matches 10; Conservative
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, ORGANISM: Conus rattus
US-10-765-926-390
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US-10-765-926-236
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                                                                                                                                      DB 14; Length 735; 43;
                                                                                                                                                                                  Indels
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                                                                                                                                                                                  4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: Olivera, Baldomero M.
APPLICANT: Warkins, Maren
APPLICANT: Garrett, James E.
APPLICANT: Garrett, James E.
APPLICANT: Garrett, James E.
APPLICANT: Garrett, James E.
APPLICANT: Garrett, G. Edward
APPLICANT: Garrier, G. Edward
APPLICANT: Jones, Robert M.
APPLICANT: Garrier, G. Edward
APPLICANT: Garrier, E. Solol-07-23
PRIOR PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR APPLICATION NUMBER: US 60/265,888
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 413
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APPLICANT: Cartier, G. Edward
TITLE OF INVENTION: Omega-Conopeptides
FILE REFERENCE: 2314-241
CURRENT APPLICATION NUMBER: US/09/910,082A
CURRENT FILING DATE: 2001-07-23
                                                                                                                                      Score 59;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 391, Application US/09910082A Publication No. US20030119731A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 392, Application US/09910082A
Publication No. US20030119731A1
                                                                                                                                                                                                                                                     254 CEKNIDDCVNSKCENGGKCV 273
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                                      TYPE: PRT ORGANISM: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Olivera, Baldomero M. McIntosh, J. Michael Watkins, Maren Garrett, James E. Shon, Ki-Joon Jacobsen, Richard
                                                                                                                             Query Match
Best Local Similarity 45.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin version 3.0
SEQ ID NO 391
LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT; ORGANISM: Conus rattus
US-09-910-082A-391
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Best Local Similarity
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US-09-910-082A-392
                                                                                    US-10-289-776-9
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT PLING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PLING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 6999
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                                                                                                                                                                                                            37.0%; Score 59.5; DB 16; Length 74; ilarity 45.5%; Pred. No. 5.1; Conservative 2; Mismatches 9; Indels
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36.6%; Score 59; DB 15; Length 601;
Best Local Similarity 45.0%; Pred. No. 36;
Matches 9; Conservative 4; Mismatches 7; Indels
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Publication No. US20030170727A1
GENERAL INFORMATION:
APPLICANT: Goodman, Corey
APPLICANT: Rid, Thomas
APPLICANT: Brose, Katja
APPLICANT: Goodman, Corey
APPLICANT: Cestier-Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
CURRENT APPLICATION NUMBER: US/10/289,776
CURRENT FILING DATE: 2002-11-06
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PRIOR PLICATION NUMBER: US/09/540,245

PRIOR FILING DATE: 2000-03-31

PRIOR PLILING DATE: 1997-11-14

PRIOR PLILING DATE: 1997-11-14

PRIOR PLILING DATE: 1998-04-07

NUMBER OF SEQ ID NOS: 20

SOFTWARE: PATENTIN VET: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-369-493-6999
Sequence 6999, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
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120 CEKNIDDCVNSKCENGGKCV 139
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PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 235
LENGTH: 74
                                                                                                            TYPE: PRT ORGANISM: Conus rattus US-10-765-926-235
                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 10; Conserva
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45.5%; Pred. No. 6.7;
tive 2; Mismatches 9; Indels
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Publication No. US20030119731A1

GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: McIntosh, J. Michael
APPLICANT: McIntosh, J. Michael
APPLICANT: McIntosh, J. Michael
APPLICANT: Jacobsen, Richard
APPLICANT: Jones, Robert M.
APPLICANT: Jones, Robert M.
APPLICANTON UNMBER: US/09/910,082A
CURRENT APPLICATION NUMBER: US 60/219,616
PRIOR APPLICATION NUMBER: US 60/265,888
PRIOR APPLICATION NUMBER: US 60/265,888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 36.3%; Score 58.5; DB 16; Best Local Similarity 45.5%; Pred. No. 2.8; Matches 10; Conservative 2; Mismatches 9;
                                                                                    APPLICANT: Jones, Robert M.
APPLICANT: Carrier, G. Edward
TITLE OF INVENTION: Omega-Conopeptides
FILE REFERENCE: 2314-241
CURRENT APPLICATION NUMBER: US/10/765,926
CURRENT FILING DATE: 2004-01-29
PRIOR PRILING DATE: 2001-07-23
PRIOR PLING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR APPLICATION NUMBER: US 60/265,888
PRIOR APPLICATION NUMBER: US 60/265,888
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: PatentIn version 3.0
SEQ ID NO 392
LENGTH: 27
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SOFTWARE: Patentin version 3.0
SEQ ID NO 238
LENGTH: 74
TYPE: PRT
ORGANISM: Conus rattus
                                       Shon, Ki-Joon
Jacobsen, Richard
         Garrett, James E.
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Matches 10; Conservative
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ORGANISM: Conus rattus
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US-09-910-082A-238
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36.3%; Score 58.5; DB 16; Length 27;
Best Local Similarity 45.5%; Pred. No. 2.8;
Matches 10; Conservative 2; Mismatches 9; Indels
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APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Olivers, Baldomero M.
APPLICANT: Olivers, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: McIntosh, J. Michael
APPLICANT: McIntosh, J. Michael
APPLICANT: McIntosh, J. Michael
APPLICANT: Garrett, James E.
APPLICANT: Garrett, Shon, Ki-Joon
APPLICANT: Jacobsen, Richard
APPLICANT: Gartier, G. Edward
TITLE OF INVENTION: Omega-Conopeptides
FILE REFERENCE: 2314-241
CURRENT APPLICATION NUMBER: US 09/910,082
PRIOR APPLICATION NUMBER: US 09/910,082
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2010-07-23
PRIOR FILING DATE: 2010-07-23
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2010-07-23
PRIOR FILING DATE: 2010-07-23
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2010-07-23
PRIOR FILING DATE: 2010-07-23
PRIOR FILING DATE: 2010-07-21
PRIOR PRIOR FILING DATE: 2010-07-21
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Sublication No. US20040132663A1
GENERAL INFORMATION:
APPLICANT: University of Utah. Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: Watkins, Maren
                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: US 60/265,888
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SEQ ID NO 392
LENGTH: 27
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Publication No. US20040132663A1
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Matches 10; Conservative
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ORGANISM: Conus rattus
                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Conus rattus
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US-10-765-926-391
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LENGTH: 27
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DB 10; Length 74;
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                                                              APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: Warkins, Maren
APPLICANT: Garrett, James E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                University of Utah Research Foundation Cognetix, Inc. Olivera, Baldomero M. McIntosh, J. Michael Watkins, Maren
                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/910,082A
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR PILING DATE: 2000-07-21
PRIOR PRILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: Patentin version 3.0
LENGTH: 74
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Best Local Similarity 45.5%; Pred. No. 6.
Matches 10; Conservative 2; Mismatche
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APPLICANT: Jacobsen, Richard
APPLICANT: Jones, Robert M.
APPLICANT: Cartier, G. Edward
TITLE OF INVENTION: Omega-Conopeptides
FILE REFERENCE: 2314-241
CURRENT APPLICATION NUMBER: US/10/765,926
CURRENT FILING DATE: 2004-01-29
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PRIOR PLICATION NUMBER: US 09/910,082

PRIOR PILING DATE: 2001-07-23

PRIOR APPLICATION NUMBER: US 60/219,616

PRIOR PILING DATE: 2000-07-21

PRIOR PILING DATE: 2000-07-21

PRIOR PILING DATE: 2001-05

NUMBER OF SEQ ID NOS: 413

SQFTWARE: PATENTIN NOS: 413

SQFTWARE: PATENTIN VERSION 3.0
                                                                                                                                                                                                                                            PPLICANT: Jones, Robert M.
PPLICANT: Cartier, G. Edward
ITLE OF INVENTION: Omega-Conopeptides
Sequence 241, Application US/09910082A
Publication No. US20030119731A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CRIXNOKCFOHLDDCCSRKCNR 22
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Publication No. US20040132663A1
GENERAL INFORMATION:
                                                                                                                                                                                                   Shon, Ki-Joon
Jacobsen, Richard
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                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 2314-241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Conus rattus
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DB 16; Length 74;

36.3%; Score 58.5;

Query Match

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                           1; Gaps
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Best Local Similarity 45.5%; Pred. No. 6.7; Matches 10; Conservative 2; Mismatches
                                                     1 CRIXNOKCFQHLDDCCSRKCNR 22
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48 CNARNSGCSQH-PQCCSGSCNK 68

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Search completed: April 18, 2005, 20:43:01 Job time: 92.5 secs

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                                                          April 18, 2005, 20:23:04 ; Search time 26.5 Seconds (without alignments) 98.032 Million cell updates/sec
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         GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                         283416 segs, 96216763 residues
                                                                                             US-10-627-685A-26
161
1 CRIXNQKCFQHLDDCCSRKCNRFNKCV
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T31070
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T09688
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B26637
T22274
                                          protein search, using sw
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Maximum Match 100%
Listing first 100 6
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seq length: 200000000
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Query
Match Length D
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1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:*
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Perfect score:
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52.5
52
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71
61
59
59
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Maximum DB
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protein C2485.5 (i
major merozoite su
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ALIGNMENTS

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C;Species: Conus magus (magus cone)
C;Date: 17-Apr-1993 #sequence_revision 11-Apr-1997 #text_change 09-Jul-2004
C;Accession: JH0699; PC2380
C;Accession: JH0699; PC2380
R;Hillyard, D.R.; Monje, V.D.; Mintz, I.M.; Bean, B.P.; Nadasdi, L.; Ramachandran, J.; Mn. Neuron 9, 69-77, 1992
A;Title: A new conus peptide ligand for mammalian presynaptic Ca2+ channels.
A;Reference number: JH0699; MUID:92337922; PMID:1352986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 3-28 < NEW>
B; Residues: 3-28 < NEW>
A; Residues: 3-28 < NEW>
A; Reference S. 3. Basus, V.J.
A; Reference number: A66297; PDB:10MN
A; Contents: annotation; conformation by (1) H-NMR, residues 3-28
A; Title: Solution structure of omega-conotoxin MVIIC, a high affinity of P-type calcium classical conformation by (1) H-NMR
A; Reference number: A56582; MUID:95248539; PMID:7731037
A; Reference number: A56582; MUID:95248539; PMID:7731037
A; Reference number: A56582; MUID:8548639; PMID:7731037
A; Refe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:P37300; GB:S40826; NID:g252126; PIDN:AAB22674.1; PID:g252127 R;Nemoto, N.; Kubo, S.; Yoshida, T.; Chino, N.; Kimura, T.; Sakakibara, S.; Kyogoku, Y.; Ribothem. Blophya. Res. Commun. 207, 695-700, 1995
A;Title: Solution structure of omega-conotoxin MVIIC determined by NMR. A;Reference number: PC2380; MUID:95169113; PMID:7864862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-601 <WLL>
A;Residues: 1-601 <WLL>
A;Cross-references: UNIPROT:Q20204; EMBL:Z69792; PIDN:CAA93668.1; GSPDB:GN00028; CESP:F4(
E;Experimental source: clone F40E10
C;Genetics:
A;Gene: CESP:F40E10.4
                        - cone shell (Conus magus) (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein F40E10.4 - Caenorhabditis elegans (fragment)
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22025
R;Smye, R.
Submitted to the EMBL Data Library, February 1996
A;Reference number: Z19503
A;Reference number: Z19503
A;Accession: T22025
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: T20205
A;Status: preliminary; translated from GB/EMBL/DDBJ
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45.0%; Pred. No. 13;
tive 4; Mismatches 7; Indels
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Omega-conotoxin MVIIC precursor [validated]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56
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Best Local Similarity 45.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA A; Residues: 1-29 <HIL>
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C44379

Omega-conotoxin SVIB [validated] - cone shell (Conus striatus)

N/Alernate names: SNX-183

C/Species: Couns eritatus (striated cone)

C/Species: Conus eritatus (striated cone)

C/Species: Conus eritatus (striated cone)

C/Species: Conus eritatus

C/Species: Construction 31-Dec-1993 #text_change 15-Sep-2000

R/Smallo, C.A. Zafazalla, G.C.; Nadaedi, D.; Hammerland, L.G.; Yoshikami, D.; Gray, W.R

B/Smallo, C.A. 2 Zafazalla, G.C.; Nadaedi, D.; Hammerland, L.G.; Yoshikami, D.; Gray, W.R

R/Smallo, C.A. 2 Zafazalla, G.C.; Nadaedi, D.; Hammerland, L.G.; Yoshikami, D.; Gray, W.R

B/Schence: C.A.; Zafazalla, G.C.; Nadaedi, D.; Hammerland, L.G.; Yoshikami, D.; Gray, W.R

A/ROCCHE Type: profein

A/ROCCHE Type
                                                                                    Kappa-conotoxin PVIIA - cone shell (Conus purpurascens)
NyAlternate names: fin-popping peptide
CySpecies: Conus purpurascens (purple cone,)
CySpecies: Conus purpurascens (purple cone,)
CyAccession: A58997
RyTerlau, H.; Shon, K.J.; Grilley, M.; Stocker, M.; Stuehmer, W.; Olivera, B.M.
Nyture 381, 148-151, 1996
A;Tetle: Strategy for rapid immobilization of prey by a fish-hunting marine snail.
A;Reference number: A58997
A;Reference number: A58997
A;Reference protein
A;Molecule type: protein
A;Molecule type: protein
A;Residues: 1-27 cTER.
A;Cross-references: UNIPROT:P56633
C;Comment: This conotoxin blocks conductance of the Shaker potassium channel.
C;Keywords: hydroxyproline; neurotoxin; venom
F;4/Modified site: 4-hydroxyproline (Pro) #status experimental
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Pred. No. 0.074;
4; Mismatches 11; Indels
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il Similarity 42.3%;
11; Conservative .
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Best Local Similarity
Matches 26; Conserv
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Matches 11; Conserv
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Mol. Microbiol. 19, 91-100, 1996
A,Title: PMysical mapping and expression of gene families encoding the N-acetyl D-galactc
A,Reference number: 870662; MUID:96419166; PMID:8821939
A,Accession: 870663
A,Accession: Preliminary; translation not shown
A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 1-194 «RAM>
A,Cross-references: UNIPROT:Q24821; EMBL:U33443; NID:g993052; PID:g993053
A,Genetics:
A,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: T09229
R;Purdy, J.E.; Mann, B.J.; Shugart, E.C.; Petri, W.A.
Mol. Blochem, Parasitol. 62, 53-59, 1993
A;Title: Analysis of the gene family encoding the Entamoeba histolytica galactose-specif;
A;Feference number: Z16622; MUID:94158976; PMID:8114826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 1-48,'I',50-118,'R',120-230,'I',232-256,'N',258-266,'A',268-872,'R',874-958,'
A;Note: the authors translated the codon ATC for residue 49 as Thr, ATT for residue 2044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic Acids Res. 17, 6463-6471, 1989
A,Title: Hypervariability of simple sequences as a general source for polymorphic DNA ma:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                galactose binding adhesin heavy chain - Entamoeba histolytica
C;Species: Entamoeba histolytica
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Accession: T09229
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Status: preliminary: translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-1292 < PUR>
A,Cross-references: UNIPROT:Q24835; EMBL:L14815; NID:g290648; PID:g290649
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Pred. No. 43;
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Pred. No. 12;
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R;Ramakrishnan, G.; Ragland, B.D.; Purdy, J.E.; Mann, B.J.
Mol. Microbiol. 19, 91-100, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       notch protein - fruit fly (Drosophila melanogaster)
N,Alternate names: neurogenic repetitive locus protein
                                                                                                                                                                                                                                                                                                                                                                                        11;
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Best Local Similarity 43.3%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                             Query Match 35.1%;
Best Local Similarity 43.3%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: A24768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Gene: hgl3
C,Keywords: lectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A24420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
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                                                                                  C;Species: Caenorhabditis elegans
C;Species: (10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: D89711
R;anonymous, The C. elegans Sequencing Consortium.
Soience 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Accession: D89711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Accession: A35844
Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-601 <STO>
A;Cross-references: UNIPROT:Q20204; GB:chr_X; PIDN:CAA93668.1; PID:g3877014; GSPDB:GN000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chain, N-acetylgalactosamine-specific - Entamoeba histolytica (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A35844
Xotch protein - African clawed frog
C;Species: Renopus laevis (African clawed frog)
C;Species: Anopus laevis (African clawed frog)
C;Date: 12-Oct-1990 #sequence_revision 12-Oct-1990 #text_change 16-Aug-2004
C;Accession: A35844
R;Coffman, C.; Harris, W.; Kintner, C.
Science 249, 1438-1441, 1990
A;Title: Xotch, the Xenopus homolog of Drosophila notch.
A;Title: Xotch, the Xenopus homolog of Drosophila notch.
A;Reference number: A35844; MUID: 90385285; PMID: 2402639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lectin heavy chain, N-acetylgalactosamine-specific - Entamoeba histolytica C;Species: Entamoeba histolytica C;Date: Ib-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004 C;Accession: S70663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-2524 «COF»
C; Superfamily: North protein; ankyrin repeat homology; EGF homology
C; Keywords: transmembrane protein
F; 146-177/Domain: EGF homology «EGF1»
F; 184-215/Domain: EGF homology «EGF2»
F; 222-254/Domain: EGF homology «EGF2»
F; 456-487/Domain: EGF homology «EGF2»
F; 456-487/Domain: EGF homology «EGF2»
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36.6%; Score 59; DB 2; Length 601;
45.0%; Pred. No. 13;
iive 4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                           protein F40E10.4 [imported] - Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           < AN4 >
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Pred. No. 58;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F:1991-2023/Domain: ankyrin repeat homology F:2024-2056/Domain: ankyrin repeat homology F:2057-2089/Domain: ankyrin repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ankyrin repeat homology
ankyrin repeat homology
ankyrin repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 XNOKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1025-1056/Domain: EGF homology <EGX3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 CEKNIDDCVNSKCENGGKCV 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 CFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35.4%;
ilarity 37.5%;
Conservative
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :1957-1989/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C,Genetics:
A,Gene: F40E10.4
A,Map position: X
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Gaps

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ATTICLE: DAYSIGNI mapping and expression of gene families encoding the N-acetyl D-galactoty. A;Reference number: $70662; MUID:96419166; PMID:8821939
A;Accession: $70664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: S23802
R;Taira, M.; Jamrich, M.; Good, P.J.; Dawid, I.B.
Genes Dev. 6, 356-366, 1992
A;Title: The LIM domain-containing homeo box gene Xlim-1 is expressed specifically in the A;Reference number: S23802; MUID: 92192449; PMID:1347750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A.Gene: lim-1
C.Superfamily: homeotic protein lim-1; homeobox homology; LIM metal-binding repeat homolo
C.Keywords: DNA binding; duplication; embryo; homeobox; nucleus; transcription regulation
E;4-54/Domain: LIM metal-binding repeat homology cLIM1>
F;63-117/Domain: LIM metal-binding repeat homology cLIM2>
F;180-236/Domain: homeobox homology cHOX>
                                                                                                                                                                                                                                                            ectin heavy chain, N-acetylgalactosamine-specific - Entamoeba histolytica (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-403 <TAL>
A;Cross-references: UNIPROT:P29674; EMBL:X63889; NID:g64829; PIDN:CAA45353.1; C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
G01507
LIM domain transcription factor LIM-1 - human
N/Alternate names: homeotic protein lim-1
C;Species: Homo sapiens (man)
C;Accession: G01507
R;Dong, W.
                                                                                                                                                                                                                                                                                                                    2,Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Species: Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: UNIPROT: Q24822; EMBL: U33444; NID: 9993054; PID: 9993055
        1;
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        Indels
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                                                                                                                                                                                                                                                                                                                                                                         R;Ramakrishnan, G.; Ragland, B.D.; Purdy, J.E.; Mann, B.J.
Mol. Microbiol. 19, 91-100, 1996
        11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 CSMGTDNVITYHDDCNSRKSQCGNFNGKCI 148
        4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 55.5; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CRIXNOKCFOHLDDCCSRK--CNRFN-KCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translation not shown
A;Molecule type: DNA
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                                                          1 CRIXNOKCFOHLDDCCSRKCNRFNKC 26
                                                                                                               1 CKGKGASCHRTSYDCCTGSCNR-GKC 25
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Pred. No.
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Best Local Similarity 44.0%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                       ; Species: Entamoeba histolytica
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Best Local Similarity 40.0
Matches 12; Conservative
        Conservative
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        10;
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     Matches
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              A;Accession: 809358
A;Molecule type: DNA
A;Title: opa: a novel family of transcribed repeats shared by the Notch locus and other
A;Reference number: A05267; MUID:85099329; PMID:2981631
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A;Mesidues: 1-25 <0LI>
C;Superfamily: omega-conotoxin
C;Keywords: acetylcholine release inhibition; amidated carboxyl end; calcium channel inh
F;1-16,8-20,15-95/Disulfide bonds: #status predicted
F;25/Modified site: amidated carboxyl end (Cys) #status predicted
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R;Olivera, B.M.; Cruz, L.J.; de Santos, V.; LeCheminant, G.W.; Griffin, D.; Zeikus, R.; Botchemistry 26, 2086-2090, 1987
A;Title: Neuronal calcium channel antagonists. Discrimination between calcium channel su A;Reference number: A34115; MUID:87299637; PMID:2441741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 omega-conotoxin MVIIB - cone shell (Conus magus)
C;Species: Conus magus (magus cone)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: JH0701; B34115
R;H1llyard, D.R.; Monje, V.D.; Mintz, I.M.; Bean, B.P.; Nadasdi, L.; Ramachandran, J.; Neuron 9, 69-77, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Superfamily: Notch protein; ankyrin repeat homology; EGF homology; Keywords: differentiation; tandem repeat; transmembrane protein;27-43/Domain: transmembrane #status predicted <TMM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: FlyBase:FBgn0004647
A;Map position: 8.96-9.36
A;Introns: 53/3; 84/3; 171/3; 240/3; 283/3; 2333/3; 2436/3; 2588/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 56; DB 1; Length 2703;
Pred. No. 79;
5; Mismatches 11; Indels
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number: S09358; MUID:89385974; PMID:2780284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transmembrane #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;2017-2049/Domain: ankyrin repeat homology <AN3>F;2050-2082/Domain: ankyrin repeat homology <AN4>F;2083-2115/Domain: ankyrin repeat homology <AN5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;1950-1982/Domain: ankyrin repeat homology <AN1>F;1983-2015/Domain: ankyrin repeat homology <AN2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 55.5; Di
Pred. No. 4.1;
                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 2504-2576,'E',2578-2611 <WHA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 XNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Accession: JH0701
Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  homology <EGF3>
homology <EGX3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;988-1019/Domain: EGF homology <EGX2>
F;1064-1095/Domain: EGF homology <EGF3
F;1187-1218/Domain: EGF homology <EGX3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /297-328/Domain: EGF homology <EGX1>
/530-561/Domain: EGF homology <EGF1>
/568-599/Domain: EGF homology <EGF>
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Best Local Similarity 33.3%;
Matches 8; Conservative
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Best Local Similarity
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Residues: 1-25 <HIL>
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C;Superfamily: homeotic protein lim-1; homeobox homology; LIM metal-binding repeat homolo C;Reywords: DNA binding; duplication; embryo; homeobox; nucleus; transcription regulation E;4-54/Domain: LIM metal-binding repeat homology <LIM1>
F;63-117/Domain: LIM metal-binding repeat homology <LIM2>
F;8181-237/Domain: homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         homeotic protein lim-1 - mouse
C;Species: Mus musculus (house mouse)
C;Accession: 148637; 542788
R;Fujii, T.; Pichel, J.G.; Taira, M.; Toyama, R.; Dawid, I.B.; Westphal, H.
Dev. Dyn. 199, 73-83, 1994
A;Fitle: Expression patterns of the murine LIM class homeobox gene lim1 in the developing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A Molecule type: mRNA
A; Residues: 1-406 <FUJ>
A; Cross-references: EMBL:227410; NID:g425216; PIDN:CAA81797.1; PID:g425217
C; Genetics:
A; Gene: LhA:
C; Superfamily: homeotic protein lim-1; homeobox homology; LIM metal-binding repeat homoloc; Keywords: DNA binding; duplication; embryo; homeobox; nucleus; transcription regulation F; 4-54/Domain: LIM metal-binding repeat homology <LIM1>
F; 63-117/Domain: LIM metal-binding repeat homology <LIM2>
F; 81-217/Domain: LIM metal-binding repeat homology <LIM2>
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R;Fujii, T.
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R;Tsuchida, T.; Ensini, M.; Morton, S.B.; Baldassare, M.; Edlund, T.; Jessell, T.M.; Pfa:
Cell 79, 957-970, 1994
A;Title: Topographic organization of embryonic motor neurons defined by expression of LII
A;Reference number: A55198; MUID:95094281; PMID:7528105
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A;Residues: 1-406 <TSU>
A;Cross-references: UNIPROT:P53411; GB:L35569; NID:g531182; PIDN:AAA62173.1; PID:g531183
C;Genetics:
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C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                Gaps
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A,Reference number: S42788
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                                                                                                                                                                                                                                                                                                                                                                                 56
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Best Local Similarity 44.0.
Best Local Similarity 44.0.
Conservative
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Submitted to the EMBL Data Library, September 1994
A,Reference number: G07570
A,Accession: G01507
A,Accession: G01507
A,Accession: G01507
A,Bolecule type: mRNA
A,Status: translated from GB/EMBL/DDBJ
A,Residues: 1-404 <DON>
A,Residues: 1-404 <DON>
A,Residues: 1-404 <DON>
A,Residues: L-404 <DON>
A,Residues: L-404 <DON>
A,Crosa-references: UNIPROT:P48742; EMBL:U14755; NID:g549845; PIDN:AAA21644.1; PID:g5498
C,Genetics:
A,Gene: hLIM-1
C,Superfamily: homeotic protein lim-1; homeobox homology; LIM metal-binding repeat homology
C,Reywords: DNA binding; duplication; embryo; homeobox, nucleus; transcription regulatic
F,4-54/Domain: LIM metal-binding repeat homology <LIML>
F,63-117/Domain: LIM metal-binding repeat homology <LIML>
F,181-237/Domain: homeobox homology <HOX>
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C;Genetics:
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Cispecies: Rattus sp. (rat)
Cispecies: Rattus sp. (rat)
Cispecies: Sattus sp. (rat)
Cispecies: Sattus sp. (rat)
Cispecies: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
Cispecession: 158187, S.; Iwahashi, Y.; Takagi, H.
Neurosci. Lett. 170, 266-268, 1994
A;Title: Distribution of Rlim, an LIM homeodomain gene, in the rat brain.
A;Reference number: 158187; MUID:94336075; PMID:7914684
A;Accession: 158187
A;Accession: 158187
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rolecule type: mRNA
A;Residues: 1-406 <RES>
A;Cross-references: GB:S71523; NID:9559635; PIDN:AAC60696.1; PID:9559636
Cigenetics:
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N.Alternate names: homeotic protein lmx2
C;Species: Mesocricetus auratus (golden hamster)
C;Species: Mesocricetus auratus (golden hamster)
C;Accession: 148186
R;Rudnick, A.; Ling, T.Y.; Odagiri, H.; Rutter, W.J.; German, M.S.
Proc. Natl. Acad. Sci. U.S.A. 91, 12203-12207, 1994
A;Title: Pancreatic beta cells express a diverse set of homeobox genes.
A;Reference number: I48186; MUID:95083670; PMID:7991607
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Local Similarity 44.0%; Pred. No. 29;
hes 11; Conservative 2; Mismatches 8: Indole
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A;Molecule type: mRNA
A;Residues: 1-406 <RES>
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Pred. No. 29;
2; Mismatches
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R;Nielsen, K.J.; Thomas, L.; Lewis, R.J.; Alewood, P.F.; Craik, D.J.
R;Nielsen, K.J.; Thomas, L.; Lewis, R.J.; Alewood, P.F.; Craik, D.J.
R;Nielsen, K.J.; Thomas, L.; Lewis, R.J.; Alewood, P.F.; Craik, D.J.
A;Gerence number: A67648; PDB:1MVI
A;Contents: annotation; conformation by (1)H-NMR, residues 1-25
R;Nielsen, K.J.; Thomas, L.; Lewis, R.J.; Alewood, P.F.; Craik, D.J.
J; Mol. Biol. 263, 297-310, 1996
A;Title: A consensus structure for omega-conotoxins with different selectivities for vol
A;Reference number: A58619; MUID:97070382; PMID:8913308
A;Contents: annotation; conformation by (1)H-NMR
R;Kohno, T.; Kim, J.I.; Kobayashi, K.; Kodera, Y.; Maeda, T.; Sato, K.
Submitted to the Brookhaven Protein Data Bank, April 1995
A;Contents: annotation; conformation by (1)H-NMR, residues 1-25
B;Contents: annotation; conformation by (1)H-NMR, residues 1-25
B;Contents: annotation; conformation by (1)H-NMR, residues 1-25
A;Title: Three-dimensional structure in solution of the calcium channel blocker omega-cc
A;Contents: annotation; conformation by (1)H-NMR
C;Sinperfamilu: conformation by (1)H-NMR
C; Superfamily: homeotic protein lim-1; homeobox homology; LIM metal-binding repeat homol C; Keywords: DNA binding; duplication; embryo; homeobox; nucleus; transcription regulatic F; 4-54/Domain: LIM metal-binding repeat homology <LIM.>
F; 63-LIT/Domain: LIM metal-binding repeat homology <LIM.>
F; 81-17/Domain: LIM metal-binding repeat homology <LIM.>
F; 181-237/Domain: homeobox homology <HOX.>
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A)residente: 1-25 child.

A)residente: 1-25 child.

A)residente: 1-25 child.

A)residente: 20, 133-1343, 1985

A)reference number: 343-1343, 1985

A)reference number: A43620, MUID:86070213; PMID:4071055

A)reference number: A-25 child.

A)residues: 1-25 child.

A)reference number: A-306-2090, 1987

A)ritle: Neuronal calcium channel antagonists. Discrimination between calcium channel subpression contains.

A)reference number: A-4115; MUID:87299637; PMID:2441741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  omega-conotoxin MVIIA [validated] - cone shell (Conus magus)
C;Species: Conus magus (magus cone)
C;Date: 17-Apr-1993 #sequence revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: JH0700; C60133; Ā34115
R;H1llyard, D.R.; Monje, V.D.; Mintz, I.M.; Bean, B.P.; Nadasdi, L.; Ramachandran, J.; Neuron 9, 69-77, 1992
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A;Reference number: JH0699; MUID:92337922; PMID:1352986
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                                                                                                                                                                                                                      DB 1; Length 406;
                                                                                                                                                                                                                                                                                               8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.3;
                                                                                                                                                                                                                   34.2%; Score 55; DB 44.0%; Pred. No. 29; iive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Mismatrches
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Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                                                                                     2 RIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: JH0700
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-25 <HIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33.9%;
Best Local Similarity 38.5%;
Matches 10; Conservative
                                                                                                                                                                                                        Query Match
Best Local Similarity 44.0
Matches 11; Conservative
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-239 cWIL>
A;Cross-references: UNIRROT:018052; EMBL:Z81587; PIDN:CAB04705.1; GSPDB:GN00019; CESP:TO6.
A;Experimental source: clone T06G6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycosyltransferase [imported] - Clostridium acetobutylicum
Gispecies: Clostridium Gispecies: Clostridium Gispecies: Clostridium Gispecies: Clostridium Gispecies: Clostridium Gispecies: Agesone and Comparative Analysis of the Solvent-Producing Bacterium Clostridium Gispecies: Agetuminary
Aireterence number: Ageson; MUID:21359325; PMID:21359325
Airetuminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:Q97GL5; GB:AE001437; PIDN:AAK80307.1; PID:g15025361; GSPDB:Gh.A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC2351
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                        C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24619
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T25933
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                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Map position: 1
A;Introns: 20/1; 76/3; 103/3; 148/2; 183/2
C;Superfamily: Caenorhabditis elegans hypothetical protein T06G6.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 252;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
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   - Caenorhabditis elegans
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                R; Kershaw, J.
submitted to the EMBL Data Library, November 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 54.5; DE; Pred. No. 24; 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 IXNOKCFOHLD-----DCCSRKCNRFNK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 INDNGCFMHFDSKKLESIELCPLQCQRFNE 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 54.5; I
Pred. No. 24;
5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.3%;
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Best Local Similarity 33.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
   protein T06G6.6
                                                                                                                                                                       A;Reference number: Z19913
A;Accession: T24619
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es 10; Conserv
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ypothetical
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A;Residues: 1-1372 <MUR>

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Mismatches

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10; Conservative

Matches

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Status: preliminary, nucleic acid sequence not shown, not compared with conceptual trar; Molecule type: mRNA
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B;Abrwood, D.R.; McClay, D.R.

B;Abrwood, D.R.; McClay, D.R.

B;Abrwood, D.R.; McClay, D.R.

A;Title: Identification and localization of a sea urchin Notch homologue: insights into A;Teference number: 220966; MUID:97454256; PMID:9310331

A;Accession: T11070

A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CjAccession: A40043
CjAccession: A40043
RjEllisen, L.W.; Bird, J.; West, D.C.; Soreng, A.L.; Reynolds, T.C.; Smith, S.D.; Sklar, Cell 66, 649-661, 1991
A;Title: TAN-1, the human homolog of the Drosophila Notch gene, is broken by chromosomal A;Reference number: A40043; MUID:91347367; PMID:1831692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-2531 <SHE>
A;Cross-references: EMBL:AF000634; NID:g2570350; PID:g2570351; PIDN:AAB82088.1
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5), ozone-inducible - Scotch pine
                                                                                                                                                                                                                                           notch homolog - sea urchin (Lytechinus variegatus)
C;Species: Lytechinus variegatus (variegated urchin)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 31-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Species: Homo sapiens (man)
.Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 16-Aug-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32.9%; Score 53; DB 2; Length 2531;
45.0%; Pred. No. 1.7e+02;
Live 3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2555;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Mismatches
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : | | :::||| | ...
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1149-1180/Domain: EGF homology <EGF>
1187-1218/Domain: EGF homology <EGF3>
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                                                                       :|||| |||| ||
106 EHLDDDCSRKRARTGSC 122
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                                     10 QHLDDCCSRKCNRFNKC 26
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Best Local Similarity 33.3%;
Matches 8; Conservative '
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Matches 9; Conservative
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Cross-references: GB:M73980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
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C;Accession: B71406
R;Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk
P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terryn, N.; Giel
avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.
A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech
erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cross-references: UNIPROT:019345; EMBL:Z54270; PIDN:CAA91028.1; GSPDB:GN00028; CESP:F1
Experimental source: clone F11C1
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A; Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal A;Reference number: A71400; MUID:98121113; PMID:9461215
A;Accession: B71406
A;Cross-references: UNIPROT:P91526; EMBL:U80815; PIDN:AAB37995.1; GSPDB:GN00022; CESP:W(
A;Experimental source: strain Bristol N2; clone W02C12
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A;Introns: 39/3; 50/3; 87/1; 148/2; 190/1; 286/1; 377/3; 417/2; 499/2
C;Superfamily: steroid hormone receptor Ad4BP; erbA transforming protein homology
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A;Molecule type: DNA
A;Residues: 1-277 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein F11C1.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                         Score 54; DB 2; Length 1372;
Pred. No. 85;
7; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 53; DB 2; Length 277;
Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                          C;Genetics:
A;Gene: CESP:W02C12.1
A;Map position: 4
A;Introns: 29/1; 66/1; 774/2; 823/2; 1046/1; 1108/2; 1298/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46 VQNKKQYQCSAEANCHVDRTCRKRCPSCRFQKCL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 IXNOKCFQ-----HLDDCCSRKCN--RFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RiPalmer, S. submitted to the EMBL Data Library, September 1995 submitted to the EMBL Data Library, September 1995 A.Reference number: 219321 A.Accession: T20764 A.Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
A;Variety: columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 53.5; I
Pred. No. 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                           4 XNOKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32.9%;
58.8%;
                                                                                                                                                                                                                   33.5%;
29.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33.2%;
Best Local Similarity 32.4%;
Matches 11; Conservative
                                                                                                                                                                                    Query Match
Best Local Similarity 29.4.
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Map position: 4COP9-4G3845
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-572 <WIL>
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Palmer, S.
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Length 293;

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6; Mismatches
                                                                                                             / Match 32.3%; Score 52; Local Similarity 30.4%; Pred. No. 188 7; Conservative 6; Mismatc
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                                                                                                                                                                                                                                  166 EGQHCEQNIDECADQPCHNGGNC 188
                                                                                                                                                                                                        4 XNOKCFQHLDDCCSRKCNRFNKC 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: FlyBase: FBgn0000368
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                   F;139-170/Domain: EGF homology <EGX1>
F;177-208/Domain: EGF homology <EGF1>
F;216-252/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Keywords: transmembrane protein
F;352-385/Domain: EGF homology «EGX1»
F;392-424/Domain: EGF homology «EGF1»
F;691-722/Domain: EGF homology «EGF»
F;767-799/Domain: EGF homology «EGF3»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C,Accession: A35672
R,Tepass, U.; Theres, C.; Knust, E.
Cell 61, 787-799, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 35.7
1es 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reference number: Z19541
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                                                                                                                Query Match
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Matches
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                     C;Accession: A33917
R;Tannich, B.; Ebert, F.; Horstmann, R.D.
A;Title: Primary structure of the 170-kDa surface lectin of pathogenic Entamoeba histoly A;Reference number: A39117; MUID:91156704; PMID:2000392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neurogenic repetitive locus 95F protein - fruit fly (Drosophila melanogaster) (fragment) C;Species: Drosophila melanogaster C;Species: Drosophila melanogaster C;Species: LeAug-1988 #sequence_revision 16-Aug-1988 #text_change 09-Jul-2004 C;Accession: B26637 B26637 B;Knust, E.; Dietrich, U.; Tepass, U.; Bremer, K.A.; Weigel, D.; Vaessin, H.; Campos-Ort EMBO J. 6, 761-766, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: EGF homologous sequences encoded in the genome of Drosophila melanogaster, and A;Reference number: A91081; MUID:87218537; PMID:3107986
A;Accession: B26637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;Molecule type: mRNA
|Residues: 1-293 <KNU>
|Cross-references: UNIPROT:P10040; GB:X05144; NID:g7519; PIDN:CAA28793.1; PID:g929536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
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N;Alternate names: 3-hydroxy-3-methylglutaryl-coenzyme A synthase
C;Species: Pinus sylvestris (Scotch pine)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          170K lectin precursor - Entamoeba histolytica (fragment)
C;Species: Entamoeba histolytica
C;Date: 30-Aug-1991 #sequence_revision 17-Apr-1993 #text_change 09-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 474;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-1280 <TAN>
A;Cross-references: GB:M60498; NID:g158958; PID:g158959
C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 52.5; DB 2;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 32.6%; Score 52.5; D
Best Local Similarity 43.5%; Pred. No. 62;
Matches 10; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            211 LSOTCYLMALDSCYKRFCNKFEK 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 XNOKCF-OHLDDCCSRKCNRFNK 25
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A,Cross-references: FlyBase:FBgn0000368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 41.4%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Keywords: transmembrane protein
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A;Residues: 1-354 <WIL>
A;Cross-references: UNIPROT:Q9XV21; EMBL:281540; PIDN:CAB04398.1; GSPDB:GN00023; CESP:F46|
A;Experimental source: clone F4683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-2139 <TEP>
A;Crosm-references: UNIPROT:P10040; GB:M33753
A;Note: the authors translated the codon GGC for residue 1928 as Cys, and TAT for residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A/Title: crumbs encodes an EGF-like protein expressed on apical membranes of Drosophila
A/Reference number: A35672; WUID:90263104; PMID:2344615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
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                      C,Species: Caenorhabditis elegans
C,Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C.Species: Drosophila melanogaster
C.Date: 21-Sep-1990 #sequence_revision 18-Nov-1992 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                 A;Map position: 5
A;Introns: 23/1; 55/1; 82/1; 112/1; 142/1; 170/1; 193/1; 223/1; 299/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Length 354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
hypothetical protein F46B3.9 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  crumbs protein - fruit fly (Drosophila melanogaster)
                                                                                                                                                                                     A;Accession: T22274
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 1.9e+02;
6; Mismatches 10
                                                                                                      R,Ainscough, R.
submitted to the EMBL Data Library, November 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32.3%; Score 52; DB
35.7%; Pred. No. 58;
tive 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CRIXN--OKCFOHLDDCCSRKCNRFNKC 26
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250 AGQNCEENVDDCPGNNCKNGGACV 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Status: not
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                                     셤
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                                                                                                                                                                                                                 Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .Species: Rattus norvegicus (Norway rat)
:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 02-Aug-2002
:Accession: S18188
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A, Residues: 1-231 - WEI>
A, Cross-references: EMBL: X57405; NID:957634; PID:957635
C; Superfamily: notch protein; ankyrin repeat homology; EGF homology
F;987-1018/Domain: EGF homology <EGF1>
F;1025-1056/Domain: EGF homology <EGF>
F;1033-1264/Domain: EGF homology <EGF>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary; not compared with conceptual translation A; Molecule type: mRNA A; Molecule type: mRNA A; Residues: 1-2471 < WEI. A; Residues: 1-2471 < WEI. A; Cross-references: UNIPROT: 090W30 A; Experimental source: Schwann cell A; Note: sequence extracted from NCBI backbone (NCBIP:127811)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2531;
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Pred. No. 2.18+02;
4; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                  Riweinmaster, G.; Roberts, V.J.; Lemke, G.
Development 116, 931-941, 1992
A;Title: Notch2: a second mammalian Notch gene.
A;Reference number: A49128; MUID:93202015; PMID:1295745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RiWeinmaster, G.; Roberts, V.J.; Lemke, G.
Development 113, 199-205, 1991
A;Title: A homolog of Drosophila Notch expressed during
A;Reference number: S18188; MUID:92111383; PMID:1764995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;1876-1908/Domain: ankyrin repeat homology <ANI>F;1909-1941/Domain: ankyrin repeat homology <ANZ>F;1943-1975/Domain: ankyrin repeat homology <ANZ>F;1947-2008/Domain: ankyrin repeat homology <ANZ>F;2076-2008/Domain: ankyrin repeat homology <ANS>F;2009-2041/Domain: ankyrin repeat homology <ANS>
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                                                                                                                                                                                     cell-fate determining gene Notch2 protein - rat
1828 EGQHCEQNIDECADQPCHNGGNC 1850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EGSNCERNIDDCPNHKCQNGGVCV 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 XNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;1029-1060/Domain: BGF homology «EGF»
F;1067-1098/Domain: BGF homology «EGK3»
F;1159-1184/Domain: BGF homology «EGF9»
F;1191-1222/Domain: BGF homology «EGF9»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32.3%;
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Best Local Similarity 33.3
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          notch protein homolog - rat
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Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                            Accession: A49128
                                                                                                                                                                                                                                                                            Accession: A49128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       253
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                                  g
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4 XNQKCFQHLDDCCSRKCNRFNKCV 27

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Cispecies: Mus musculus (house mouse)
Cibacte 22-56p-1993 #sequence revision 18-Nov-1994 #text_change 16-Aug-2004
Cibacte 22-56p-1993 #sequence revision 18-Nov-1994 #text_change 16-Aug-2004
Cibacession: A46019, S25144; C49175; B46438; A46438; PH1569; S32109
Ridel Amo, F.F.; Gendron-Maguire, M.; Swiatek, P.J.; Jenkins, N.A.; Copeland, N.G.; Gridl Genomics 15, 259-264, 1993
A;Title: Cloning, analysis, and chromosomal localization of Notch-1, a mouse homolog of I A;Reference number: A46019; MUID:93194170; PMID:8449489
                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-2531 < DBL>
A;Cross-references: UNIPROT:Q01705; GB:Z11886; GB:S47228; NID:g288502; PIDN:CAA77941.1; F
A;Note: sequence extracted from NCBI backbone (NCBIP:127318)
R;Franco del Amo, F.; Smith, D.E.; Swiatek, P.J.; Gendron-Maguire, M.; Greenspan, R.J.; h
Bubmitted to the EMBL Data Library, April 1992
A;Description: Expression pattern of Motch, a mouse homolog of Drosophila Notch, suggests
A;Reference number: S25144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A Molecule type: mRNA
A;Residues: 1551-2108, Q, 21110-2114, ALP', 2118-2170 <FRA>
A;Cross-references: EMBL:Z11886
R;Lardelli, M.; Lendahl, U.
Exp. Cell Ress. 204, 364-372, 1993
A;Title: Motch A and Motch B--two mouse Notch homologues coexpressed in a wide variety of A;Reference number: A49175; MUID:93178563; PMID:8440332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Title: Mouse notch: expression in hair follicles correlates with cell fate determination. Reference number: A46438; MUID:93252998; PMID:8486742. A46438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: nucleic acid
A;Residues: 1865-1932,'RR',1935-1937,'L',1938-1967,'I',1969-2044,'IE',2047-2052,'S',2054-
A;Experimental source: embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Note: sequence extracted from NCBI backbone (NCBIN:131246, NCBIP:131247)
C;Comment: This protein has many EGF repeats and lin-12[#1172]/Notch repeats.
C;Comment: This protein is one of the neurogenic proteins controlling the decision betwee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ,Molecule type: mRNA
,Residues: 1161-1547 <LAR>
,Cross-references: EMBL:X68278; NID:g287987; PIDN:CAA48339.1; PID:g287988
,Experimental source: embryo
,Note: sequence extracted from NCBI backbone (NCBIP:126159)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    on of chromosome 2
protein; ankyrin repeat homology; EGF homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Accession: C49175 status: preliminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                  compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position: 2
A; Note: proximal region of chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <EG07>
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                                    N;Alternate names: motch protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   631-641, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          homology
homology
homology
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homology
homology
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homology
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homology
                                                                                                                                                                                                                                                                                                                                                                                       Molecule type: nucleic acid
notch-1 protein - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kopan, R.; Weintraub, Cell Biol. 121, 631-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;911-942/Domain:
F;949-980/Domain:
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probable vitellogenin receptor - fruit fly (Drosophila melanogaster)
(Species: Drosophila melanogaster
(Species: Drosophila melanogaster
(Spacies: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
(Spacession: T13171
(Rischonbaum, C.P.; Lee, S.; Mahowald, A.P.
(Rischonbaum, C.P.; Lee, S.; Mulb:95183490; PMID:7878005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecule type: mRNA
Residues: 1-1984 <SCH>
Cross-references: UNIPROT:P98163; EMBL:Ul3637; NID:G535345; PID:G535346; PIDN:AAB60217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J.; Rivier, J.; de Santos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Kerwords: acetylcholine release inhibition; calcium channel inhibitor; hydroxyproline; F;1-16,8-19,15-26/Disulfide bonds: #status predicted F;4,7/Modified site: 4-hydroxyproline (Pro) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ij
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C;Species: Conus geographus (geography cone)
C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F129-166/Domain: LDL receptor ligand-binding repeat homology (LDL8) F129-166/Domain: LDL receptor ligand-binding repeat homology (LDL8) F124-220/Domain: LDL receptor ligand-binding repeat homology (LDL10) F126-304/Domain: LDL receptor ligand-binding repeat homology (LDL1) F1025-1062/Domain: LDL receptor ligand-binding repeat homology (LDL1) F1025-1062/Domain: LDL receptor ligand-binding repeat homology (LDL2) F1118-1153/Domain: LDL receptor ligand-binding repeat homology (LDL2) F1118-1153/Domain: LDL receptor ligand-binding repeat homology (LDL3) F1154-1193/Domain: LDL receptor ligand-binding repeat homology (LDL3) F1243-1279/Domain: LDL receptor ligand-binding repeat homology (LDL5) F1243-1279/Domain: LDL receptor ligand-binding repeat homology (LDL5) F1283-1318/Domain: LDL receptor ligand-binding repeat homology (LDL5) F1283-1318/Domain: LDL receptor ligand-binding repeat homology (LDL5) F1283-1318/Domain: LDL receptor ligand-binding repeat homology (LDL5)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32.0%; Score 51.5; DB 2; Length 1984; 36.7%; Pred. No. 2.1e+02; live 3; Mismatches 9; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: A43620
R; Oilvera, B.M.; Gray, W.R.; Zeikus, R.; McIntosh, J.M.; Varga, Science 230, 1338-1343, 1985
A; Title: Peptide neurotoxins from fish-hunting cone snails.
A; Reference number: A43620; MUID:86070213; PMID:4071055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Status: preliminary; translated from GB/EMBL/DDBJ
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31.0%; Pred. No. 14;
ive 5; Mismatches
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           27
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                                             17 CREESRRCMQR--DVCAARCARRRRMQQCV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /Map position: 1:90-124/Domain: LDL receptor ligand-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cross-references: FlyBase: FBgn0004649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: UNIPROT: P05483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C:Superfamily: omega-conotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CRIXNQKCFQHLDDCC-
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Best Local Similarity 31.0
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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Best Local Simi
Matches 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          omega-conotoxin MVIID precursor - cone shell (Conus magus) (fragment)
C;Species: Conus magus (magus cone)
C;Species: Conus magus (magus cone)
C;Date: 27-Mar-1997 #sequence_revision 11-Apr-1997 #text_change 09-Jul-2004
C;Accession: A58537
R;Monje, V.D.; Haack, J.A.; Naisbitt, S.R.; Miljanich, G.; Ramachandran, J.; Nasdasdi, I
Neuropharmacology 32, 1141-1149, 1993
A;Title: A new Conus peptide ligand for Ca channel subtypes.
A;Reference number: A58537; MUID:94150815; PMID:8107968
A;Reference number: A58537
A;Molecule type: mRNA
A;Residues: 1-29 <MONS
A;Cross-references: UNIPROT:Q26350; GB:S69322; NID:G545399; PIDN:AAB29902.1; PID:G545406
C;Superfamily: omega-conotoxin
C;Superfamily: omega-conotoxin
C;Superfamily: omega-conotoxin MVIID #status predicted <MAT>
F;4-29/Product: omega-conotoxin MVIID #status predicted
F;4-19,11-23,18-28/Disulfide bonds: #status predicted
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R;Cui, L.W.; Li, Y.; Liu, B.Y.
Acta decension: JC1088

A;Title: Localization and nuclectide sequence of propionyl acylase gene of Streptomyces
A;Reference number: JC1088

A;Reference number: JC1088

A;Reference number: JC1088

A;Residues: 1-113 < CUI>
A;Residues: 1-113 < CUI>
Cisuperfamily: Streptomyces mycarofaciens propionyl acylase
C;Reywords: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ï
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C;Species: Streptomyces mycarofaciens
C;Date: 27-Aug-1995 #sequence_revision 19-Cct-1995 #text_change 09-Jul-2004
C;Accession: JC1088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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~hes 12; Indels
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                                                                                                                                                                                                                                                                      F;1917-1946/Domain: ankyrin repeat homology <AN1>F;1949-1981/Domain: ankyrin repeat homology <AN2>F;1949-2016/Domain: ankyrin repeat homology <AN3>F;2016-2048/Domain: ankyrin repeat homology <AN3>F;2049-2081/Domain: ankyrin repeat homology <AN5>F;2049-2081/Domain: ankyrin repeat homology <AN5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 51.5; I
Pred, No. 13;
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Pred. No. 31;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 52;
Pred. No. 3
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                                                                                                                      <EG18><EGF4><EG19>
                                                                                                                                                                                                                                    homology <EGF>
                                                                                                                                                               homology
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ilarity 33.3%;
Conservative
                                                                                       homology
homology
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Best Local Similarity 34.6%;
Matches 9; Conservative
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Matches 8; Conserv
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Best Local Similarity
Matches 10; Conserv
                                                                        F;1149-1180/Domain: E;1141-1218/Domain: E;1233-1264/Domain: E;1352-1383/Domain: E;1391-1425/Domain: a;1349-1281/Domain: a;1349-1281/Domain: a
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acetylcholinesterase (EC 3.1.1.7) (clone lambda-AChE8) - marbled electric ray (fragment) C;Species: Torpedo marmorata (marbled electric ray)
R;Sikorav, J.L.; Duval, N.; Anselmet, A.; Bon, S.; Krejci, E.; Legay, C.; Osterlund, M.;
EMBO J. 7, 2983-2993, 1988
A;Fitle: Complex alternative splicing of acetylcholinesterase transcripts in Torpedo electric electric number: S01293; MUID: 89030590; PMID: 3181125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chin, CW.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Mature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C.C., C.A.; Li, J.H.; Li, Y.; Liu, S.Y.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I A;Authors: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Fitle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: E86452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 1-100 <SIK>
A; Residues: 1-100 <SIK>
A; Cross-references: EMBL:X13174; NID:g64418; PIDN:CAA31572.1; PID:g64419
A; Note: the authors translated the codon CTT for residue 66 as Leu
C; Superfamily: cholinesterae; cholinesterae homology
C; Keywords: alternative splicing; carboxylic ester hydrolase; glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                            Gape
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Pred. No. 33;
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46.7%; Pred. No. 76;
iive 5; Mismatches 3; Indels
                            Length 53;
                                                                                            Indels
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                            31.7%; Score 51; DB 2;
llarity 39.3%; Pred. No. 22;
Conservative 4; Mismatches 11
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                                                                                                                                                                                         25 CADTGAVCV-HSDECCSGACSPVFNYCL 51
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74 RLASSKWWAHSDPLCSRRC 92
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172 CRVFRKKNYQKIDDC 186
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Query Match
Best Local Similarity
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Matches 8; Conserv
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Matches 7; Conserv
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                                                                                                                                                                                                         N.Alternate names: shaker peptide GVIIB
C;Species: Conus geographus (geography cone)
C;Species: Conus geographus (geography cone)
C;Accession: B43620
R;Olivera, B.M.; Gray, W.R.; Zeikus, R.; McIntosh, J.M.; Varga, J.; Rivier, J.; de Santc Science 230, 1338-1343, 1985
A;Title: Peptide neurotoxins from fish-hunting cone snails.
A;Reference number: A43620; MuID:86070213; PMID:4071055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RiAhrens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohrmann, G.F. Virology 229, 381-399, 1997
Virology 229, 381-399, 1997
A;Title: The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis A;Reference number: Z17011; MUID:97271300; PMID:9126251
A;Accession: T10405
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C;Species: Lymantria dispar nuclear polyhedrosis virus, LdMNPV
C;Species: Lymantria dispar nuclear polyhedrosis virus, LdMNPV
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T30499
R;Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; Rohr Virology 253, 17-34, 1999
A;Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantria d A;Reference number: Z20836; MUID:99124785; PMID:9897315
A;Accession: T30499
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:P05483
C;Superfamily: omega-conotoxin
C;Keywads: acetylcholine release inhibition; calcium channel inhibitor; hydroxyproline;
F;1-16,8-19,15-26/Disulfide bonds: #status predicted
F;4,7/Modified site: 4-hydroxyproline (Pro) #status experimental
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C.Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 11-May-2000
C.Accession: T10405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           conotoxin-like protein 1 - Orgyia pseudotsugata nuclear polyhedrosis virus
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A;Residues: 1-53 «KUZ»
A;Cross-references: UNIPROT:Q9YMH9; EMBL:AF081810; PIDN:AAC70335.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31.7%; Score 51; DB 2; Length 29; 31.0%; Pred. No. 14; tive 5; Mismatches 9; Indels
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                                                                                                                                                   B43620
omega-conotoxin GVIIB - cone shell (Conus geographus)
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A;Molecule type: DNA
A;Residues: 1-53 <AHR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CRIXNQKCFQHLDDCC----SRKCNRF 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CRIXNOKCFOHLDDCCSRKCNR-FNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 CAETGAVCV-HSDECCSGACSPVFNYCL 51
                         CKSPGTPCSRGMRDCCTSCLLYSNKCRRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 31.7%;
Best Local Similarity 39.3%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 31.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Molecule type: protein A, Residues: 1-29 <OLI>
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T10405
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Gaps

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hypothetical protein ZKZ87.4 - Caenorhabditis elegans
C;Species: T27822
R;McMurray, A.
Submitted to the EMBL Data Library, April 1996
A;Recession: T27822
A;Recession: T27822
A;Recession: T27822
A;Recession: T2782
A;Recession: T2782
A;Recession: T2782
A;Residues: Draliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-1208
A;Residues: 1-1208
A;Residues: Companion of the CK287
A;Resperimental source: clone ZK287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Nap position: 5
A;Introns: 44/1; 131/3; 167/1; 259/1; 319/1; 355/1; 484/3; 713/3; 765/1; 840/2; 1036/1; )
                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: T46722

R;Volckaert, G; Ivens, A.C.; Lawson, D.; Quail, M.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, December 1999
A;Reference number: Z23137
A;Accession: T46722
                                                                                                                                                                                                                                                                                                                           conserved hypothetical protein [imported] - Leishmania major N;Alternate names: probable proline synthetase associated protein C;Species: Leishmania major C;Species: Leishmania major C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #cext_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C72850
Conotoxin homolog - Autographa californica nuclear polyhedrosis virus
C;Species: Autographa californica nuclear polyhedrosis virus, AcMNPV
A;Note: dsDNA virus
C;Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 09-Jul-2004
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                                                           DB 2; Length 371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1208;
                                                                                                           Indels
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Best Local Similarity 47.8%; Pred. No. 1.9e+02;
Matches 11; Conservative 1; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-389 <VOL>
                                                     Score 50.5; DE Pred. No. 89; 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31.4%; Score 50.5; I 60.0%; Pred. No. 92; Live 2; Mismatches
                                                                                                                                                                                                  31 CRNINQ-CFONYNSPIKCRACRFRKC 55
                                                                                                                                                      1 CRIXNOKCFOHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           804 GNQNNFQSFDS-CSRACGATIVC 825
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                                             Query Match
Best Local Similarity 42.3%;
Matches 11; Conservative
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Best Local Similarity 60.0
Matches 9; Conservative
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A, Gene: CESP: ZK287.4
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                                                                      C; Accession: T30176
R;Sell, C; Hoff III, H.B.
Submitted to the EMBL Data Library, May 1996
A; Description: Cloning of a novel mRNA regulated by the insulin like growth factor type A; Reference number: Z20762
A; Accession: T30176
A; Accession: T30176
A; Accession: T30176
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-1687 <SEL>
A; Cross-references: UNIPROT: C61204; EMBL: U57368; NID: g1336627; PID: g1336628; PIDN: AAB013
A; Experimental source: strain C57BL/6J; clone DBI-1; whole embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Andlecule type: DNA
A;Residues: 1-131 cBRA>
A;Cross-references: UNIPROT:Q23053; EMBL:U64837; PIDN:AAB04836.1; GSPDB:GN00023; CESP:TZ
A;Experimental source: strain Bristol N2; clone T2784
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A;Residues: 1-371 <WIL>
A;Cross-references: UNIPROT:O17932; EMBL: 283233; PIDN:CABO5765.1; GSPDB:GN00023; CESP:KQC)Genetics: clone K06B4
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JF repeat transmembrane protein - mouse
Species: Mus musculus (house mouse)
Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
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T123369
T123369
T123369
T123369
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: D-Oct-1999 #sequence_revision 15-Cct-1999 #text_change 09-Jul-2004
R; Lloyd, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 131;
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A) Reference number: 219732
A) Accession: T23369
A) Status: preliminary; translated from GB/EMBL/DDBJA; Molecule type: DMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 31.4%; Score 50.5; Similarity 33.3%; Pred. No. 45 9; Conservative 4; Mismatche
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A;Introns: 40/1; 53/2; 98/1; 118/3
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A;Introns: 8/3; 120/3; 242/1
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A, Gene: CESP:T27E4.5
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A;Residues: 1-1474 <RIE>
A;Cross-references: UNIPROT:Q23870; EMBL:U00796; NID:g2702254; PID:g2702256; PIDN:AAC186:
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ,Residues: 1-204,'G',206-221,'A',223-380,'D',382-386,'H',388-444,'HN',447-450,'V',452-55
|Cross-references: GB:M23121; NID:g212746; PIDN:AAA49086.1; PID:g212749
|Accession: B33379
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Residues: 1-204,'G',206-221,'A',223-380,'D',382-386,'H',388-444,'HN',447-450,'V',452-55
Accession: C33379
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\(\forear-references: GB:ND3121\)
\(\forear-referenc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecule type: mRNA
Residues: 27-181,'R',183-204,'G',206-221,'A',223-380,'D',382-386,'H',388-444,'HN',447-4
Cross-references: EMBL:X08030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tran
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Molecule type: mRNA
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A;Residues: 1-1810 <JON>
A;Cross-references: UNIPROT:Q90824; GB:J04519; NID:g211717; PIDN:AAA48745.1; PID:g211718
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N.Contains: tenascin 190K; tenascin 200K
N.Contains: tenascin 190K; tenascin 200K
N.Contains: callue gallue (chicken)
C.Speciess (Gallue gallue)
C.Speciess (Gallue)
C.Species (Gallue)
C.Sp
                                                                                                                                                                                                                                                                                                                                                                 31.1%; Score 50; DB 2; Length 1474; 52.9%; Pred. No. 2.5e+02; ive 3; Mismatches 5; Indels
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Matches 9; Conserv
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J. Virol. 66, 6563-6571, 1992
A;Title: Characterization of a baculovirus gene encoding a small conotoxinlike polypepti A;Tele: Characterization of A;Tele: MID:93021384; PMID:1404603
A;Accession: A44003
A;Status: preliminary; not compared with conceptual translation
C; Accession: C73850; A44003
R; Ayres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D.
Xizology 202, 586-605, 1994
A; Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus.
A; Reference number: A72850; MUID:94303173; PMID:8030224
A; Status: preliminary
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-53 < AXR>
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A;Residues: 1-403 <WLL>
A;Residues: 1-403 <WLL>
A;Residues: UNIPROT: 062412; EMBL: AL021479; PIDN: CAA16320.1; GSPDB: GN00023; CESP: A;Experimental source: clone Y22F5A
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Genetics 148, 1117-1125, 1998
AyTitle: Dictyostellum discoideum nuclear plasmid Ddp5 is a chimera related to the Ddp1
A;Reference number: Z14684; MUID:98198836; PMID:9539429
A;Accession: T18281
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Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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C;Species: Dictyostelium discoideum
C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18281
R;Rieben Jr., W.K.; Gonzales. C.M.: Ganzales of maintimes of maint
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A,Molecule type: DNA
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Bubmitted to the EMBL Data Library, January 1998
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Pred. No. 28;
4; Mismatches
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Accession: T26551
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Gene: CESP:Y22F5A.1
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A; Residues: 1-53 < ELD
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interleukin-1 beta precursor - rabbit
Nicternate names: hematopoietin-1; IL-1 beta; lymphocyte proliferation potentiating fact. C.Species: Oryclolagus cuniculus (domestic rabbit)
C;Bote: 25-May-1989 #sequence revision 22-Nov-1996 #text_change 09-Jul-2004
C;Accession: A27714; A30584; JU0082; A32166
E;Mori, S.; Goto, F.; Goto, K.; Obkawara, S.; Maeda, S.; Shimada, K.; Yoshinaga, M. Biochem. Biophys. Res. Commun. 150, 1237-1243, 1988
A;Title: Cloning and sequence analysis of a cDNA for lymphocyte proliferation potentiatirly A;Recession: A27714; MUID:88134238; PMID:2449207
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Afresidues: 1-268 «CMN»
Afcrossidues: 1-268 «CMN»
Afcrossidues: 1-268 «CMN»
Afcrossidues: 1-268 «CMN»
Bfoung, P.R.; Sylvester, D.
Protein Eng. 2, 545-551, 1989
Affitle: Cloning of rabbit interleukin-1 beta: differential evolution of IL-1 alpha and 11
Afreference number: A94230; MUID:89315718; PMID:2787507
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A)Status: not compared with conceptual translation
A)Molecule type: mRNA
A)Molecule type: mRNA
A)Residues: 1-268 - WNOR
A)Cross-references: UNIPROT: P14628
A)Cross-references: UNIPROT: P14628
J. Immunol. 142, 2299-2306, 1989
A)Title: Rabbit IL-1. Cloning, expression, biologic properties, and transcription during
A)Reference number: A30584; MUD: 89176242; PMID: 2784458
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A,Residues: 1-268 <VOU>
C,Comment: This protein lacks a conventional signal sequence for protein export. Cleavage
C,Comment: This protein-lbeta, unlike interleukin 1-alpha, is inactive.
C,Comment: Interleukin-lbeta precursor is less heavily myristoylated than interleukin-lal
C,Superfamily: interleukin-l
C,Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
F;117-268/Product: interleukin-l beta #status predicted <LLB>
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Glycoprotein A - mouse
C.Species: Mus musculus (house mouse)
C.Species: O2-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 15-Jun-2001
C.Accession: JE0120
R.Haidaris, C.G.; Medzihradsky, O.F.; Gigliotti, F.; Simpson-haidaris, P.J.
DNA Res. S., 77-88, 1998
A.Title: Molecular characterization of mouse Pneumocystis carinii surface glycoprotein A. A.Title: Molecular characterization of mouse Pneumocystis carinii surface glycoprotein A. A. Molecula type: mRNA
A.Molecule type: mR
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                                                           F;34/Modified site: 6-bromotryptophan (Trp) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Indels
                                                                                                                                                                                                                                                                                            5; Mismatches
                                                                                                                                                                                 Score 49.5;
Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 30.7%; Score 49.5; I Similarity 37.0%; Pred. No. 93; 10; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 CKTNKMSCSLH-EECCRFRCCFHGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                       1 CRIXNOKCFOHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 OKCFOHLDDCCSRK-----CNRFNK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : || | | | | : | | : | | : | | 33 KSCFQDLDLCCPDEGIQLRISCQPYNK 59
                                                                                                                                                                      Query Match
Best Local Similarity 30.8%;
Matches 8; Conservative
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Matches
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() Species: Rattus norvegicus (Norway rat)
() Species: Rattus norvegicus (Norway rat)
() Species: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
() Accession: T08618
() Biol. Chem. 273, 5235-5242, 1998
() A. Biol. Chem. 273, 5235-5242, 1998
() A. Richter Chem. 273, 5235-5242, 1998
() A. Richter Chem. Chem. 216459; MUID:98148073; PMID:9478979
() A. Reference number: 216459; MUID:98148073; PMID:9478979
() A. R
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A;Cross-references: UNIPROT:O70244; EMBL:AF022247; NID:g3834379; PIDN:AAC71661.1; PID:g3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:Q7M4K5
A;Cross-references: UNIPROT:Q7M4K5
A;Note: Injection of rile in 13- to 15-day-old mice caused hyperactivity, circular motic ward swimming or swimming in a vertical direction and death.
F;13/Modified site: gamma-carboxyglutamic acid (Glu) #status predicted
F;14/Modified site: gamma-carboxyglutamic acid (Glu) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Superfamily: intrinsic factor-B12 receptor cubilin; BGF homology
C; Seywords: egg yolk; endocytosis; glycoprotein; intestine; kidney; peripheral membrane
F;1-20/Domain: signal sequence #Eratus predicted <SIG>
F;21-3623/Product: intrinsic factor-B12 receptor CUBILIN #status predicted <MAT>
F;133-164/Domain: BGF homology <BGF>
F;31-36-467/Domain: BGF homology <BGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Species: Conus radiatus
C; Date: 20-Jan-2003 #sequence_revision 20-Jan-2003 #text_change 09-Jul-2004
C; Accession: A59457
R; Olivera, B.
submitted to the Protein Sequence Database, January 2003
A; Description: Novel Excitatory Conus Peptides Define a New Conotoxin Superfamily.
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F;773-857/Domain: fibronectin type III repeat homology <FN3C>F;865-949/Domain: fibronectin type III repeat homology <FN3D>F;865-949/Domain: fibronectin type III repeat homology <FN3D>F;1036-1128/Domain: fibronectin type III repeat homology <FN3F>F;1037-1219/Domain: fibronectin type III repeat homology <FN3G>F;1228-1110/Domain: fibronectin type III repeat homology <FN3G>F;1318-1399/Domain: fibronectin type III repeat homology <FN3I>F;407-1487/Domain: fibronectin type III repeat homology <FN3I>F;1405-1575/Domain: fibronectin type III repeat homology <FN3I>F;1405-1575/Domain: fibronectin type III repeat homology <FN3I>F;1405-1778/Domain: fibronectin type III repeat homology <FN3I>F;139-1798/Domain: fibronectin type III repeat homology <FN3I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31.1%; Score 50; DB 1; Length 1810; 35.3%; Pred. No. 2.9e+02; ive 3; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 3623;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            356 RCENGLCVCHEGFVGDDCSQKRCPKTCNNRGRCV 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
31.1%; Score 50; DB 2; I
Best Local Similarity 29:2%; Pred. No. 4.66+02;
Matches 7; Conservative 6; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 RIXNOKCFOHL----DDC----CSRKCNRFNKCV 27
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Best Local Similarity 35.37
Matches 12, Conservative
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A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-37 <OLI>
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Page 15

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A;Cross-references: UNIPROT:Q9UUM3; EMBL:AL049495; PIDN:CAB39853.1; GSPDB:GN00066; SPDB:EA;Experimental source: strain 972h-; cosmid c2A9_3p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein T07E3.4 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: G88492
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Atcle: Genome sequence of the nematode C. elegans: a platform for investigating biology
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see webbaites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_elegans/A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: G88492
A;Status: preliminary
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A;Residues: 1-427 <STO>
A;Cross-references: UNIPROT:Q22310; GB:chr III; PIDN:AAA21083.1; PID:g532471; GSPDB:GN00
A;Note: weak similarity to glycogen branching enzyme
                                                                                                               conserved hypothetical protein SPBC2A9.11c - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
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C;Species: Caenorhabditis elegans
C;Accession: T32289
R;Scheet, P.; Maggi, L.
Submitted to the EMBL Data Library, September 1997
A;Description: The sequence of C. elegans cosmid F42G2.
A;Reference number: Z21146
A;Accession: T32289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                   C;Accession: T40102
R;Barrell, B.G; Rajandream, M.A.; Lyne, M.; Skelton, J.; Churcher, C. submitted to the BMBL Data Library, March 1999
A;Accession: T40102
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Pred. No. 1.4e+02;
6; Mismatches 8; Indels
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Local Similarity 24.4%; Pred. No. 1.4e+02;
es 11; Conservative 7; Mismatches 7;
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A;Molecule type: DNA
A;Residues: 1-395 <BAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 IXNQKCFQHLDDCCS--RKCN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 33.3%;
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Genetics:
A;Gene: SPDB:SPBC2A9.11c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Introns: 216/3; 260/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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TO1055

Hypothetical protein YUP8H12R.38 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 09-Jul-2004
C;Accession: T01055
R;Theologis, A.; Vysotskaia, V.S.; Osborne, B.I.; Schwartz, J.R.; Federspiel, N.A.; Kwan Oefner, P.; Davis, R.W.
submitted to the EMBL Data Library, May 1998
A;Description: Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence.
A;Reference number: 214227
A;Retus: translated from GB/EMBL/DDBJ
A;Rotaus: translated from GB/EMBL/DDBJ
A;Rotaus: 1-1516 <THE>
A;Resulus: Cycos - Federaces: UNIPROT: 064548; EMBL: AC002986; NID: 92494106; PID: 93152587; GSPDB: GNG
C;Genetics: And A; Accession: UNIPROT: 064548; EMBL: Accession: Cycos - Federaces: UNIPROT: 
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Cispecies: 20-59p-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jan-2000
Cipate: 20-58p-1999 #sequence 21-Jan-2000
Cipate: 2
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A;Map position: 1
A;Introns: 59/2; 97/3; 185/1; 319/1; 379/1; 809/3; 908/3; 1001/3; 1044/3; 1111/3; 1159/2
C;Superfamily: Pneumocystis carinii major surface glycoprotein MSG100
C;Keywords: glycoprotein
F;248,612,717,779,1063/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                    1;
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                                                                                                                                                                                                          Query Match 30.7%; Score 49.5; DB 2; Length 1282; Best Local Similarity 33.3%; Pred. No. 2.6e+02; Matches 9; Conservative 7; Mismatches 10; Indels 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       366 CQEYLEKCYFYGSSCKDTKCDKVNNKC 392
                                                                                                                                                                                                                                                                                                                                                                                                               1 CRIXNOKCFQHLDDCCSRKCNRF-NKC 26
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F;23-34,28-43,45-54,62-88,180-191,185-200,202-211,218-229,223-238,240-249,256-267,261-276
57,451-466,468-477,484-495/Distlicae bonds: #steure predicted
F;489-504,506-515,522-533,527-542,544-553,560-571,565-580,589-591,598-609,603-618,620-625
08,810-819,826-837,831-846,848-857,864-875,869-884,886-895,902-913,907-922,924-933/Distuli
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C;Species: Mus musculus (house mouse)
C;Date: 21-Jan-1994 #sequence_revision 05-Jan-1996 #text_change 16-Aug-2004
C;Accession: A49175; PH1570; S32113
R;Lardelli, M.; Lendahl, U.
R;Lardelli, M.; Lendahl, U.
A;Title: Motch A and Motch B--two mouse Notch homologues coexpressed in a wide variety of A;Reference number: A49175; WUID:93178563; PMID:8440332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Comment: EGF homology repeats 10-17 are spliced out in the short form (fibropellin Ib) :1-19/Domain: signal sequence #status predicted <SIG>:20-1064/Product: fibropellin I #status predicted <FIB>
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A;Experimental source extracted from NCBI backbone (NCBIP:126158)
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C;Comment: This protein is one of the neurogenic proteins controlling the decision betwee
C;Superfamily: Notch protein; ankyrin repeat homology; EGF homology
                    A;Title: A sea urchin gene encodes a polypeptide homologous to epidermal growth factor.
A;Reference number: A29316; MUID:87319677; PMID:3498216
                                                                                                                                                                                                                                                                                        R;Hunt, L.T.; Barker, W.C.
PASEB J. 3, 1760-1764, 1989
A;Title: Avidin-11ke domain in an epidermal growth factor homolog from a sea urchin.
A;Reference number: A43131; MUID:89196806; PMID:2784773
A;Contents: annotation
                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 'S',280-481,786-1064 <HUR>
A;Cross-references: GB:M17421; NID:g161474; PIDN:AAA30050.1; PID:g552260
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40.0%; Pred. No. 2.6e+02;
ive 3; Mismatches 9; Indels
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;57-175/Domain: Clr/Cls repeat hom
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A; Residues: 1-1203 <LAR>
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les 8; Conserv
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                                                                                                 A; Accession: A29316
A; Status: preliminary
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F;902-933/Domain:
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Best Local S
Matches 8
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                                    A;Cross-references: UNIPROT:017102; EMBL:AF024499; PIDN:AAB70358.1; GSPDB:GN00020; CESP: A;Experimental source: strain Bristol N2; clone F42G2 (Senetics) 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               integrin beta chain precursor - fruit fly (Drosophila melanogaster)
(Species: Drosophila melanogaster
(Species: Drosophila melanogaster
(Space: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 16-Aug-2004
(SAccession: A3088)
R;MacKrell, A.J.; Blumberg, B.; Haynes, S.R.; Fessler, J.H.
Proc. Natl. Acad. Sci. U.S.A. 85, 2633-2637, 1988
A;Title: The lethal myospheroid gene of Drosophila encodes a membrane protein homologous
A;Reference number: A30889; MuID:88190122; PMID:3128792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Molecule type: mRNA
A,Residues: 1-846 <MAC>
A,Cross-references: UNIPROT:P11584; GB:J03251; NID:g157954; PIDN:AAA28714.1; PID:g157955
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C;Date: 13-May-1992 #sequence revision 17-Sep-1997 #text_change 09-Jul-2004
C;Date: 13-May-1992 #sequence revision 17-Sep-1997 #text_change 09-Jul-2004
C;Accession: A40136; B40136; C40136; A29316; A43131
R;Deladillo-Reynoso, M.G.; Rollo, D.R.; Hursh, D.A.; Raff, R.A.
J. Mol. Evol. 29, 314-327, 1989
A;Title: Structural analysis of the uEGF gene in the sea urchin Strongylocentrotus purpu
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A; Status: preliminary
A; Moreite type: mRNA
A; Moleus: 1-114 < DEL>
A; Cross-references: UNIPROT: P10079; GB:X17530; NID:g10225; PID:g667061
A; Accession: B40136
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A;Cross-references: FlyBase:FBgn0004657
C;Superfamily: Integrin beta chain; laminin-type EGF-like homology
C;Keywords: cell adhesion; cytoskeleton; transmembrane protein
                                                                                                                                                                                                                                                                                                                 30.4%; Score 49; DB 2; Length 833; ilarity 26.9%; Pred. No. 2.2e+02; Conservative 6; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; not compared with conceptual translation A;Molecule type: DNA A;Residues: "K, 747-821,898-978 < DE3> K;Hursh, D.A.; Andrews; M.E.; Raff, R.A. Science 237, 1487-1490, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 846;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 30.4%; Score 49; DB 2; Length 846
Best Local Similarity 32.3%; Pred. No. 2.3e+02;
Matches 10; Conservative 6; Mismatches 11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 181-251,329-370,'R',372-408,'RA',411-441 <DE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  669 CIVNDQGRFSGRHCEKCPICSGRCQELKDCV 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CRIXNOKCF--OHLDDC--CSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87 QVVQNNCFQHLSPLYSKFCEHYGHMI 1.12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 RIXNOKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 7; Conserv
A;Residues: 1-833 <SCH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fibropellin Ia
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A40136
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C;Accession: S45306
R;Lardelli, W.; Dahlstrand, J.; Lendahl, U.
R;Lardelli, W.; Dahlstrand, J.; Lendahl, U.
A;Title: The novel Notch homologue mouse Notch 3 lacks specific epidermal growth factor-1
A;Reference number: S45306; MUD:95001556; PMID:7918097
A;Accession: S45306
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                               %;Cross-references: UNIPROT:061982; EMBL:X74760; NID:9483580; PIDN:CAA52776.1; PID:948358 C; Superfamily: notch protein; ankyrin repeat homology; EGF homology
F;163-195/Domain: EGF homology eEGF2>
F;163-105/Domain: EGF homology eEGF2>
F;854-885/Domain: EGF homology eEGF2>
F;1839-1871/Domain: ankyrin repeat homology eAN1>
F;1805-1938/Domain: ankyrin repeat homology eAN2>
F;1906-1938/Domain: ankyrin repeat homology eAN3>
F;1907-2004/Domain: ankyrin repeat homology eAN4>
F;1907-2004/Domain: ankyrin repeat homology eAN4>
F;1907-2004/Domain: ankyrin repeat homology eAN5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Bierkamp, C.; Campos-Ortega, J.A.
Mech. Dev. 43, 87-100, 1993
A;Title: A zebrafish homologue of the Drosophila neurogenic gene Notch and its pattern of
A;Reference number: S42612; MUID:94128602; PMID:8297791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-2437 <BLE>
A;Residues: 1-2437 <BLE>
A;Residues: 1-2437 <BLE>
A;Cross-references: UNIPROT:P46530; EMBL:X69088; NID:g433866; PIDN:CAA48831.1; PID:g43380
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology
F;755-786/Domain: EGF_homology <EGFI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Brachydanio rerio (zebra fish)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S42612
      notch 3 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
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Pred. No. 4.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.4%; Score 49; DB 2; Similarity 25.0%; Pred. No. 4.4e+02; 6; Conservative 6; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;1915-1947/Domain: ankyrin repeat homology <AN1>F;1948-1980/Domain: ankyrin repeat homology <AN2>F;1948-1980/Domain: ankyrin repeat homology <AN3>F;1982-2014/Domain: ankyrin repeat homology <AN3>F;2018-2047/Domain: ankyrin repeat homology <AN4>F;2048-2080/Domain: ankyrin repeat homology <AN5>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transmembrane protein precursor - zebra fish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1116 AGDSCEDNIDECASQPCQNGGSCI 1139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              249 TGQTCEHNVDDCTQHACENGGPCI 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 XNQKCFQHLDDCCSRKCNRFNKCV 27
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Best Local Similarity 29.2%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 1-2318 <LAR>
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Best Local Similarity
Matches 6; Conserv
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C;Species: Arabidopsis thaliana ($\text{mouse-ear}$ cress)

C;Accession: T06694

R;Quetier, F.; Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artigusubmitted to the Protein Sequence Database, April 1999

A;Accession: T06694

A;Accession: T06694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: T06692
R;Quetier, F.; Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artigu submitted to the Protein Sequence Database, April 1999
A;Reference number: 215793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Introns: 823/3; 866/3; 930/3; 947/2; 1051/3; 1094/1; 1161/1; 1193/1; 1253/3; 1325/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Accession: T06692
A; Molecule type: DNA
A; Residues: 1-1291 <QUE>
A; Residues: 1-1291 <QUE>
A; Cross-references: UNIPROT: Q9SU54; EMBL: AL049658; GSPDB: GN00061; ATSP:T17F15.220
A; Experimental source: cultivar Columbia; BAC clone T17F15
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A; Reaidues: 1-128 «QUE»
A; Cross-references: UNIPROT:Q9SU52; EMBL:AL049658; GSPDB:GN00061; ATSP:T17F15.240
A; Experimental Bource: cultivar Columbia; BAC clone T17F15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypochetical protein T17F15.220 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr.1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                Length 1203;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.4%; Score 49; DB 2; Length 1528; 42.1%; Pred. No. 3.4e+02; Live 3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Introns: 863/3; 906/3; 970/3; 987/2; 1091/3; 1134/1; 1201/1
                                                                                                                                                                             30.4%; Score 49; DB 2; 1
llarity 29.2%; Pred. No. 2.9e+02;
Conservative 6; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
                                                                                                                                                                                                                                                                                                                                     4 XNQKCFQHLDDCCSRKCNRFNKCV 27
         homology <EGF1>
homology <EGF>
homology <EGX2>
homology <EGF3>
homology <EGF3>
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Matches 8; Conservative
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Matches 8; Conservative
                                                                                                                                                                             Query Match
Best Local Similarity
Matches 7; Conserv
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A,Gene: ATSP:T17F15.240
A,Map position: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene: ATSP:T17F15.220
                                                              EGF
FGF
F;482-513/Domain: E;560-591/Domain: E;674-705/Domain: E;712-743/Domain: E;836-867/Domain: E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Map position:
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RESULT 66

Matches

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A; Molecule type: DNA
A; Residues: 1-461 < LBEV.
A; Residues: 1-461 < LBEV.
A; A; Residues: 1-461 < LBEV.
A; A; Cross-references: UNIPROT: PS4873; EMBL: AL078606
A; Experimental source: cultivar Columbia; BAC clone T26M18
R; Montamat, F.; Guilloton, M.; Karst, F.; Delrot, S.
Gene 167, 197-201, 1995
A; Title: Isolation and characterization of a cDNA encoding Arabidopsis thaliana 3-hydrox)
A; Reference number: JC4567; MUID: 96144274; PMID: 8566777
                                                                                                                                                                                                                                                                                                                                                                                                                                                  C,Accession: A45545
R;Blackman, M.J.; Ling, I.T.; Nicholls, S.C.; Holder, A.A.
Mol. Biochem. Parasitol. 49, 29-33, 1991
A;Title: Proteolytic processing of the Plasmodium falciparum merozoite surface protein-1 A;Reference number: A45545; MUID:92131048; PMID:1775158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;MOJECTLE type: mRNA
A;Residues: 1-305,'S',307-341,'N',343-461 <MON>
A;Cross-references: EMBL:X83882; NID:g1143389; PIDN:CAA58763.1; PID:g1143390
C:Comment: This enzyme mediates the conversion of three acetyl-CoA molecules to one molecivity, and uptakes amino acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5) - Arabidopsis thaliana
N;Alternate names: 3-hydroxy-3-methylglutaryl-coenzyme A synthase; protein T26M18.30
S;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T09341; JC4557
R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft, submitted to the Protein Sequence Database, June 1999
A;Reference number: Z16650
A;Accession: T09341
                                                                                                                                                                                                                                                                                                                                                major merozoite surface antigen - malaria parasite (Plasmodium falciparum) (fragments)
C;Species: Plasmodium falciparum
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Introns: 21/3; 57/2; 101/3; 149/3; 202/3; 227/2; 252/3; 271/2; 300/3; 347/3; 397/3 C; Superfamily: hydroxymethylglutaryl-CoA synthase C; Superfamily: hydroxymethylglutaryl-CoA synthase C; Keywords: carbon-carbon lyase; coenzyme A; glycoprotein; oxo-acid-lyase F;117/Active site: Cys (covalent substrate-binding) #status predicted F;269/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 11-400 cBLA>
A;Residues: 11-400 cBLA>
A;Cross-references: UNPROT:Q03999
A;Cross-reference extracted from NCBI backbone (NCBIN:77612, NCBIP:77621)
C;Superfamily: major merozoite surface antigen
C;Keywords: glycoprotein; merozoite; surface antigen; tandem repeat
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30.1%; Score 48.5; DB 2; Length 461;
Best Local Similarity 39.1%; Pred. No. 1.7e+02;
Matches 9; Conservative 4; Mismatches 9; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                    170 CASQNQKTNQCANECNNQCANSCSPSSQTSSYSKCV 205
       Local Similarity 30.6%; Pred. No. 1.4e+02; nes 11; Conservative 7; Mismatches 9;
                                                                                                            1 CRIXNQKCFQHLDDC---CSRKC----NRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 48.5; DB 2;
Pred. No. 1.6e+02;
4; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300 QNSGCFRHLDEREECKCLLNYKQEGDKCV 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 XNOKCFOHLDDCCSRKC----NRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 30.1%;
l Similarity 37.9%;
11; Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 11, Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Gene: ATSP: T26M18.30
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       Best Loca
Matches
                                                                                                                                                                                                                                                                               RESULT 71
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Rivan den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.
Biochim. Biophys. Acta 453, 400-409, 1976
Biochim. Biophys. Acta 453, 400-409, 1976
A;Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic
A;Reference number: A90612; MUID:77065676; PMID:999896
A;Accession: A00820
A;Accession: A00820
A;Residues: 1-124 <VAN>
A;Residues: 1-124 <VAN>
A;Residues: 1-24 <VAN>
A;Coss-references: UNIPROT:P00675
A;Note: a second component of chinchilla ribonuclease has 32-Asp
C;Superfamily: pancreatic ribonuclease;
C;Superfamily: pancreatic ribonuclease;
C;Keywords: glycoprotein, hydrolase; nucleic acid digestion; pancreas
C;Keywords: glycoprotein, hydrolase; nucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;34/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 69
J01739
hypothetical 14.7K protein - shallot virus X
N.Alternate names: ORF6 protein
C.Species: shallot virus X
C.Species: shallot virus X
C.Species: shallot virus X
C.Species: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C.Species: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C.Species: 30, Sep-1993 #sequence _revision 30-Sep-1993 #text_change 09-Jul-2004
C.Species: 30, Sep-1993 #sequence _revision 30-Sep-1993 #text_change 09-Jul-2004
R.Kanyuka, K.V.; Vishnichenko, V.K.; Levay, K.E.; Kondrikov, D.Y.; Ryabov, E.V.; Zavriev
A.Fithe: Nucleotide sequence of shallot virus X RNA reveals a 5'-proximal cistron closel
A.Reference number: J01734; MUID:93019008; PMID:1339468
A.Recession: J01739.
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A.Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele A.Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A.Statuus: preliminary
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;Cross-references: UNIPROT:Q9TY01; GB:chr_V; PID:g4883503; GSPDB:GN00023; CESP:C24B5.5
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(899152

Protein C19B5.5 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: (899152
C;Accessions, Caelegans Sequencing Consortium.
Science 282, 2012-2018, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30.1%; Score 48.5; DB 1; Length 124; llarity 27.5%; Pred. Nc. 72; Conservative 6; Mismatches 8; Indels 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 128;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |::||:|||:|||65 CKNGQSNCYQSNSNMHITDCRLISNSKYPNCSYRTSRENK 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CRIXNOKCFQ-----HLDDC-----CSRKCNRFNK 25
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A;Residues: 1.128 «KAN»
A;Cross-references: UNIPROT: 004580
A;Experimental source: strain X
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Best Local Similarity
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Best Local Similarity
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C;Genetics: A;Gene: C24B5.5

g ò

Query Match

us-10-627-685a-26.rpr

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Nucleic Acids Res. 17, 5401, 1989

A;Title: Nucleotide and deduced amino acid sequence of the gpl95 (MSA-1) gene from Plasmc A;Reference number: S04850; MUID:89345116; PMID:2668887

A;Recession: S04850

A;Molecule type: mRNA
A;Residues: 1504-16339 cMYL2>
A;Cossidues: 1504-16339 cMYL2>
C;Superfamily: major merozoite surface antigen
C;Superfamily: major merozoite; surface antigen
C;Keywords: glycoprotain; merozoite; surface antigen
C;F1-19,Domain: signal sequence #status predicted <SIG>
F;20-1639/Product: major merozoite surface antigen #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (8t)
                                                                                                  A;Molecule type: mRNA
A;Residues: 1-1639 <MYL>
A;Croser zeferences: UNIPROT:P04933; EMBL:X15063; NID:g9896; PIDN:CAA33163.1; PID:g9897
R;Myler, P.J.
Nucleic Acids Res. 17, 5401, 1989
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N;Alternate names: 195K glycoprotein
C;Species: Plasmodium falciparum
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S
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Pred. No. 4e+02;
4; Mismatches 9; Indels 5
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Pred. No. 4.1e+02;
4; Mismatches 9;
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A;Molecule type: DNA
A;Residues: 1-1104. AWEB1>
A;Cross-references: UNIPROT:P04934; EMBL:X03831
A;Cross-r.i.s.; Sim, B.K.L.; Lyon, J.A.; Wolff, R. Nucleic Acids Res. 16, 1206, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1539 ONSGCFRHLDEREECKCLLNYKOEGDKCV 1567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :| || || || || || ENSGCFRHLDEREECKCLLNYKOEGDKCV 1629
R;Myler, P.J.
submitted to the EMBL Data Library, April 1989
A;Reference number: S05603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 XNOKCFOHLDDCCSRKC----NRFNKCV 27
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Local Similarity 37.9%;
hes 11; Conservative
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Best Local Similarity 37.9%;
Matches 11; Conservative '
                                                                               Accession: S05603
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Matches
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A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule: 1-651 <TOL>
A;Cross-references: UNIPROT:Q25924; EMBL:235329; NID:g535257; PIDN:CAA84558.1; PID:g5352
A;Cross-references: UNIPROT:Q26924; EMBL:235329; NID:g535257; PIDN:CAA84558.1; PID:g5352
A;Experimental source: atrain R0-71
C;Superfamily: major merozoite; surface antigen
C;Keywords: glycoprotein; merozoite; surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 major merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum) (st
C;Species: Plasmodium falciparum
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jun-2000
C;Accession: A25120
R;Mackay, M; Goman, M; Bone, N; Hyde, J.E.; Scaife, J.; Certa, U.; Stunnenberg, H.; E
Briso J. 4, 3823-3829, 1895
A;Title: Polymorphism of the precursor for the major surface antigens of Plasmodium falc
A;Reference number: A91030; MUID:86136024; PMID:3004972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Comment: The merozoite stages of different strains have strain-specific surface antige
;Comment: P. falciparum has three stages: sporozoite, merozoite, and gametocyte. The me
;Superfamily: major merozoite surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Keywords: glycoprotein; merozoite; surface antigen; tandem repeat; transmembrane prote F;1-19/Domain: signal sequence #status predicted <SIG> 7:20-1631/Product: major merozoite surface antigen #status predicted <MAT> F;67-84/Region: 3-residue repeats (S-G-T/P) F;1614-1631/Domain: membrane anchor #status predicted <MBN> F;1614-1631/Domain: membrane anchor #status predicted <MBN> F;97,259,755,759,835,911,955,1049,1156,1165,1436,1563/Binding site: carbohydrate (Asn) (
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                                                                                                                                                                                                             - malaria parasite (Plasmodium falciparum) (strain RO-71)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - malaria parasite (Plasmodium falciparum)
                                                                                                                                                                                                                                                              A,Variety: strain RO-71
C;Date: 06-Jan-1995 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: S47282
R;Tolle, R.; Bujard, H.; Cooper, J.A.
submitted to the RMBL Data Library, July 1994
A;Description: Plasmodium falciparum: recombination within the C-terminal region of
A;Reference number: S47282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 48.5; DB 2;
Pred. No. 2.2e+02;
4; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1531 QNSGCFRHLDEREECKCLLNYKQEGSKCV 1559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      551 QNSGCFRHLDEREECKCLLNYKQEGDKCV 579
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                                                         LSQTCYLMALDSCYKHLCNKFEK 230
                        XNOKCF-OHLDDCCSRKCNRFNK
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37.9%;
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Matches 11; Conservative
                                                                                                                                                                                                             merozoite surface antigen 1 - mal
C;Species: Plasmodium falciparum
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Best Local Similarity 37.9.
Thes 11; Conservative
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C;Comment: The merozoite
C;Comment: P fall:
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S05603
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A;Cross-references: SGD:S0003092
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Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: CESP: Y43F8C.16
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Best Local S:
Matches 9
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                                                        A; Accession: S06361
A; Molecule type: DNA
A; Cross-references: EMBL:X03831
C; Comment: The merozoite stages of different strains have strain-specific surface antige
C; Comment: P. falciparum has three stages: sporozoite, merozoite, and gametocyte. The me
C; Keywords: glycoprotein: merozoite surface antigen; tandem repeat
C; Keywords: glycoprotein: merozoite; surface antigen tandem repeat
C; Keywords: glycoprotein: merozoite surface antigen
C; Keywords: glycoprotein: merozoite surface
C; Keywords: glycoprotein: merozoite 
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A45946

C; Species: Plasmodium falciparum
C; Species: Plasmodium falciparum
C; Species: Plasmodium falciparum
C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C; Accession: A45948
R; Chang, S.P.; Kramer, K.J.; Yamaga, K.M.; Kato, A.; Case, S.E.; Siddiqui, W.A.
Exp. Parasitol. 67, 1-11, 1988
A; Title: Plasmodium falciparum: gene structure and hydropathy profile of the major meroz A; Recession: A45948; MUID:89005525; PMID:3049134
A; Rate: preliminary
A; Statuus: preliminary
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'Title: Merozoite surface protein sequence from the Camp strain of the human malaria
Reference number: 806361; MUID:88143999; PMID:3278296
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502007
502007
C) Conceaning I - rabbit
C) Species: Oryctolagus cuniculus (domestic rabbit)
C) Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C) Accession: S02007
R;Ammer, H.; Henschen, A.
FBBS Lett. 242, 111-116, 1988
A;Title: Primary structure of rabbit sperm protamine, the first protamine of its type 1
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30.1%; Score 48.5; DB 1; Length 1726;
Best Local Similarity 37.9%; Pred. No. 4.1e+02;
Matches 11; Conservative 4; Mismatches 9; Indels 5
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Pred. No. 4.1e+02;
4; Mismatches 9; Indels
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Pred. No. 45;
5; Mismatches 10
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A,Residues: 1-1726 <CHA>
A;Cross-references: UNIPROT:Q25922; GB:M37213
C;Superfamily: major merozoite surface antigen
C;Keywords: surface antigen
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C;Superfamily: sperm histone
C;Keywords: DNA binding; nucleus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30.1%;
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Best Local Similarity 34.6%;
Matches 9; Conservative
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A, Molecule type: protein
A, Residues: 1-49 < AMM>
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S64135

hypothetical protein YGL124c - yeast (Saccharomyces cerevisiae)

NAlternate names: hypothetical protein G2889

Cispecies: Saccharomyces cerevisiae

Cispecies: Saccharomyces cerevisiae

Cispecies: Saccharomyces cerevisiae

Cispecies: SACCESSION: S64135; S72027

Riceran, E.; Rodriguez-Torres, A.M.; Rodriguez-Belmonte, E.; Tizon, B.; Cadahia, J.L.; Cabahited to the Protein Sequence Database, May 1996

A:Reference number: S64134
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A; Residues: 1-644 < CERA
A; Residues: 1-644 < CERA
A; Residues: 1-644 < CERA
A; Cross-references: UNIPAPOT: P53129; EMBL: Z72646; NID: g1322684; PIDN: CAA96832.1; PID: e2433:
A; Experimental source: strain S288C
B; Tizon, B.; Rodriguez-Torres, A.M.; Rodriguez-Belmonte, E.; Cadahia, J.L.; Cerdan, E.
Yeast 12, 1047-1051, 1996
A; Title: Identification of a putative methylenetetrahydrofolate reductase by sequence ans A; Title: Omnuber: S72026; MUID: 97051592; PMID: 8896269
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:09XWN5; EMBL:AL032637; PIDN:CAA21616.1; CESP:Y43F8C.16
A;Experimental source: clone Y43F8C
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                                                                                                                                                                                         hypothetical protein Y43F8C.16 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct.1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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C;Superfamily: Caenorhabditis elegans hypothetical protein Y43F8C.16
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A;Residues: 1-644 <TIZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match
29.8%; Score 48; DB 2; Length 296;
Local Similarity 37.5%; Pred. No. 1.5e+02;
tes 9; Conservative 4; Mismatches 11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-296 <WIL>
                                                                                                                                                                                                                                                                                                C.Accession: 176875
R.Ainscough, R.
Submitted to the EMBL Data Library, October 1998
A.Reference number: 220279
A.Accession: 126875
14 CRRRRRCRRRRRCCQRR--RVRKC 37
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A; Molecule type: mRNA
A; Residues: 1-880 <VAE>
A; Cross-references: UNIPROT: P10041; EMBL: X06289; NID: 97852; PID: 97853
R; Knust. E. 1. Dietrich, U.; Tepass, U.; Bremer, K.A.; Weigel, D.; Vaessin, H.; Campos-Orte
EMBO J. 6, 761-766, 1987
A; Title: EGF homologous sequences encoded in the genome of Drosophila melanogaster, and t
A; Reference number: A91081; MUID: 87218537; PMID: 3107986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-1429 <YOC>
A;Cross-references: UNIPROT:P14585; EMBL:M12069; NID:g156357; PIDN:AAA70191.1; PID:g1563E
            Title: The neurogenic gene Delta of Drosophila melanogaster is expressed in neurogenic; Reference number: S00670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A)Cross-references: FlyBase:FBgn0000463
C;Superfamily: neurogenic protein delta; EGF homology
C;Keywords: transmembrane protein
F;I-18/Domain: signal sequence #status predicted <SIG>F:19-8P/Product: neurogenic repetitive locus delta protein #status predicted <MAT>F;19-88/Domain: EGF homology <EGFI>F;533-564/Domain: EGF homology <EGFI>
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C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 16-Aug-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                         ;Accession: A26637
;Molecule type: mRNA
;Residues: 422-436, ET', 439-458, 'A',460-489, 'T',491-621 <KNU>
;Cross-references: GB:X05140; NID:97851; PIDN:CAA28786.1; PID:9929563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
29.8%; Score 48; DB 2; Length 880;
Best Local Similarity 28.6%; Pred. No. 3e+02;
Matches 6; Conservative 5; Mismatches 10; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Greenwald, I.
Cell 43, 583-590, 1985
A;Reference number: A24769; MUID:86079540; PMID:3000611
A;Accession: A24769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 449 RCETNIDDCLGHQCENGGTCI 469
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Best Local Similarity 35.0
Matches 7; Conservative
6, 3431-3440, 1987
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A; Residues: 173-712 <GRE>
                                                                              Accession: S00670
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                                       A31246
A31246
A31246
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A31246
A31246
C;Species: Drosophila melanogaster)
C;Species: Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 02-Aug-2002
C;Accession: A31246
A;Title: Delta, a Drosophila neurogenic gene, is transcriptionally complex and encodes
A;Title: Delta, a Drosophila neurogenic gene, is transcriptionally complex and encodes
A;Refedence number: A31246
A;Molecule type: mRNA
A;Residues: 1-832 <KOP>
A;Cross-references: GB:Y00222
C;Genetics:
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Cibate: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
CiAccession: S19087
Simuskavitch, M.A.T.
submitted to the EMBL Data Library, June 1991
A;Reference number: S19087
A;Accession: S19087
A;Accession: S19087
A;Reference number: Manay
A;Rolecule 'type: manay
A;Rolecule 'type: manay
A;Residues: 1-833 *MUS>
A;Cross-references: UNIPROT:P10041; EMBL:Y00222
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C;Species: Drosophila melanogaster
C;bate: 31-Dec-1988 #recurence_revision 31-Dec-1988 #text_change 09-Jul-2004
C;Accession: S00670; Az6637
R;Vaessin, H.; Bremer, K.A.; Knust, E.; Campos-Ortega, J.A.
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S19087
gene Delta protein precursor – fruit fly (Drosophila melanogaster)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Superfamily: neurogenic protein delta; EGF homology F;295-328/Domain: EGF homology <EGX1> F;422-450/Domain: EGF homology <EGF1> F;457-488/Domain: EGF homology <EGF> F;533-564/Domain: EGF homology <EGF>
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F;378-415/Domain: EGF homology < EGF1>
F;457-488/Domain: EGF homology < EGF5>
F;533-564/Domain: EGF homology < EGF5>
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A,Cross-references: FlyBase:FBgn0000463
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A,Cross-references: FlyBase:FBgn0000463
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28.6%;
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Matches 6; Conservative
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Accession: S02392
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notch3 protein - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: A-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C;Accession: S78549; S71825
R;Joutel, A.; Tournier-Lasserve, E.
submitted to the EMBL Data Library, April 1997
A;Reference number: S78549
A;Rocession: S78549
A;Rocession: S78549
A;Rocession: S78549
A;Rocession: S7001>
A;Rocession: S7001>
A;Rocession: S71825; MUIDP:97032728; PMID:8878478
A;Title: Notch3 mutations in CADASIL, a hereditary adult-onset condition causing stroke A;Rocession: S71825; MUID:97032728; PMID:8878478
A;Rocession: S71825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 67-113;138-194;268-333,'G',335-346;536-613;716-765;1240-1279;1815-1888 <JOUZ
A;Cross-references: EMBL:U97669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;Su, X.Z.; Hartwole, V.M.; Wertheimer, S.F.; Guinet, F.; Herrfeldt, J.A.; Peterson, D.S. 11 82, 89-100, 1995.
Fittle: The large diverse gene family var encodes proteins involved in cytoadherence an Reference number: Z20487; MUID:95330813; PMID:7606788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a type of stroke and
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A;Cross-references: UNIPROT:Q26032; EMBL:L40609; NID:g886376; PID:g886377; PIDN:AAA75397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2321;
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5; Mismatches 9; Indels
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Molecule type: DNA
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578 RCESQVDECRSQPCRHGGKCL 598
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F,162-194/Domain: BGF homology <BGFI>
F,240-271/Domain: BGF homology <BGX2>
F,318-349/Domain: BGF homology <BGX2>
F,9473-264/Domain: BGF homology <BGR3>
F,953-884/Domain: BGF homology <BGR3>
F,928-959/Domain: BGF homology <BGFS>
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Best Local Similarity 33.33
Matches 7; Conservative
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A;Map position: 19p13.1
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162-194/Domain: EGF
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A;Introns: 2597/3
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alpha-2-macroglobulin receptor precursor - human
NyAlternate names: CD91; LDL receptor-related protein 1; low density lipoprotein receptor
C;Species: Homo sapiens (man)
C;Date: 14-Aug-1998 #sequence revision 14-Aug-1998 #text_change 09-Jul-2004
C;Accession: S02392; S30027; I37998; A39210; S12538
R;Herz, JJ: Hamann, U; Rogne, S.; MyKlebost, O.; Gausepohl, H.; Stanley, K.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Title: Surface location and high affinity for calcium of a 500-kd liver membrane protes:
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EMBO J. 9; 1769-1776, 1990
A;Title: Proteolytic processing of the 600 kd low density lipoprotein receptor-related prairitle: Proteolytic processing of the 600 kd low density lipoprotein receptor-related prairitle: Proteolytic processing of the 600 kd low density lipoprotein receptor-related prairitle: Proteolytic processing of the 600 kd low density lipoprotein receptor-related protein (LRP) promotes allocation; site of proteolytic cleavage
Biochim. Biophys. Acta 1009, 229-236,
Biochim. Biophys. Acta 1009, 229-236,
A;Title: Structure of the low-density lipoprotein receptor-related protein (LRP) promotes A;Reference number: 137998; MUID:90089395; PMID:2597675
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A;Gene: GDB:LRP1; APR; LRP; A2MR
A;Cross-referencés: GDB:119694; OMIM:107770
A;Map position: 12q13.1-12q13.3
C;Complex: The alpha-2-macroglobulin receptor complex consists of noncovalently-associate
C;Complex: The alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-binding
C;Superfamily: alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-binding
C;Superfamily: alpha-2-macroglobulin receptor 51GS-
F;1-19/Domain: signal sequence #status predicted <51GS-
F;2-0-3943/Product: alpha-2-macroglobulin receptor 515K chain #status predicted <515K>
F;2-0-3943/Product: alpha-2-macroglobulin receptor 515K chain #status predicted <515K>
F;72-108/Domain: LDL receptor ligand-binding repeat homology <LDL1>
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Strickland, D.K.; Ashcom, J.D.; Williams, S.; Burgess, W.H.; Migliorini, M.; Argraves, Biol. Chem. 265, 17401-17404, 1990
Strickland, D.K.; Sequence identity between the alpha2-macroglobulin receptor and low density lipcing Sequence in Month of Month
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Molecule type: protein
Residues: 150-166;234-238,'X',240-245,'X',247-252;'G',686-695;902-916;1096-1109;'S',174
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Cross-references: UNIPROT:Q07954; EMBL:X13916; NID:G34338; PIDN:CAA32112.1; PID:G34339
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Status: preliminary; translated from GB/EMBL/DDBJ
Molecule type: DNA
Residues: 1-11 <RES>
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Query Match
29.8%; Score 48; DB
Best Local Similarity 33.3%; Pred. No. 6.8e
Matches 9; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                    1052 CKGKAKSCTQKDGDCTKCKAACDNYNK 1078
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F)148-188/Domain: EGF homology <EG2-
198-239/Domain: LDL receptor WTD-containing
F)240-281/Domain: LDL receptor WTD-containing
F)282-334/Domain: LDL receptor WTD-containing
F)335-378/Domain: LDL receptor WTD-containing
F)379-420/Domain: LDL receptor WTD-containing
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A; Residues: 3275-3864 <KRI>
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homology <YW24>
homology <YW25>
homology <YW26>
homology <YW27>
homology <YW27>
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<LDLN>
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<LDLQ>
<LDLR>
<LDLR>
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The homology cEG12>
The receptor YWTD-containing repeat homology cW10.
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F;2944-2980/Domain:
F;2946-3021/Domain:
F;3029-3068/Domain:
F;3069-3113/Domain:
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F;3201-3241/Domain:
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F;3294-3330/Domain:
F;3334-3369/Domain:
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F;3413-3448/Domain:
F;3453-3489/Domain:
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F;3654-3690/Domain:
F;3695-3731/Domain:
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F;1754-1796/Domain:
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F;1850-1886/Domain:
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F,3575-3609/Domain:
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N'Alternate names: CD91; LDL receptor-related protein 1; low density lipoprotein receptor
C;Species: Mus musculus (house mouse)
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A;Molecule type: mRNA
A;Residues: 1-4545 cVANI>
A;Residues: 1-4545 cVANI>
A;Cross-references: 1-4545 cVANI>
A;Cross-references: UNIRROT:061291; EMBD:X67469; NID:g49941; PIDN:CAA47817.1; PID:g49942
R;van Leuven, F.; Stas, L.; Raymakers, L.; Overbergh, L.; de Strooper, B.; Hilliker, C.;
Bjochim. Bjophys. Acta 1173, 71-74, 1993
A;Title: Molecular cloning and sequencing of the murine alpha-2-macroglobulin receptor of A;Reference number: S32554; MUID:93250049; PMID:8485155
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A,Accession: 52.5-5-4
A,Accession: 52.5-5-4
A,Accession: 52.5-5-4
A,Accession: 52.5-5-4
A,Accession: 52.5-5-4
A,Accession: 52.5-5-4
A,Cross -references: EMB1.X67469
C,Complex: The alpha-2-macroglobulin receptor complex consists of noncovalently-associat cited protein (see PIR:X70281).
C,Superfamily: alpha-2-macroglobulin receptor; EGF homology, LDL receptor ligand-binding C,Keywords: beta-hydroxyasparagine; beta-hydroxyaspartic acid; calcium binding; glycopro F,1-19/Domain: signal sequence #status predicted <51G.
F,20-3944/Domain: alpha-2-macroglobulin receptor $15K chain #status predicted <41KA>F;20-3944/Domain: alpha-2-macroglobulin receptor $15K chain #status predicted <515K>F;20-3944/Domain: LDL receptor ligand-binding repeat homology <LDL1>F;31-19/Domain: LDL receptor ligand-binding repeat homology <W002>F;31-19/Domain: LDL receptor YWTD-containing repeat homology <W003>F;31-138/Domain: LDL receptor YWTD-containing repeat homology <W003>F;33-335/Domain: LDL receptor YWTD-containing repeat homology <W003>F;33-335/Domain: LDL receptor YWTD-containing repeat homology <W004>F;33-421/Domain: LDL receptor YWTD-containing repeat homology <W004>F;33-421/Domain: LDL receptor YWTD-containing repeat homology <W004>F;33-421/Domain: LDL receptor YWTD-containing repeat homology <W005>F;33-421/Domain: LDL receptor YWTD-containing repeat homology <W006>F;33-421/Domain: LDL receptor YWTD-containing repeat homology <W006>F;32-46/Domain: LDL receptor YWTD-containing repeat homology <W006>F;32-42-46/Domain: LDL receptor YWTD-containing repeat homology <W006>F;32-42-42/Domain: LDL receptor YWTD-containing repeat homology <W006>F;32-42-42/Domain: LDL receptor YWTD-
LDL receptor ligand-binding repeat nomology successions of the homology security sec
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F;445-454/Domain: transmembrane #status predicted <INT>
F;445-454/Domain: intracellular #status predicted <INT>
F;165,2998/Modified site: erythnro-beta-hydroxyasparagine fast) #status predicted
F;2558/Modified site: erythnro-beta-hydroxyaspartic acid (Asp) #status predicted
F;4075,4125,4278/Binding site: carbohydrate (Asn) (covalent) #status predicted
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F;4013-4056/Domain: LDL receptor YWTD-cont
F;4100-4142/Domain: LDL receptor YWTD-cont
F;4151-4182/Domain: LDL receptor YWTD-cont
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F;4200-4231/Domain: EGF homology «EG15»
F;4200-4331/Domain: EGF homology «EG19»
F;4318-4373-4408/Domain: EGF homology «EG19»
F;4318-4374/Domain: EGF homology «EG20»
F;4317-4408/Domain: EGF homology «EG21»
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F;3944-4544/Product:
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F;3828-3860/Domain:
F;3868-3911/Domain:
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F;479-520/Domain: EGF homology <EG3>
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F;512-664/Domain: LDL receptor YWTD-containing repeat homology <YW08>
F;661-711/Domain: LDL receptor YWTD-containing repeat homology <YW09>
F;712-753/Domain: LDL receptor YWTD-containing repeat homology <YW10>
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F;885-891/Domain: LDL receptor ligand-binding repeat homology <UDL3>
F;896-932/Domain: LDL receptor ligand-binding repeat homology <LDL5>
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F;1105-1141/Domain: LDL receptor ligand-binding repeat homology <LDL6>
F;1105-1141/Domain: LDL receptor ligand-binding repeat homology <LDL6>
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F;1490-1532/Domain: LDL receptor YWTD-containing repeat homology <WH15>
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F;1490-1532/Domain: LDL receptor YWTD-containing repeat homology <WH15-
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F;2260-2242/Domain:
F;224-225/Domain:
F;2345-2389/Domain:
F;2390-2430/Domain:
F;2431-24/4/Domain:
F;2483-2518/Domain:
F;2557-2601/Domain:
F;266-2640/Domain:
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F;1935-1977/Domain:
F;1978-2020/Domain:
F;2021-2064/Domain:
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F;1628-1670/Domain:
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;2905-2940/Domain;
;2945-2981/Domain;
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F;2819-2854/Domain:
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Pancreatic ribonuclease (EC 3.1.27.5) - reindeer (tentative sequence)
NyAlternate names: RNase 1; RNase A
C;Species: Rangifer tarandus (reindeer)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: B91418; A00812
R;Ledijenaar-van den Berg, G; Beintema, J.J.
R;Reijenaar-van den Berg, G; Beintema, J.J.
A;Ttle: The amino acid sequences of reindeer, moose and fallow deer pancreatic ribonucle
A;Reference number: A91418; MUD: 76003215; PMID:1157925
A;Accession: B91418
A;Molecule type: protein
A;Residues: 1.124 <LEI>A;Cross references: UNIPROT: P00666
C;Superfamily: pancreatic ribonuclease
C;Superfamily: pancreatic ribonuclease
C;Superfamily: pancreatic ribonuclease
C;Gywords: hydrolase; nucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
                                                         in: LDL receptor YWTD-containing repeat homology <YW40>
in: LDL receptor YWTD-containing repeat homology <YW41>
in: LDL receptor YWTD-containing repeat homology <YW41>
in: alpha-2-macroglobulin receptor 85K chain #status predicted <85K>
in: 85K chain extracellular #status predicted <8KT>
in: BDL receptor YWTD-containing repeat homology <YW42>
in: LDL receptor YWTD-containing repeat homology <YW44>
in: LDL receptor YWTD-containing repeat homology <YW44>
in: BDF homology <EG16>
in: EGF homology <EG18>
in: EGF homology <EG18>
in: EGF homology <EG19>
in: EGF homology <EG22>
in: EGF homology <EG22>
in: EGF homology <EG22>
in: EGF homology <EG22>
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 08-Dec-2000
C;Accession: A39384
R;Bellefroid, E.J.; Poncelet, D.A.; Lecocq, P.J.; Revelant, O.; Martial, J.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 3608-3612, 1991
A;Title: The evolutionarily conserved Krueppel-associated box domain defines a subfamily A;Reference number: A39384; MUID:91219421; PMID:2023909
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;442-4445/Domain: transmembrane #status predicted <TMM>;4446-445/Domain: intracellular #status predicted <INT>
;1446-4545/Domain: intracellular #status predicted <INT>
;167,299/Modified site: erythno-beta-hydroxyasparatic acid (Asp) #status predicted ;2959/Modified site: erythno-beta-hydroxyaspartic acid (Asp) #status predicted ;4076,4126,4279/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 4545; 9e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29.5%; Score 47.5; D
25.0%; Pred. No. 94;
iive 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | : : | | : | | CKNGQSNCYQSNSAMHITDCRETGSSKYPNCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CRIXNOKCFQHLDDCCSRKC--NRFN-KC 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29.8%; Score 48; 44.8%; Pred. No. 9
EGF homology < LDL receptor Y LDL receptor Y
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Best Local Similarity 25.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 13; Conserv
                                                                                                                      ;3945-4545/Domain:
;3945-4421/Domain:
;3971-4013/Domain:
                                ;3829-3861/Domain:
;3869-3912/Domain:
;3913-3970/Domain:
                                                                                                                                                                                                                :4014-4057/Domain:
                                                                                                                                                                                                                                             :4058-4100/Domain:
                                                                                                                                                                                                                                                                             :4101-4143/Domain:
                                                                                                                                                                                                                                                                                                             4152-4183/Domain:
                                                                                                                                                                                                                                                                                                                                             ;4201-4232/Domain:
                                                                                                                                                                                                                                                                                                                                                                      4237-4268/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                   ;4273-4304/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                4309-4340/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :4378-4409/Domain:
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C;Accession: S49371
R;Stonnet, V.; Guesdon, J.L.
submitted to the EMBL Data Library, October 1994
A;Description: Nucleotide sequences and molecular organization of the two small cryptic I
A;Reference number: S49367
                                                                                                                                                                                                                                                                     A Status: preliminary
Modecule type: DNA
A;Residues: 1-253 <STO>
A;Cross-references: UNIPROT:Q46019; EMBL:X82079; NID:g557228; PIDN:CAA57593.1; PID:g5572
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A;Experimental source: clone F02D8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cross-references: UNIPROT: Q03923; EMBL: U35376; NID: g1017721; PIDN: AAA79179.1; PID: g101
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A;Map position: 19p12-19p12
C;Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transcription repressor zinc finger protein 85 - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C;Accession: G02075
R;Poncelet, D.A.
Submitted to the EMBL Data Library, September 1995
A;Reference number: G09169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ).Species: Caenorhabditis elegans
:)Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
:)Accession: T20506
                                  C;§pecies: Campylobacter coli
C;Date: 16-Feb-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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29.5%; Score 47.5; DB 2;
Best Local Similarity 34.6%; Pred. No. 1.5e+02;
Matches 9; Conservative 5; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
29.5%; Score 47.5; DB 2;
Best Local Similarity 34.4%; Pred. No. 2.7e+02;
Matches 11; Conservative 7; Mismatches 9;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 CRLNDSKMDYKEIFFAIDDCLKKLCN 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CRIXNOK-----CFQHLDDCCSRKCN 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: 5
A;Introns: 27/3; 57/3; 195/3; 235/3
         protein - Campylobacter coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lypothetical protein F02D8.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-595 < PON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-285 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: GDB: ZNF85
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C;Genetics:
A;Gene: Ac-IAP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          apoptosis inhibitor - Autographa californica nuclear polyhedrosis virus
C;Species: Autographa californica nuclear polyhedrosis virus
A;Note: abDNA virus
C;Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 09-Jul-2004
C;Accession: H72858
R;Ayres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D.
Virology 202, 586-605, 1994
A;Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus.
A;Reference number: A72850; MUD:94303173; PMID:8030224
A;Accession: H72858
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-249 <AYR>
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C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Datession: T41814
R;Gomi, S.; Majima, K.; Maeda, S.
J. Gen. Virol. 80, 1323-1337, 1999
A;Title: Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus.
A;Reference number: Z22020; MUID:99281911; PMID:10355780
                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                            A;Residues: 1-196 <BEL>
A;Cross-references: GB:M61866; NID:g454818; PIDN:AAA52689.1; PID:g184336
C;Keywords: DNA binding; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 29.5%; Score 47.5; DB 2; Length 249; Best Local Similarity 34.3%; Pred. No. 1.5e+02; Matches 12; Conservative 6; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 249;
                                                                                                                                                     Length 196
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A;Molecule type: DNA
A;Residues: 1-249 <KAMA>
A;Crose-references: UNIPROT:092435; EMBL:L33180; PIDN:AAC63743.1
A;Experimental source: isolate T3
C;Genetics:
A;Note: iap2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IAP2 orf71 - Bombyx mori nuclear polyhedrosis virus (isolate T3)
                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Species: Bombyx mori nuclear polyhedrosis virus, BmSNPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 29.5%; Score 47.5; DB 2;
Best Local Similarity 34.3%; Pred. No. 1.5e+02;
Matches 12; Conservative 6; Mismatches 8;
                                                                                                                                               Query Match

29.5%; Score 47.5; DB 2;
Best Local Similarity 34.4%; Pred. No. 1.3e+02;
Matches 11; Conservative 7; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            202 CKVCFDREKSVCFMPCRHLAVCTECSRRCKRCCVC 236
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                                                                                                                                                                                                                                                                                                           107 CRHENLPLRKGCESMDECKMHKGGCNGLNQCL 138
                                                                                                                                                                                                                                                                     1 CRIXN---QKCFQHLDDCCSRK--CNRFNKCV 27
A, Molecule type? DNA
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Query Match
Best Local Similarity 37.5'
Matches 9, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: PFB0855c
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                                                                                                                                                                                                                                                                                                                                          transcription regulator, AraC family agpT [imported] - Agrobacterium tumefaciens (strain C)Species: Agrobacterium tumefaciens
C)Species: Agrobacterium tumefaciens
C)Accession: AG3129
C;Accession: AG3129
C;A
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A,Residues: 1-295 «KUR»
A,Cross-references: UNIPROT:Q8U6Z7; GB:AE0)8689; PIDN:AAL45453.1; PID:g17743157; GSPDB:G
C,Genetics:
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B99158
agpt protein (AF215048) [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: B99158
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2321-2328, 2001
Science 294, 2321-2328, 2001
A;Fitle: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-295 <KUR>
A, Cross-references: UNIPROT: Q8U6Z7; GB: AE007870; PIDN: AAK88788. L; PID: G15158539; GSPDB: G
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B71604
rRNA methylase (SpoU family) (OO, TP) PFB0855c - malaria parasite (Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ster, E.W.
Affile: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AG3129
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Pred. No. 1.9e+02;
3; Mismatches 7; Indels
                                                   Indels
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       Pred. No. 1.9e+02;
5; Mismatches 6;
                                                                                                                                               3 IXNQKCFQHLD--DCCSRKCNRF 23
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132 LQQETVDHLAECCSRLVN 149
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132 LQQETVDHLAECCSRLVN 149
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A,Map position: linear chromosome
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A;Map position: linear chromosome
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Best Local Similarity
Matches 9; Conserv
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C;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #text_change 09-Jul-2004
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004
R;Garcher, M.J; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V., Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.; Science 282, 1126-1132, 1998
Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Teference number: A71600; MUID:99021743; PMID:9804551
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C;Genetics:
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26564
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted to the EMBL Data Library, September 1999 A;Reference number: 220234 A;Accession: T26564 A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33 CKIKNQSCF--INPCTHKNNDKRN 54
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Q9iat6 brachydanio Q91gmB oryza sativ P072G7 drosophila P05485 conus magus Q24822 entamoeba h	Q8mztl entamoeba h Q8mztz entamoeba h P32022 entamoeba h P60254 scorpio mau Q9psu2 xenopus lae	Q7xks9 oryza sativ P37137 xenopus lae Q63zr3 xenopus lae P29674 xenopus lae	P48742 homo saplen P53411 gallus gall P63008 mesocricetu	P63007 mas muscuru P63007 rattus norv Q26107 plasmodium	Q80w06 mus musculu Q80w06 mus sapien Q8nbs4 homo sapien O88671 rattus norv	088516 mus musculu Q9nyj7 homo sapien Q81286 plasmodium Q7rrt3 plasmodium	P05484 conus magus Q646v4 phytophthor Q646v5 phytophthor Q646w1 phytophthor	018052 caenorhabdi Q97g15 clostridium 018720 entamoeba d P58920 conus catus	Q80lt7 adoxophyes Q90476 brachydanio Q45117 chironomus	Q68kf8 xenopus lae P91526 caenorhabdi	Q9de37 brachydanio P83183 eledone cir O693n8 taxus x med	Q19345 caenorhabdi P59868 pandinus im	Q61z11 methanococc Q7xz30 griffithsia	Q86152 dictyostell O23297 arabidopsis	O44635 caenorhabdi O7qct2 anopheles g	016004 lytechinus P46531 homo sapien	Q8wnzu plecotus to Q646us phytophthor	Q646u/ pnycopninor Q6pyv0 schistosoma	P93773 pinus sylve Q6k5w7 oryza sativ	P23502 entamoeba h 09xv21 caenorhabdi	Q8msx5 drosophila P40589 drosophila	9ibg4 xenopus 1 96vi2 pneumocys	10040	
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5.1.6 Compugen Ltd.	Search time 117 Seconds (without alignments) 118.172 Million cell updates/sec			0.00				cted by chance to have a cof the result being printed score distribution.		Description	conus	conus	conus		281x03 plasmodium Q81x03 plasmodium Q8wny8 myotis daub	O to	Q9u4az plasmodium Q7pm27 anopheles	Q20204 caenorhabdı Q8kle3 mus musculu	Q6uy11 homo sapien P60252 opistophtha	P60253 opistop O7g0m5 anophel	042374 brachyd 080282 fugu ru		Q24821 entamoeba h Q8mu89 entamoeba h Q8mzt3 entamoeba h	Q24835 entamoeba h Q8i218 plasmodium
GenCore version (c) 1993 - 2005	using sw model	-10-627-685A-26 1 CRIXNQKCFQHLDDCCSRKCNRFNKCV .27	, Gapext 0.5	12079187		Match 0% Match 100% first 100 summaries	<pre>Prot_03:* uniprot sprot:* uniprot_trembl:*</pre>	results predi to the score of the total	SUMMARIES	DB ID	21	2 Q6XE2 2 Q71KT	CX011		2 Q8IK(1 HSP1	- 7	000			ч 2		1401	2 Q2482 2 Q8MU8 2 Q8MZT	
	searc 1 18,	US-10-627-685A-2 161 1 CRIXNQKCFQHLDD	BLOSUM62DX Gapop 10.0	1612378 segs, 5	th: 0 th: 2000	Minimum Ma Maximum Ma Listing fi	UniProt_03:* : uniprot_e : uniprot_t	No. is the number of greater than or equal derived by analysis		cy ch Length	i	.3 67	اطط	N m c	5 4 10	م م د	7 40 1	٥٥	04	4.4	4.4	4.4		ਜ਼ਜ਼
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strategy for rapid immobilization of prey by a fish-hunting marine
                                        05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Four-loop conotoxin preproprotein (Fragment).
Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Neogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
NCBI_TAXID=41690;
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28-FBE-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last amotation update)
Kappa-conotoxin PVIIA precursor (Fin-popping peptide).
Conus purpurascens (Purple cone)
Bukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Canogastropoda; Sorbecconcha; Hypsogastropoda;
Neogastropoda; Canoidea; Conidae; Conus.
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MEDLINE=98079023; PubMed=9417043; DOI=10.1074/jbc.273.1.33;
Shon K.-J., Stocker M., Terlau H., Stuchmer W., Jacobsen R.B.
Walker C.S., Grilley M.M., Watkins M., Hillyard D.R., Gray W.
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MEDLINE=22068471; PubMed=12074021; DOI=10.1038/381148a0;
Terlau H., Shon K.-J., Grilley M.M., Stocker M., Stuehmer W.,
                                                                                                                                                                                                                                                                                             ; Score 161; DB 2; Length 67;
Pred. No. 1.4e-12;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Kappa-conotoxin PVIIA is a peptide inhibiting the shaker K+
                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                      Duda T.F. Jr., Palumbi S.R.;
Submitted (FEB-2002) to the EMBL/GenEank/DDBJ databases.
EMBL, AF440312; AAQ05864.1; -.
HSSP; P56633; 1Av3.
                                                                                                                                                                                               GO, GO:0005576; C:extracellular; IEA.
GO; GO:0008200; F:ion channel inhibitor activity; IEA.
GO:0009405; P:pathogenesis; IEA.
InterPro; IPR004214; Conotoxin.
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67 AA; 7712 MW; E7E77CC61873E1DB CRC64;
                          67 AA.
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                                                                                                                                                                                                                                                                                             100.08;
                                                                                                                                                                                                                                     Pfam; PF02950; Conotoxin; 1.
                                                                                                                                                                                                                                                                                                       96.3%;
                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                               26; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=41690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRUCTURE BY NMR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Olivera B.M.
                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                           Query Match
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                     Q71KT2
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Q71KT2
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WUTGENESIS OF ARG-47; ILE-48; PRO-49; ASN-50; GLN-51; LVS-52; PHE-54; PHE-54; GLN-55; HIS-56; LEU-57; ASP-58; ASP-59; SER-62; ARG-63; LVS-64; ARG-67; PHE-68; ASN-69 NND LVS-70.

MEDLINE-20387356; PubMed-10818087; DOI=10.1074/jbc.C900990199; Jacobsen R.B., Koch B.D., Lange-Malecki B., Stocker M., Verhey J., Van Wagoner R.M., Vyazovkina A., Olivera B.M., Terlau H.; Single amino acid substitutions in kappa-conotoxin PVIIA disrupt interaction with the shaker K+ channel ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Molecular simulation of the interaction of kappa-conotoxin-PVIIA with the Shaker potassium channel pore.";
Eur. Biophys. J. 30:528-536(2001).
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-!- TISSUE SPECIFICITY: Expressed by the venom duct.
-!- MASS SPECTROMETRY: MW=3268.4; METHOD=FAB; RANGE=46-72; NOTE=Ref.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAUTION: Because analogs resulting of mutagenesis of Hyp-49, Asn-50, Leu-57 and Asp-59 gave very low yields upon folding, the results of mutagenesis on these residues should be interpreted
                                                                                                                                                                                                                                                   MEDLINE=98217295; PubMed=9548922; DOI=10.1021/bi9730341; Savarin P., Guenneugues M., Gilquin B., Lamthanh H., Gasparini S., Zinn-Justin S., Menez A.; "Three-dimensional structure of kappa-conotoxin PVIIA, a novel potassium channel-blocking toxin from cone snails."; Blochemistry 37:5407-5416(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Terlau H., Boccaccio A., Olivera B.M., Conti F., "The block of Shaker K+ channels by kappa-conotoxin PVIIA is state
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        causes the sudden tetanus of prey (STOP) syndrome, which is a single, lethal "fin-pop" in envenomated fish. In mice, induces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: Belongs to the conotoxin O-superfamily. Kappa-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      With caution...
With caution...
With caution...
With caution...
With caution...
With Assay 7.
We see 1.27.
We
"Solution structure and proposed binding mechanism of a novel potassium channel toxin kappa-conotoxin PVIIA.";
Structure 5:1585-1597(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Potential.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Biol. Chem. 275:24639-24644 (2000).
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MEDLINE=99329121; PubMed=10398696;
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MEDLINE=22017751; PubMed=12023223;
Naranjo D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gen. Physiol. 114:125-140(1999).
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STRUCTURE BY NMR
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SIGNAL
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Four-loop conotoxin preproprotein (Fragment).
Comus purpuraacens (Purple cone).
Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Canoidea; Conidae; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
50-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Four-loop conotoxin preproprotein (Fragment).
Conus purpurascens (Purple cone).
Eukaryota; Metazza, Mollusca; Gastropoda, Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidee; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 73; DB 2; Length 67;
Pred. No. 0.088;
3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44.1%; Score 71; DB 2; Length 67; 50.0%; Pred. No. 0.15; 7; Indels iive 3; Mismatches
                                                                                                                                                                                                                                                                                                        Duda T.F. Dr. Prop. 1. Palumbi S.R.; Submitted (PEB-2002) to the EMBL/GenBank/DDBJ databases. Submitted (PEB-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AF480313; AAQ05865.1; GO; GO:0008200; F: ion channel inhibitor activity; IEA. GO; GO:0008405; P: pathogenesis; IEA. InterPro; IPR004214; Conotoxin. Pfam; PF02950; Conotoxin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Duda T.F. Jr., Palumbi S.R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF480315; AA05867.1; -.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR004214; Conotoxin.
Pfam; PF02950; Conotoxin; 1.
NOW TER
41 67 four-loop conotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 41 67 four-loop conotoxin.
67 AA; 7358 MW; E311E06BB6AF702E CRC64;
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67 AA; 7488 MW; 1B483B1BB6AF7755 CRC64;
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                                                                                                                      67 AA.
                                              99
                                 1 CRIXNOKCFOHLDDCCSRKCNRFNKC
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Best Local Similarity 50.07
Best Local Similarity
Best Local Similarity
Best Local Similarity
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Best Local Similarity 50.0
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                       RESULT 4
Q71KT1
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                                                                                   I-AR: 3-fold decrease of toxicity.
N-A: 100% reduction of toxicity.
N-A: 100% reduction of toxicity.
Q-A: 13-fold decrease of toxicity.
K-A,R: 100% reduction of toxicity.
F-A,H: 100% reduction of toxicity.
F-A,H: 1-fold decrease of toxicity.
N-A: 3-fold decrease of toxicity.
H-A: 3-fold decrease of toxicity.
L-A: 100% reduction of toxicity.
L-A: 100% reduction of toxicity.
D-A: 1.5-fold decrease of toxicity.
                                                          4-hydroxyproline.
R->A,K,Q: 100% reduction of toxicity
                                                                                                                                                                                                                                                  D->A: 100% reduction of toxicity.
S->A: 1.5-fold decrease of toxicity.
R->A: 3.5-fold decrease of toxicity.
K->A: 1.2-fold decrease of toxicity.
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                                                                                                                                                                                                                                                                                                                5-fold decrease of toxicity.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Four-loop conotoxin (Fragment).
Conus ermineus (Atlantic fish-hunting cone).
Bukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Canoiqastropoda; Sorbeoconcha; Hypsogastropoda;
NCBI_TaxID=55423;
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Pred. No. 0.019;
6; Mismatches 7; Indels
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Duda T.F. Jr., Palumbi S.R.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AY236862; AAP75888.1; -. GO: 0005576; C:extracellular; IEA. GO: 0005200; F: on channel inhibitor activity; IEA GO: GO: 0009405; P: pathogeneais; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8317 MW; 53BFAF79EE751C16 CRC64;
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   Kappa-conotoxin PVIIA
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Matches 26; Conservative
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Best Local Similarity 46.2
Matches 12; Conservative
PEPTIDE
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Ramilo C., Zafaralla G.C., Nadasdi L., Hammerland L.G., Yoshikami D.,
Gray W.R., Kristipati R., Ramachandran J., Miljanich G., Olivera B.M.
Cruz L.J.;
                                                                                                                                                                                          05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Conus purpurascens (Purple cone)
Conus purpurascens (Purple cone)
Eukaryota; Metazoa, Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conidae; Conidae; Conus.
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Apogastropoda, Caenogastropoda, Sorbeoconcha, Hypsogastropoda,
Neogastropoda, Conoidea, Conidae, Conus.
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STRUCTURE BY NMR.
MEDLINE=97070382; PubMed=8913308; DOI=10.1006/jmbi.1996.0576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 71; DB 2; Length 67;
Pred. No. 0.15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

Duda T.F. Jr., Palumbi S.R.;

Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AF480141, AA005866.1;

GO; GO:0008200; F.ion channel inhibitor activity; IEA.

GO; GO:0004965; F.ion channel inhibitor activity; IEA.

InterPro; IPR004214; Conotoxin; IEA.

Pfam; PP02950; Conotoxin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       four-loop conotoxin.
33E83B1BB6AF7435 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CXOB CONST STANDARD; PRT; 12 AH. P288B1; Q9UB25; 10-DEC-1992 (Rel. 24, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 25-OCT-2004 (Rel. 45, Last annotation update) Omega-conotoxin SYIB precursor (SNX-183). Conus striatus (Striated cone).
                                                                                                                                                                  67 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
       20
                            1 CRIXNOKCFOHLDDCCSRKC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CKKSGRKCFPHQKDCCGRAC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 46-71, AND SYNTHESIS.
CRIXNOKCFOHLDDCCSRKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 67
67 AA; 7529 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44.1%;
50.0%;
                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 50.0
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Venom duct;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=41690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alpha and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=6493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Venom;
                                          42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TER
                                                                                                                                                      Q71KT0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONST
                                                                                                         RESULT 6
Q71KT0
                                                                                                                                                      8
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
MEDLINE=9524066; PubMed=7708756; Daquinag A.C., Nakamura S., Takao T., Shimonishi Y., Tsukamoto T.; Daquinag A.C., Nakamura S. Takao T., Shimonishi Y., Tsukamoto T.; Prinary structure of a potent endogenous dopa-containing inhibitor of phenol oxidase from Musca domestica."; Proc. Natl. Acad. Sci. U.S.A. 92:2964-2968(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa; Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Muscoidea,
Muscidae, Musca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cysteine amide (G-72 provides amide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inhibitor;
inhibitor; Neurotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-UL-2004 (Rel. 44, Last annotation update)
17rosinase inhibitor (Phenol oxidase inhibitor) (Phenoloxidase inhibitor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 6-9, CHARACTERIZATION, AND DEVELOPMENTAL STAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 71; DB 1; Length 72;
Pred. No. 0.16;
4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          group).
1F753546AAD39908 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Omega-conotoxin SVIB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE, CHARACTERIZATION, AND MASS SPECTROMETRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF02250; Conotoxin; 1.
3D-structure; Amidation; Calcium channel
Direct protein sequencing; Ionic channel
Presynaptic neurotoxin; Signal; Toxin.
SIGNAL Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46 CKLKGOSCRKTSYDCCSGSCGRSGKC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; C44379; C44379.
PDB; 1MVJ; NWR; @=46-72.
InterPro; 1PR004214; Conotoxin.
                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF146346; AAD31906.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7741 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Musca domestica (House fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22
45
71
61
65
71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Hemolymph;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rissum=Hemolymph;
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J. Biol. Chem. 275:3535-35344(2000).
-!- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind and block voltage-sensitive calcium channels (VSCC) (By similarity). This toxin blocks N-, P-, and Q-type calcium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097;
Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
Carlton J.W., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
Chan M.S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S.,
Pertea M., Allen J., Selengt J., Haft D., Mather M.W., Vaidya A.B.,
Martin D.M., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lewis R.J., Nielsen K.J., Craik D.J., Loughnan M.L., Adams D.A., Sharper.I.A., Luchian T., Adams D.J., Bond T., Thomas L., Jones A., Matheson J.-L., Drinkwater R., Andrews P.R., Alewood P.F.; Moyel omega-conotoxins from Conus catus discriminate among neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; NG84; 1DW4.
Amidation; Calcium channel inhibitor; Direct protein sequencing;
Ionic channel inhibitor; Neurotoxin; Presynaptic neurotoxin; Toxin.
DISULFID 1 16 By similarity.
DISULFID 8 20 By similarity.
ATTALL 15 26 By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the venom duct.
-!- SIMILARITY: Belongs to the conotoxin O-superfamily. Omega-type
                                                                                                                                                                                                                                                                   Conús catus (Cat cone).
Bukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoldea; Conidae; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Venom;
MEDLINE=20519630; PubMed=10938268; DOI=10.1074/jbc.M002252200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmodium falciparum (isolate 3D7).
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 66; DB 1; Length 26; Pred. No. 0.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cysteine amide.
56EFC382335C4A8B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Hypothetical protein.
                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41.0%; Scor.
38.5%; Pred. No. v...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 2050 AA
     688 CSMGTDNVIRYHDDCCSRKSQCGNFNGKC 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CKGKGOSCSKLMYDCCTGSCSRRGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2003 (TrEMBLrel. 23, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 20
15 26
26 26
26 AA; 2790 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             calcium channel subtypes."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 38.5
                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE, AND SYNTHESIS.
                                                                                                                                                                                                                                                 Omega-conotoxin CVIC.
                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=101291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORFNames=PF10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          channels.
                                                                                                                         CONCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
MOD RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QBIK03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q81K03
                                                                            RESULT 10
CXOC_CONCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QBIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7
                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                  SYNTHESIS, AND DISULFIDE BONDS.
MEDLINE=99152007; PubMed=10026302; DOI=10.1021/bi9819834;
Daquinag A.C., Sato T., Koda H., Takao T., Fukuda M., Shimonishi Y.,
                                                                                                                                                                                                                                                                                                                                                                                       -1- SUBUNIT: Monomer.
-1- SUBCELLULAR LOCATION: Secreted.
-1- DEVELOPMENTAL STAGE: POI activity increases throughout pupariation, and is highest in final instar pupae. No activity newly emerged adults.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- MASS SPECTROMETRY: MW-4213.1; MW_ERR=0.2; METHOD=Electrospray; RANGE=1-38; NOTE=Ref.1.
Direct protein sequencing; Hydroxylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dodson J.M., Clark C.G., Lockhart L.A., Leo B.M., Schroeder J.W.,
Mann B.J.;
                      Tsukamoto T., Ichimaru Y., Kanegae N., Watanabe K., Yamaura I., Katsura Y., Funatsu M.; "Identification and isolation of endogenous insect phenoloxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .,
Y
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32 32 3',4'-dihydroxyphenylalanine.
38 AA; 4204 MW; E597BE0BFF286792 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 68; DB 1; Length 38;
Pred. No. 0.22;
7; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1
1125 1125
1125 AA; 126050 MW; 8DA832DE48A717C4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03, Created)
04, Last sequence update)
26, Last annotation update)
                                                                                                                       Biochem. Biophys. Res. Commun. 184:86-92(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1125 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gal/GalNAc lectin heavy subunit (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CRIXNQKCFQHLDDCCSRK--CNRFN-KC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 CLANGSKCYSH-DVCCTKRCHNYAKKCV 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CRIXNQKCFQHLDDCCSRKCNRF-NKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, U85822; AAB50229.1; -.
HSSP; P60045; 1MF4.
GO; GO:0005529; F:sugar binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Entamoebidae; Entamoeba.
NCBI_TaxID=46681;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR006209; EGF_like.
PROSITE; PS00022; EGF_1; UNKNOWN_1.
MEDLINE=92231987; PubMed=1567460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1997 (TrEMBLrel. 01-JUL-1997 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUL-1997 (TrEMBLrel. 01-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR006209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=hgl2;
Entamoeba dispar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-SAW 760;
                                                                                                                                                                                                                                                   rsukamoto T.;
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P92135

RESULT 9 P92135

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Direct proposed propo

RAYRAR RAYRA RAYRAR RAYRAYRAR RAYRAR RAYRAYRAR RAYRAR RAYR

MOD RES SEQUENCE Query Match

Matches

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Gaps

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10; Indels

SEQUENCE Query Match

Matches

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McFadden G.I.,

us-10-627-685a-26.rup

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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mol. Phylogenet. Evol. 22:333-341(2002).
-!- FUNCTION: Protamines substitute for histones in the chromatin of sperm during the haploid phase of spermatogenesis. They compact sperm DNA into a highly condensed, stable and inactive complex (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21881971; PubMed=11884158; DOI=10.1006/mpev.2001.1051;
Van Den Bussche R.A., Hoofer S.R., Hansen E.W.;
"Characterization and phylogenetic utility of the mammalian protamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pram; PF00286; Protramine Pi; 1.
PROSITE; PS00048; PROTAMĪNE Pi; FALSE NEG.
Chromosomal protein; DNA condensation; DNA-binding; Nuclear protein; Nucleosome core; Spermatogenesis; Testis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Myotis daubentoni (Daubenton's bat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Chiroptera; Microchiroptera; Vespertilionidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
    Cummings L.M., Subramanian G.M., Mungall C., Tuucci D.J., Hoffman S.L., Newbold C., Davis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39.1%; Score 63; DB 2; Length 2050; 40.0%; Pred. No. 30;
                                                                                                                                "Genome sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                                    l protein.
2050 AA; 243182 MW; 0A0586A5B42A3B8C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 62; DB 1; Length 46; Pred. No. 1.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0 0 By similarity.
46 AA; 6397 MW; CDEDDD686E6A7BED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE SPECIFICITY: Testis. SIMILARITY: Belongs to the protamine P1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BIMILIARILY/.
SUBCELLULAR LOCATION: Nuclear (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-OCT-2004 (Rel. 45, Created)
25-OCT-2004 (Rel. 45, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            574 CNKLNEKCTQECNKLNEKCTQECNKLNEKC 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40.0%; Pred. No.
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                                                                                                                                                                                                              Nature 419:498-511(2002).
EMBL; AE014829; AAN35235.1; -.
HSSP; Q93IC2; 1MWX.
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                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 40.0%,
-hes 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                         Venter J.C., Carucci
Fraser C.M., Barrell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sperm protamine Pl.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=98922;
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                                                                                                                                                                                                                                                                                                                                          Hypothetical
SEQUENCE 20
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QBWNYB;
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HSP1 MYODA
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RAH KAH KAH KAH BER KA
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND SYNTHESIS.
MEDLINE=92337922; PubMed=1352986; DOI=10.1016/0896-6273(92)90221-X;
MEDLINE=92337922; PubMed=1352986; DOI=10.1016/0896-6273(92)90221-X;
Hillyard D.R., Monje V.D., Mintz I.M., Bean B.P., Nadasdi L.,
Ramachandran J., Miljanich G.P., Azimi-Zoonooz A., McIntosh J.M.,
Cruz L.J., Imperial J.S., Olivera B.M.;
"A new Conus peptide ligand for mammalian presynaptic Ca2+ channels.";
Neuron 9:69-77(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Structure-activity relationships of omega-conotoxins MVIIA, MVIIC and 14 loop splice hybrids at N and P/Q-type calcium channels."; J. Mol. Biol. 289:1405-1421(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nielsen K.J., Adams D., Thomas L., Bond T., Alewood P.F., Craik D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Solution structure of omega-conotoxin MVIIC, a high affinity ligand of P-type calcium channels, using 1H NMR spectroscopy and complete tralaxation matrix analysis.";
J. Mol. Biol. 248:106-124(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Tyri3 is essential for the binding of omega-conotoxin MVIIC to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and omega-conotoxin GVIA.
SUBCELLUIAR LOCATION: Secreted.
TISSUE SPECIFICITY: Expressed by the venom duct.
SIMILARITY: Belongs to the conotoxin O-superfamily. Omega-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, S40826; AAB22674.1; -.
PRI; JH0699; MRG 43-29.
PDB; ICNN; NMR; 63-3-29.
PDB; ICNN; NMR; 63-2-29.
PDB; ICNN; NMR; 63-2-29.
PDB; ICNN; NMR; 63-2-29.
PDB; ICNN; NMR; 60-3-29.
PDG; ICNN; NMR; 60-3-29.
PDG; ICNN; MATCOCON; IN; Presynaptic neurotoxin; Toxin.
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MUTAGENESIS OF TYR-15.
MEDLINE-95408251; PubMed=7677735;
Kim J.I., Takahashi M., Martin-Moutot N., Seagar M.J., Ohtake A.,
                                                                                                                       Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda; Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda; Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRUCTURE BY NMR.
MEDLINE=99303703; PubMed=10373375; DOI=10.1006/jmbi.1999.2817.
                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95248539; PubMed=7731037;
Farr-Jones S., Miljanich G.P., Nadasdi L., Ramachandran J.,
                                                  01-OCT-1994 (Rel. 30, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Omega-conotoxin MVIIc precursor (SNX-230) (Fragment).
      29 AA.
    PRT;
                                      (Rel. 30, Created)
  STANDARD;
                                                                                                            Conus magus (Magus cone)
                                                                                                                                                                                                                                                                                                                                                                               STRUCTURE BY NMR.
                                  01-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                       Basus V.J.;
CONMA
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Gaps

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Indels

1 CRIXNQKCFQHLDDCCSRK-----CNRFNKC 26

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MEDLINE=20144115; PubMed=10677532; DOI=10.1073/pnas.040545897; Smith J.D., Graig A.G., Kriek N., Hudson-Taylor D., Kyes S., Fagen T., Pinches R., Baruch D.I., Newbold C.I., Miller L.H.; "Identification of a Plasmodium falciparum intercellular adhesion molecule.1 binding domain: a parasite adhesion trait implicated in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
ENSANGPO00001402 (Fragment).
Name-ENSANGG0000011913;
Anopheles gambiae str. PEST.
Anopheles gambiae str. PEST.
Bukaryota; Metazoa; Atthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NGT_TAXID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anopheles Genome Sequencing Consortium;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37.3%; Score 60; DB 2; Length 1685; 33.3%; Pred. No. 60; tive 7; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 36.6%; Score 59; DB 2; Length 638; Local Similarity 36.0%; Pred. No. 34; onservative 5; Mismatches 11; Indels ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1685 AA; 193671 MW; DIFD42666B0551E CRC64;
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                                                                                                                                                                                                                                                     Cerebral malaria.";
Proc. Natl. Acad. Sci. U.S.A. 97:1766-1771(2000).
BMBL. AF193424; AAF18980.1;
GO, GO.0005539; F.GJYcosaminoglycan binding; IEA.
GO; GO:0009405; P:gJYcosaminoglycan binding; IEA.
R InterPro; IPR00454; Bub ATPase_Csub.
R InterPro; IPR004559; PFEMP.
R Pfam; PF03011; PFEMP; 1.
RP PROSITE; PS00605; ATPASE_C; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CRIXNQKCFQHLDDC--CSRKCNRFNK 25
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EMBL, AARBO1008980; EAA14483.2; -.
HSSP; P19438; IEXT.
InterPro; IPR0063341; DUF139.
InterPro; IPR006209; EGF like.
Pfam; PP02363; C tripleX; 15.
Pfam; PP00008; EGF; 11.
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Best Local Similarity 33.34
Best Local Similarity
Conservative
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                                                                                                           SEQUENCE FROM N.A.
                                                       NCBI_TaxID=5833;
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Anopheles.
     Omega-conotoxin MVIIc.
Essential for calcium channel binding
                                                                                                                                 Hydroxyproline (Probable).
Cysteine amide (G-29 provides amide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anopheles Genome Sequencing Consortium,
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                     group).
Y->A: High decrease in binding.
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                                                                                                                                                                                                                                                                                                                                                                                                                          Score 61; DB 1; Length 29;
Pred. No. 1.2;
4; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        207 AA; 22432 MW; 2F4552091F91FBE8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         preliminary data.

EMBL; AAAB01008897; EAA08999.2; -.
GO; GO:0005576; C:extraccllular; IEA.
GO; GO:0008200; F:ion channel inhibitor activity; IEA.
GO; GO:009405; P:pathogenesis; IEA.
InterPro; IPR004214; Conotoxin.
                                                                                                                                                                                                                                                                                                                                                                        AC7A68948474728A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O9U4A2;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Variant surface protein PfEMP1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        207 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1685 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CRIXNQKCFQHLDDCCSRKCNRFN-KCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28 CAKNNEYCLTH-RDCCSGSCLSFSYKCV 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 CKGKGAPCRKTMYDCCSGSCGRRGKC 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2004 (TrEMBLrel. 26, C
01-MAR-2004 (TrEMBLrel. 26, L
01-MAR-2004 (TrEMBLrel. 26, L
ENSANGP0000015215 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 38.5%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                           3071 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro, IPR004214; Conotox
Pfam; PF02950; Conotoxin; 2.
NON TER 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 46.4
nes 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=ENSANGG00000012726
     NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=PEST;
                                                 DISULFID
DISULFID
DISULFID
MOD_RES
MOD_RES
                                                                                                                                                                                                                                                                                                                                             STRAND
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                              MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14

O7PQD5
AC Q7PQD5;
DT 01-MAR.-;
DT
                              BINDING
                                                                                                                                                                                                                                          TURN
STRAND
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Q9U4A2
ID Q9U4A:
AC Q9U4A:
DT 01-MA:
DT 01-MA:
DE Varia:
                                                                                                                                                                                                                                                                                                                         TURN
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                                              01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 24, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein F40E10.4.
Name=alt-1; ORFNames=F40E10.4;
Caenorhabditis elegans.
Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                  "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                         Sayer.;
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; AL022270; CAB63434.2;
EMBL; Z69792; CAB63434.2;
EMBL; AL022270; CAS93668.3; JOINED.
EMBL; Z69792; CAA93668.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wormbebse, maceurouvous; sul-1.

Wormbebse, maceurouvous; sul-1.

GO; GO:0005509; F:calcium ion binding; IEA.

GO; GO:0005198; F:sarlcium ion binding; IEA.

GO; GO:0005155; F:sarlcium ion binding; IEA.

InterPro; IPR00152; Asx hydroxyl S.

InterPro; IPR0016015; Asx hydroxyl S.

InterPro; IPR0016017; EGF Ca.

R InterPro; IPR00189; EGF Li.

R InterPro; IPR00171; Laminin G.

R InterPro; IPR001611; LRR.

R InterPro; IPR001611; LRR.

R InterPro; IPR001613; IRR Crem.

R InterPro; IPR001729; TSP N.

R Pfam; PF0010129; TSP N.

R Pfam; PF0210; Laminin G 2; 1.
                                                                                                                                                                                                                                                                                                               Smye R.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases
                              PRT; 1410 AA
                                                                                                                                                                                            STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00010; ASX HYDROXYL; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Z69792; CAA93668.3; -. PIR; D89711; D89711. D89711. PR; T22025; T22025. HSSP; P00740; 1EDM. WormBase; WBGene00004854; elt-1.
                                                                                                                                                                                                                                                 investigating biology.";
Science 282:2012-2018(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO0010; EGFBLOOD.
SMART; SM00041; CT; 1.
SMART; SM00041; CT; 1.
SMART; SM00179; EGF C3; 3.
                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYP; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SM00082; LRRCT; 4.
SM00013; LRRNT; 4.
SM00369; LRR_TYP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF01463; LRRCT; I.Pfam; PF01462; LRRNT; 4.Pfam; PF00560; LRR 1; 17.
                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                     STRAIN=Bristol N2
                                                                                                                                                         NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PSO
PROSITE; PSO
PROSITE; PSO
                        Q20204
Q20204;
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SMART;
SMART;
RESULT 17
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REATENINFERON N.A. (ISOFORM 1).

REATENINFERON TISSUE=Salivary gland;

RATENINFERON TISSUE=Salivary gland;

RATENINFERON TISSUE=Salivary gland;

RATENINFERON TISSUE=Salivary gland;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Batchenco L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brachenco M., Soarsa M.B., Bonaldo M.E., Casavant T.L.; Scheetz T.E.,

RA Brownstein M.J., Ubdin T.B., Toohiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Ubdin T.B., Toohiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Nockernan K.J., Malek J.A., Gunaarane D.H.,

RA Norlay K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Hillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Hillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Hillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Haresley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Schnerch A., Schein J.E., Villalon D.E.,

RA Generation and initial analysis of more than 15,000 full-length human R. Proc. Natl. Acad. Sci. U.S.A., 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. The Buropean Bioinformatics Institute. The Buropean Bioinformatics of the Buropean Bioinformatics Institute. The Buropean Bioinformatics of Bioinformati
                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QBKIE3, QQQYP3, STANDARD, PKI; 382 AA. 25-007-2004 (Rel. 45, Leated) 25-007-2004 (Rel. 45, Last sequence update) 25-007-2004 (Rel. 45, Last annotation update) Multiple EGF-like-domain protein 9 precursor (Endothelial cell Name-Egfis).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fukudome K., Tsuneyoshi N., Kimoto M.;
"Endothelial cell specific protein S-1.";
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
-! SUBCELLUTAR LOCATION: Type I membrane protein (Potential).
                                                                                                                                                                                                                                 36.6%; Score 59; DB 2; Length 1410;
45.0%; Pred. No. 68;
1ive 4; Mismatches 7; Indels
PROSITE; PS50026; EGF_3; 7.
PROSITE; PS01187; EGF_CA; 2.
PROSITE; PS50025; LAM_G_DOMAIN; 1.
EGF-like domain; Hypothetical protein.
SEQUENCE 1410 AA; 158221 MW; D33716A9C98EBA9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Journal 10 Cold-OBKIES-2; Sequence=VSP 011768; Note=No experimental confirmation available; -!- SIMILARITY: Contains 6 EGF-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    382 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 259-382 FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=Q8K1E3-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  944 CEKNIDDCVNSKCENGGKCV 963
                                                                                                                                                                                                                                                                                                                                                                                8 CFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                    Local Similarity 45.0
les 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EFL9 MOUSE
                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EFL9 MOUSE
                                                                                                                                                                                                                                                                           Best Loc
Matches
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(Human)
                          NCBI_TaxID=9606;
   sapiens
                                                                                                                                                                                                                                                                                                                                                                                              Name=1
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 (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                          EGF-like 4.

EGF-like 4.

EGF-like 5, calcium-binding (Potential).

EGF-like 6, calcium-binding (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EEL9_HUMAN

BEL9_HUMAN

C GUVII; 098024 (Rel. 45, Created)

DT 25-OCT-2004 (Rel. 45, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annocation update)

DF Multiple EGF-like-domain protein 9 precursor (UNQ2903/PRO28633).

GN Name=EGFL9;
                                                                                                                  SMART; SM00179; EGF CA; 2.
PROSITE; PS0010; ASX HYDROXYL; 2.
PROSITE; PS00022; EGF 1; 6.
PROSITE; PS01186; EGF 2; 6.
PROSITE; PS01186; EGF 2; 5.
PROSITE; PS01187; EGF 7; 6.
Alternative splicing; Calcium; Calcium-binding; EGF-like domain;
                                                                                                                                                                                                                                                                                                                                                                                                                     N-linked (GlcNAc. .) (Potential).
Missing (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                   Potential.
Multiple EGF-like-domain protein
Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 58; DB 1; Length 382;
Pred. No. 28;
2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             F2C82AD649CA0B3C CRC64; .
                                                                                                                                                                                                                 Cytoplasmic (Potential)
                                                                                                                                                                                                                                                                           By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                             similarity
entities requires a license agreement (S. or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                      /FTIG=VSP
                                  BAA88686.1; ALT_INIT
                                                        InterPro; IPR000152; Aax hydroxyl_S.
InterPro; IPR000742; BGF_2.
InterPro; IPR001881; BGF_Ca.
InterPro; IPR001438; BGF_II.
InterPro; IPR006209; BGF_II.
Pf00008; EGF; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         209 CTINLDDCASRPCQRGARC 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 CFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                           Repeat; Signal; Transmembrane.
SIGNAL 1 26
                                                                                                                                                                                                                                                                                                                                                                                                                                              382 AA; 40404 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               36.0%;
52.6%;
                         EMBL; BC019431; AAH19431.1;
EMBL; AB011019; BAA88686.1;
                                                                                                          EGFBLOOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 52.6'
Matches 10; Conservative
                                      HSSP, P00750; ITPG.
MGD; MGI:2146838; Egfl9.
                                                                                                                                                                                                                                                                            PRINTS; PRODO10;
                                                                                                                                                                                                            TRANSMEM
DOMAIN
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DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                   DISULFID
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De Enkaryote, Mescasa (hordata, Cranithi, Werebrata, Buteleoscomi, Namanilia, Butheria primates, Carathini, Hominidae, Homo.

MEDINEZ-287796, PubMed-1975.09, DOI-10.1010/Gr.133001.

R. Gilly, R. Courney, L. Abaya E. Baker K., Baldwin D. Brunh J., R. Chen J., Chon J., Chon J. C., Currelly E., Currelly C., Currelly E., Currelly E., Charley C., Currelly E., Charley C., Carathini, Hominia S., Lee J., R. Andrews E., M. C., Mana P. E., Haldens S., R. Haray A., Kim H., S., Kilmons E., Sanchez C., Schemfield J., R. Manay A., Kim K., Konn J., S., Kilmons E., Sanchez C., Schemfield J., Sanchez C., Sanchez
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                FASEB J. 17:1765-1767(2003).
-1- FUNCTION: Potently and reversibly modifies channel gating behavior of the type 1 ryanodine receptor (RyR1) by inducing prominent subconductance behavior. Binds a different site as ryanodine (By
                                                                                                                                                                                                                                                                                                                         similarity).
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the venom gland.
-!- SIMILARITY: Belongs to the scorpion calcine family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 CFQHL-----DDCCSRKCNR 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36 CLPHLKRCKENNDCCSKKCKR 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 47.6
nes 10; Conservative
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Matches
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                                                                                                                                                                                                                                                                                                                                                                 EGF-like 2.
EGF-like 3.
EGF-like 4.
EGF-like 5.
EGF-like 5. calcium-binding (Potential).
By Similarity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCXI OPICA STANDARD; PRT; 66 AA.
B60252;
29-MAR-2004 (Rel. 43, Created)
29-MAR-2004 (Rel. 45, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Opicalcine I precursor.
Opistophthalmus carinatus (African yellow leg scorpion).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones; Iurida; Scorpionoidea; Scorpionidae; Scorpionidae; Opistophthalmus.
InterPro; IPR006210; IEGF.
InterPro; IPR001841; Znf_ring.
Pfam; PP000018; EGF; 5.
PRINTS; PR00010; EGFELCOD.
SMART; SM00119; EGF CA; 4.
PROSITE; PS00012; EGF CA; 4.
PROSITE; PS00012; EGF CA; 4.
PROSITE; PS00118; EGF CA; 5.
PROSITE; PS01186; EGF C; 6.
PROSITE; PS01187; EGF CA; 6.
PROSITE; PS01187; EGF CA; 7.
PROSITE; PS01187; EGF CA; 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                           Multiple EGF-like-domain protein Extracellular (Potential).
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TISSUB-Venom gland;
MEDLINE=22838230; PubMed=12958203; DOI=10.1096/fj.02-1044fje;
Zhu S.-Y., Darbon H., Dyason K., Verdonck F., Tytgat J.;
"Evolutionary origin of inhibitor cystine knot peptides.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     701AC6B043863EA7 CRC64;
                                                                                                                                                                                                                                                                                                                                 Cytoplasmic (Potential)
EGF-like 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 58; DB
Pred. No. 28;
2; Mismatches
                                                                                                                                                                                                                                                                                                                     Potential [ ]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 CFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                       Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     383 AA; 40547 MW;
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les 10, Conservative
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46
57
71
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88
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                                                                                                                                                                                                                                     Repeat; Signal;
SIGNAL
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TRANSMEM
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Gaps

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2; Mismatches

8

Score 57; Pred. No

DB 1; Length 66; 3; Indels

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TISSUBE-Venom gland;
TISSUBE-Venom gland;
MEDLINE=22838230; PubMed=12958203; DOI=10.1096/fj.02-1044fje;
Zhu S.-Y., Darbon H., Dyason K., Verdonck F., Tytgat J.;
Zhu S.-Y., Darbon H., Dyason K., Verdonck F., Tytgat J.;
"EVOLUTIONARY Origin of inhibitor cystine knot peptides.";
"RASEB J. 17:155-1767(2003).
-!- FUNCTION: Potently and reversibly modifies channel gating behavior of the type 1 ryanodine receptor (RyR1) by inducing prominent subconductance behavior. Binds a different site as ryanodine (By
                                                                                                                                                                                                                                                                                                      Opistophthalmus carinatus (African yellow leg scorpion).
Bukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Iurida; Scorpionoidea; Scorpionidae; Scorpioninae; Opistophthalmus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity).
--- SUBCELLUIAR LOCATION: Secreted.
--- TISSUE SPECIFFICITY: Expressed by the venom gland.
--- SIMILARITY: Belongs to the scorpion calcine family.
Calcium channel inhibitor; Cleavage on pair of basic residues;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 By similarity.
6DC7632E9F205F5D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ionic channel inhibitor; Neurotoxin; Signal; Toxin.
22 GGAAL
PROPEP 23 33 By similarity.
CHAIN 34 66 Opicalcine 2.
DISULFID 36 50 By similarity.
DISULEID 43 54 By similarity.
SEQUENCE 66 AA; 7644 MW; 6DC7632E9F205F5D CRC64
| SCYZ OPICA | STANDARD; | PRT; | 66 AA. | |
| AC | SCYZ OPICA | STANDARD; | PRT; | 66 AA. |
| AC | SCYZ OPICA | STANDARD; | PRT; | 66 AA. |
| DT | 29-MAR-2004 (Rel. 43, Last sequence update) |
| DT | 25-OCT-2004 (Rel. 45, Last annotation update) |
| DE | Opicalcine 2 precursor. | |
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                         SEQUENCE FROM N.A.
Westin J., Lardelli M.;
Whree novel Notch genes in zebrafish: implications for vertebrate
Notch gene evolution and function.";
Dev. Genes Evol. 207:51-63(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Takifugu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 35.4%; Score 57; DB 2; Length 752; Best Local Similarity 37.5%; Pred. No. 68; Matches 9; Conservative 2; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cobbe N.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ54332; CAD58847.2; -.
HSSP; Q9XOR4; 1E69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fugu rubripes (Japanese pufferfish) (Takifugu rubripes)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82103 MW; 30939E16E0327F8A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q80252;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                         ZENI; ZDB-CRNE-000329-4; notch2.
GO; GO:0016020; C:membrane; IEA.
GO; GO:000509; F:calcium ion binding; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0030154; F:receptor activity; IEA.
INCEPPO: IPR000152; Apx hydroxyl_S.
INCEPPO: IPR0001438; EGF_CA.
INCEPPO: IPR0001438; EGF_CA.
INCEPPO: IPR000800; NOCGI.
INCEPPO: IPR000800; NOCGI.
INCEPPO: IPR000800; NOCGI.
FFam; PF00006; EGF_LA, I.
Pfam; PF00006; NOCGI, 2.
PRINTS; PR00010; EGFELOD.
PRINTS; PR00010; EGFELOD.
PRINTS; RN000179; EGF CA, I.
SWART; SN000179; EGF CA, I.
       Brachydanio rerio (Zebrafish) (Danio rerio)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 XNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00010; ASX HYDROXYL; 9. PROSITE; PS00022; EGF 1; 17. PROSITE; PS01106; EGF 3; 15. PROSITE; PS50026; EGF 3; 17. PROSITE; PS01107; EGF CA; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0016020; C:membrane; IEA. GO; GO:0005634; C:nucleus; IEA.
                                                                                                                                                                                            EMBL; Y10354; CAA71380.1; -. HSSP; P00740; 1EDM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGF-like domain; Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         752 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=smclb;
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NON TER
SEQUENCE
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Q802S2
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                                       Gaps
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Ouery Match " 35.4%; Score 57; DB 1; Length 66; Best Local Similarity 47.6%; Pred. No: 8; Matches 10; Conservative 2; Mismatches 3; Indels
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                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05, Last sequence update)
26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0016020; C:membrane; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0007509; F:calcium ion binding; IEA.
GO; GO:0007150; F:calcium ion binding; IEA.
InterPro; IPR001774; DSL.
InterPro; IPR001774; DSL.
InterPro; IPR001431; EGF_Ca.
InterPro; IPR001438; EGF_II.
InterPro; IPR001438; EGF_II.
FIGHT, PF01414; DSL; 1.
PEGM; PF010008; EGF; 7.
                                                                                                                                                                                                                                                                                                  Name=ebiG2886; ORFNames=ENSANGG0000002379;
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01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preliminary data.
EMBL; AAABO1008980; EAA14361.1; -.
HSSP; P00740; 1EDM.
                                                                                            36 CLPHLKRCKENNDCCSKKCKR 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS00010; ASX HYDROXYL; 3. PS00022; EGF_1; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Notch receptor protein (Fragment). Name=notch2; Synonyms=Notch6;
                                                                        8 CFQHL-----DDCCSRKCNR 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; PS01186; EGF_1; 9.
; PS01186; EGF_2; 9.
; PS01026; EGF_3; 7.
; PS01187; EGF_CA; 2.
                                                                                                                                                                                                                           01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF07645; EGF CA; 1.
PRINTS; PR00010; EGFBLOOD.
PROSITE; PS00010; ASX HYDF
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                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       650
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                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EGF-like domain
                                                                                                                                                                                                             Q7Q0M5;
01-MAR-2004 (
01-MAR-2004 (
                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=PEST
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                                                                                                                                                                                            Q7Q0M5
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042374
                                                                                                                                                             RESULT 22
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Gaps

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calcium-binding (Potential).
                                                                                                                                                                                                                                                                                  gnaling pathway; Repeat; Signal; Transmembrane
                                                                                                                                                                                                                                                                                                           Neurogenic locus notch protein homolog.
Extracellular (Potential).
DR Pfam; PF00008; EGF; 36.

Pfam; PF00006; NoD2; 1.

Pfam; PF00066; NoD2; 1.

Pam; PF00026; Notch; 3.

PRINTS; PR01415; ANKTRIN.

DR PRINTS; PR01415; ANKTRIN.

DR SMART; SM0010; EGFELOOD.

DR SMART; SM00179; EGF CA; 24.

DR SMART; SM00179; EGF CA; 24.

DR PROSITE; PS50089; ANK REPEAT; 4.

DR PROSITE; PS00102; EGF 1; 34.

DR PROSITE; PS01186; EGF 2; 29.

DR PROSITE; PS01186; EGF 2; 29.

DR PROSITE; PS01187; EGF CA; 21.

TRANK repeat; Differentiation; EGF-like domain; Glycoprotein;

W Neurogenesis; Notch signaling pathway; Repeat; Signal: Transmenters.
                                                                                                                                                                                                                                                                                                                                                                              EGF-like 2.
EGF-like 3.
EGF-like 3.
EGF-like 4.
EGF-like 5.
EGF-like 6.
EGF-like 6.
EGF-like 6.
EGF-like 9.
EGF-like 9.
EGF-like 10.
EGF-like 11.
EGF-like 11.
EGF-like 12.
EGF-like 12.
EGF-like 12.
EGF-like 13.
EGF-like 14.
EGF-like 14.
EGF-like 14.
EGF-like 15.
EGF-like 14.
EGF-like 16.
EGF-like 17.
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calcium-binding
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EGF-like 1.
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EGF-like 30, C
EGF-like 31, C
EGF-like 33, C
EGF-like 33.
EGF-like 35.
EGF-like 35.
EGF-like 36.
Lin/Notch 1.
Lin/Notch 2.
Lin/Notch 2.
Lin/Notch 3.
ANK 2.
ANK 3.
ANK 4.
ANK 6.
ANK 6.
By similarity.
By similarity.
By similarity.
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EGF-like 19,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kinther C.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
SUBMITTED LOCATION: Type I membrane protein.
DEVELOPMENTAL STAGE: Expressed almost uniformly in early embryos.
SIMILARITY: Belongs to the NOTCH family.
SIMILARITY: Contains 6 ANK repeate.
SIMILARITY: Contains 3 Lin/Notch repeats.
      R GO; GO:0005524; F:ATP binding; IEA.

R GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. ..;
GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. ..;
R GO; GO:0006810; P:transport; IEA.

R InterPro; IPR003439; ABC_transporter.

R InterPro; IPR003405; SMC_C.

R InterPro; IPR003405; SMC_C.

R InterPro; IPR003495; SMC_N.

R Pfam; PF06443; SMC_N.

R Pfam; PF06470; SMC_hinge; 1.

R Pfam; PF06470; SMC_hinge; 1.

R Pfam; PF06463; SMC_N; 1.
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                 01-MXY-1991 (Rel. 18, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Newrogenic locus notch protein homolog precursor (XOTCH protein)
Name=XOTCH;
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                                                                                                                                                                                               35.4%; Score 57; DB 2; Length 1245; 42.9%; Pred. No. 1.1e+02; 1ve 4; Mismatches 8; Indels
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MEDLINE=90385285; PubMed=2402639;
Coffman C., Harris W., Kintner C.;
"Xocch, the Xenopus homolog of Drosophila notch.";
Science 249:1438-1441(1990).
                                                                                                                                                                                                                                                                                                                                                             PRT; 2524 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopus laevis (African clawed frog).
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1056 RKCSQEFEQVKFQRCQRFNKC 1076
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InterPro; IPR0001215; Ask hydroxyl_S.
InterPro; IPR000142; BGF_2.
InterPro; IPR001481; BGF_Ca.
InterPro; IPR001488; BGF_II.
InterPro; IPR001481; IRR01488; IRR0161060; IRR0161060; IRR0161060; IRR
                                                                                                                                                                                                                                                       6 OKCFOHLDDCCSRKCNRFNKC 26
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                                                                                                                                                                                          Query Match
Best Local Similarity 42.99
Matches 9, Conservative
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Pfam; PF00023; Ank; 6.
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NOTC_XENLA
ID NOTC_XENLA
AC P21783;
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Proc. Natl. Acad. Sci. U.S.A. 100:1316-1321(2003).
EMBL; AE015944; AA036841.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=Magsachusetts / E88;
STRAIN=Magsachusetts / E88;
MEDLINE=22457253; PubMed=12552129; DOI=10.1073/pnas.0335853100;
Brueggemann H., Baeumer S., Fricke W.F., Wiezer A., Liesegang H.,
Decker I., Herzberg C., Martinez-Arias R., Merkl R., Henne A.,
Gottschalk G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clostridium tetani.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
NCBI_TaxID=1513;
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STRAIN=HM1:IMSS;
STRAIN=HM1:IMSS;
STRAIN=HM1:IMSS;
Samakirishnan G., Ragland B.D., Purdy J.E., Mann B.J.;
Submitted (AuG-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U33443; AAA75551.1; -.
EMBL; U33443; AAA75551.1; -.
GO; GO:0005259; F:sugar binding; IEA.
InterPro; IPR006209; EGF_like.
PROSITE; PS00022; EGF_L', UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  153 AA; 17382 MW; 6334C88F39A8E189 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-UNN-2003 (TrEMBLrel. 24, Created)
01-UNN-2003 (TrEMBLrel. 24, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Membrane-associated protein.
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Last annotation update)
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Pred. No. 2e+02
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequ
01-MAR-2004 (TrEMBLrel. 26, Last sequ
01-MAR-2004 (TrEMBLrel. 26, Last anno
GalNAc lectin heavy subunit (Fragment
Name=hgl4;
Entamoeba histolytica.
Eukaryota; Entamoebidae; Entamoeba.
NCBI_TaxID=5759;
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OrderedLocusNames=CTC02367;
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les 9; Conservative
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DB 2; Length 372;

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372 AA; 41994 MW; 3812E4DC7B310B13 CRC64;
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35.1%; Score 56.5; D
Local Similarity 43.3%; Pred. No. 42;
18s 13; Conservative 3; Mismatches
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MEDLINE=22314996; PubMed=12427470; DOI=10.1016/S0014-4894(02)00113-3;
Beck D.L., Tanyuksel M., Mackey A.J., Haque R., Trapaidze N.,
Pearson W.R., Loftus B., Petri W.A. Jr.;
                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                           3;
                                                                                                                                    Query Match
35.1%; Score 56.5; DB 2; Length 194;
Best Local Similarity 43.3%; Pred. No. 24;
Matches 13; Conservative 3; Mismatches 11; Indels
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                                                     194 194
194 AA, 21501 MW; BD0C3HD9406AA858 CRC64;
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372 AA; 41984 MW; 5BE2A013D596D124 CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Gal/GalNAc lectin heavy subunit region D (Fragment)
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Exp. Parasitol. 101:157-163(2002).
EMBL; AF533541; AAM97358.1; -.
GO; GO:0005529; F:sugar binding; IEA.
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NCBI_TaxID=5759;
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Entamoeba histolytica.
Eukaryota; Entamoebidae; Entamoeba.
NCBI_TaxID=5759;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 43.3
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Entamoeba histolytica
Lectin.
NON TER
NON TER
SEQUENCE
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=hgl;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               08MU89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lectin.
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                                                                                                                                                                                                                                                                                                                                                                                          RESULT 28
Q8MU89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 29
108M2T3
10 08M2T4
AC Q8M2T4
DT 01-OC
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Mann B.J., Torian B.E., Vedvick T.S., Petri W.A.Jr. ;
"Sequence of a cysteine-rich galactose-specific lectin of Entamoeba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-HM-1:IMSS;
MEDLINE=94158976; PubMed=8114826; DOI=10.1016/0166-6851(93)90177-Y;
Purdy J.E., Mann BJ., Shugart B.C., Petri W.A.;
"Analysis of the gene family encoding the Entamoeba histolytica galactose-specific adhesin 170-kDa subunit.";
Mol. Blochem. Parasitol. 62:53-59(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 Potential.
145176 MW; E3123F4C7B6FDB98 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=HM-1:IMSS;
Purdy J.E., Mann B.J., Petri W.A.Jr.;
Submitted (OCT-1993) to the EMBL/GenBank/DDBJ databases.
EMBL; L14815; AAA18828.1; -.
                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Galactose-specific adhesin 170kD subunit precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Erythrocyte membrane protein 1 (PfEMP1).
Name=VAR; Synonyms=PPD0020c;
                                                                                                                                                                                                                                                                                                                                                                            histolytica.";
Proc. Natl. Acad. Sci. U.S.A. 88:3248-3252(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 35.1%; Score 56.5; DB 2; Similarity 43.3%; Pred. No. 1.3e+02; 13; Conservative 3; Mismatches 11;
  PRT; 1292 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 3467 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CRIXNOKCFQHLDDCCSRK--CNRFN-KCV 27
                                                                                                                                                   Entamoeba histolytica.
Bukaryota, Entamoebidae, Entamoeba.
NCBI_TaxID=5759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR006209; EGF like.
PROSITE; PS00022; EGF_1; UNKNOWN_1.
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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PIR; T09229; T09229.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 1292 AA;
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Q81218
ID Q8121
AC Q8121
AC Q8121
DT 01-MA
DT 01-MA
DE Eryth
GN Name=
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InterPro; IPR001841; Znf_ring
    Pfam; PF01414; DSL; 1.
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Q9LGM8
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                                               MEDLINE-22255708; PubMed=12368867; DOI=10.1038/nature01095;
MEDLINE-22255708; PubMed=12368867; DOI=10.1038/nature01095;
MIDIAL N., Berriam M., Churcher C., Harris B., Haarris D., Mungall K., Bowman S., Akkin K., Baker S., Barron A., Brooks K., Buckee C.O., Burrows C., Cherevach I., Chillingworth C., Corton C., Croin A., Davies R., Davis P., Dearden F., Coston C., Reltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z., Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P., Hamper D., Kerhornou A., Mights A., Konfortov B., Kyes S., Larke N., Lawson D., Lemard N., Line A., Maddison M., Mclean J., Mooney P., Moule S., Murphy L., Oliver K., Ormond D., Price C., Quail M.A., Rabbinowitsch E., Asandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M., Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K., Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J., Stevens K., Sulston J.E., Craig A., Newbold C., Barrell B.G;
Mature 499:527-531(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20054100; PubMed=10585570; DOI=10.1016/S0925-4773(99)00231-2; Smithers L.E., Haddon C., Jiang Y.-J., Lewis J.; "Sequence and embryonic expression of deltaC in the zebrafish."; Mech. Dev. 90:119-123(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Сарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brachydanio rezio (Zebrafish) (Danio rerio).

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               21;
                                                                                                                                                                                                                                                                                                                                                                                                                                    35.1%; Score 56.5; DB 2; Length 3467; 31.9%; Pred. No. 3e+02; ive 3; Mismatches 8; Indels 21;
Plasmodium,falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   318 CRIRNHKLRKIKDACRNDKERLYCSONGYDCTKRIEKGSSCSRENKC 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CRIXNOK-----KCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01011; PFEMP; 2.
PROSITE; PS0190; CYTOCHROME C; UNKNOWN 1.
SEQUENCE 3467 AA; 398216 WW; E8FCBA37025989D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                            EMBL; AL034557; CAD49096.1; -.
GO; GO:0005539; F:glycosaminoglycan binding; IEA.
GO; GO:0009405; P:pathcognesis; IEA.
InterPro; IPR00345; CytC, heme_BS.
InterPro; IPR004258; PFEMP.
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EMBL; AF146429; AAF27299.1; -.
HSSP; P00740; 1EDM.
ZFIN; ZDB-GENE-C000125-4; dlc.
GO; GO:0016020; C:membrane; IEA,
GO; GO:0005509;-F:calcium ion binding; IEA,
GO; GO:00071254; P:cell communication; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000152; Asx hydroxyl_S. InterPro; IPR001774; DSL. InterPro; IPR000742; EGF 2. InterPro; IPR001881; EGF Ca. InterPro; IPR001881; EGF II. InterPro; IPR0016209; EGF II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 31.9
Matches 15, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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Q91AT6
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Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y., M. Sasaki T., Matsumoto T., Yamamoto K., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H., Hobokwa X., Maukwa M., Arikawa K., Chiden Y., Hayashi M., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H., Hijshita S., Mando T., Aoki H., Arita K., Hamada M., Harada C., M. Hijshita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M., Ikoh S., Itoh T., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K., Karasawa W., Kategiri S., Kikuta A., Kobayashi T., Mukai Y., Machita K., Machara T., Mizunayashi T., Mukai Y., Nakamura M., Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M., A., Shomura A., Song J., Takazaki Y., Tarasawa K., Tauji K., Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K., Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y., Yano M., Jiang J., Golobori T., Ito H., Hahn J.H., Kim H.I., Eun M.Y., The genome sequence and structure of rice chromosome I.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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GO: O0:00005634; C:nucleus; IEA.

GO: O0:0000151; C:ubiquitin ligase complex; IEA.

GO: C0:0000150; F:transcription factor activity; IEA.

GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.

GO: GO:0006875; F:zinc ion binding; IEA.

GO: GO:000655; P:regulation of transcription, DNA-dependent; IEA.

GO: CO:000658; ZFe2S fd_BS.

InterPro: IPR000967; Znf_PHD.

InterPro: IPR001965; Znf_PHD.
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01-0TN-2001 (TrEMBLrel. 17, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to Arabidopsis thaliana chromosome V P1 MJJ3 (Similar to Arabidopsis thaliana chromosome V P1 MJJ3.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                                            34.8%; Score 56; DB 2; Length 664; 34.5%; Pred. No. 81;
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Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; APO02521; BAA86756.2; --.
EMBL; APO02533; BAB08195.2; --.
                                                                                                                                                                                                                                                                                                                  664 AA; 72547 MW; 0AD6C34C8579116B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 708 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CR--IXNOKCFQHLDDCCSRKCNRFNKCV 27
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Pubmed=12447438; DOI=10.1038/nature01184;
                                                                                                            α.
                             SWART; SM00051; DSL; 1.

SMART; SM00179; EGF CA; 4.

PROSITE; PS00010; ASX HYDROXYI

PROSITE; PS00186; EGF 1; 8.

PROSITE; PS01186; EGF 2; 8.

PROSITE; PS01187; EGF CA; 2.

EGF-11ke domain.

SEQUENCE 664 AA; 72547 MW;
PRINTS; PRO0010; EGFBLOOD
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                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 34.5
Les 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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MEDLINE=87064624; PubMed=3097517;
Kidd S., Kelley M.R., Young M.W.;
"Sequence of the notch locus of Drosophila melanogaster: relationship of the encoded protein to mammalian clotting and growth factors.";
Mol. Cell. Biol. 6:3094-3108(1986).
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STRAIN-OFFGON-R; TISSUB-Embryo;
STRAIN-OFFGON-R; TISSUB-Embryo;
MEDLINE-86679539; DubMed=3935325; DOI=10.1016/0092-8674(85)90229-6;
Wharton K.A., Johansen K.M., Xu T., Arravanis-Tsakonas S.;
"Nucleotide sequence from the neurogenic locus notch implies a gene product that shares homology with proteins containing EGF-like
                                                                                                                                                                                                                                                                                                                                                                                                                9
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P07207, 097458; P04154; Q9W4T8;
P07207, 097458; P04154; Q9W4T8;
O1-NOV-1986 (Rel. 03, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Neurogenic locus Notch protein precursor.
Name-N; ORFNames-GC3396;
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Haxapoda; Insecta; Pterygota;
Eukaryota; Badopterygota; Diptera; Brachycera; Muscomorpha;
Ephdycidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                      34.8%; Score 56; DB 2; Length 708; 40.0%; Pred. No. 86;
                                                                                                                                                                                                                                                                                                                                                                                                           10; Indels
Pfam; PF01422; zf-NF-X1; 5.
SWART; SW00438; ZnF NFX; 7.
PROSITE; PS00197; ZFE2S FERREDOXIN; UNKNOWN_1.
PROSITE; PS01359; ZF_PHD 1; UNKNOWN_1.
PROSITE; PS50089; ZF_RING 2; 1.
SEQUENCE 708 AA; 77563 MW; C886D4.2B927FC928 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          395 CRCGGLKKEVPCYQEL--TCERKCQRLRNC 422
                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CRIXNOK----CFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                             Pred.
                                                                                                                                                                                                                                                                                                                                                    Local Similarity 40.0
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Cell 43:567-581(1985).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                              Query Match
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NOTC DROME
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Matches
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Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mourt S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Relson D.R., Pacleb J.M.,
Relson D.R., Pacleb J.M.,
Relson M., Stupski M.P., Santh T.,
Spier B., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spier B., Stradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas K. Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Williams S.M., Woodage T., Weinstock G.W. D., Yang S., Yao Q.A.,
A. J. Yeh R.-F., Zaveri J.S., Zhan M., Zhou K., Zhu S., Zhu X., Smith H.O.,
A. Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
R. The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22426669; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.B.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.B., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stappeton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Gregon-R;
MEDLINB=20166011; PubMed=10731137; DOI=10.1126/science.287.5461.2220;
Benos P.V. Gatt M.K., Ashburner M., Murphy L., Harris D.,
Barrell B.G., Ferraz C., Vidal S., Brun C. Demailles J., Cadieu E.,
Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Borkova D.,
Minnan B., Raffatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,
Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablos B.,
Modolell J., Peter A., Schoettler P., Werner M., Mourkioti F.,
Beinert N., Dowe G., Schaefer U., Jaeckle H., Bucheton A.,
Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S.,
Glover D.M.; Salles C., Tait E.A., Valenti P., Saunders R.D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NECURINE-85099329; PubMed=2981631; DOI=10.1016/0092-8674(85)90308-3; Wharton K.A., Yedvobnick B., Finnerty V.G., Artavanis-Tsakonas S.; "Opa: a novel family of transcribed repeats shared by the Notch locus and other developmentally regulated loci in D. melanogaster.";
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MEDLINE-87257846; PubMed=3037327;
Kelley M.R., Kidd S., Berg R.L., Young M.W.;
"Restriction of P-element insertions at the Notch locus of Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=55401878; PubMed=7671825;
Matsuno K., Diederich R.J., Go M.J., Blaumueller C.M.,
Artavanis-Tsakonas S.;
"Deltex acts as a positive regulator of Notch signaling through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Diederich R.J., Matsuno K., Hing H., Artavanis-Tsakonas S.; "Cytosolic interaction between deltex and Notch ankyrin repeats implicates deltex in the Notch signaling pathway."; Development 120:473-481(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "From sequence to chromosome: the tip of the X chromosome of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          systematic review.";
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERACTION WITH DX, AND MUTANT SU42C.
MEDLINE=942I5489; PubMed=8162848;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mol. Cell. Biol. 7:1545-1548(1987).
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Gaps

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-I- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind and block voltage-sensitive calcium channels (VSCC).
-I- SUBCELLULAR LOCATION: Secreted.
-I- TISSUB SPECIFICITY: Sersessed by the venom duct.
-I- SIMILARITY: Belongs to the conotoxin O-superfamily. Omega-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Neuronal calcium channel antagonists. Discrimination between calcium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP, P05484; 1DW4.
Amidation; Calcium channel inhibitor; Direct protein sequencing;
Ionic channel inhibitor; Neurotoxin; Presynaptic neurotoxin; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 channel subtypes using omega-conotoxin from Conus magus venom.";
Biochemistry 26:2086-2090(1987).
                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Olivera B.M., Cruz L.J., de Santos V., Lecheminant G.W., Gril
Zeikus R.D., McIntosh J.M., Galyean R., Varga J., Gray W.R.,
Rivier J.E.;
    Length 2703;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 55.5; DB 1; Length 25; Pred. No. 5.2;
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Ramakrishnan G., Ragland B.D., Purdy J.E., Mann B.J.;
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cysteine amide.
E4B9CE5EFAA3734D CRC64;
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Last annotation update)
    Score 56; DB 1;
Pred. No. 2.8e+02;
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                                             5; Mismatches
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822 TGQKCETNIDDCVTNPCGNGGTCI 845
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=87299637; PubMed=2441741;
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  34.8%;
ilarity 33.3%;
Conservative ;
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Best Local Similarity 38.5%;
Matches 10; Conservative
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                                                                                                                                                                                                                                    STANDARD;
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      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Via its ANK repeats.
SUBCELLULAR LOCATION: Type I membrane protein. Upon activation and S1 cleavage, it is released from the cell membrane and enters into the nucleus in conjunction with Su(H).
FTM: Upon binding its ligands such as Delta or Serrate, it is cleaved (S2 cleavage) in its extracellular domain, close to the transmembrane domain. S2 cleavage is probably mediated by Kuz. It is then cleaved (S3 cleavage) downstream of its transmembrane domain, releasing it from the cell membrane. S3 cleavage requires
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WEDLINE=21575956; PubMed=11719214; DOI=10.1016/S0960-9822(01)00562-0;
                                                                                 MEDLINE=99221487; PubMed=10206646; DOI=10.1038/19091;
Struhl G., Greenwald I.;
"Presenilin is required for activity and nuclear access of Notch in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'General outlines of the molecular genetics of the Notch signalling
                                                                                                                                                                                                            S3 CLEAVAGE BY PSN.
MEDLINE=99221488; PubMed=10206647; DOI=10.1038/19096;
Ye Y., Lukinova N., Fortini M.E.;
"Neurogenic phenotypes and altered Notch processing in Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Notch alleles reveal a Deltex-dependent pathway repressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ramain P., Khechumian K., Seugnet L., Arbogast N., Ackermann C.,
Heitzler P.;
                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21657146; PubMed=11799064; DOI=10.1101/gad.942302; Lieber T., Kidd S., Young M.W.; "kuzbanian-mediated cleavage of Drosophila Notch."; Genes Dev. 16:209-221(2002).
interactions with the Notch ankyrin repeats."; Development 121:2633-2644(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Belongs to the NOTCH family. SIMILARITY: Contains 6 ANK repeats. SIMILARITY: Contains 36 EG-like domains. SIMILARITY: Contains 3 Lin/Notch repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22256570; PubMed=12369105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Curr. Biol. 11:1729-1738(2001).
                                                                                                                                                                                                                                                                                                                    Nature 398:525-529(1999).
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                                                                                                                                                Drosophila."
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SEQUENCE FROM N.A.
MEDUTNE=2214996; PubMed=12427470; DOI=10.1016/S0014-4894(02)00113-3;
BECK D.L., Tanyuksel M., Mackey A.J., Haque R., Trapaidze N.,
Pearson W.R., Loftus B., Petri W.A. Jr.;
"Entamoeba histolytica: Sequence conservation of the Gal/GalNAc lectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Entamoeba histolytica: sequence conservation of the Gal/GalNAc lectin
                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22314996; PubMed=12427470; DOI=10.1016/S0014-4894(02)00113-3; Beck D.L., Tanyuksel M., Mackey A.J., Haque R., Trapaidze N., Pearson W.R., Loftus B., Petri W.A. Jr.;
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                                                                                                                                          DB 2; Length 194;
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                                                                                                            21438 MW; 8A9DF5FC481C671D CRC64;
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372 372
372 AA; 41994 MW; 49AA800CGECE259F CRC64;
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                                                                                                                                                                                                                                                                                              372 AA
                                                                                                                                                                     4; Mismatches
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                                                                                                                                         Score 55.5; |
Pred. No. 32;
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        PIR; S70664; S70664.

GO; GO:0005529; F:sugar binding; IEA.
InterPro; IPR006209; EGF like.
PROSITE; PS00022; EGF_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from clinical isolates.",
Exp. Parasitol. 101:157-163(2002).
EMBL, AFS01278, AAM22199.1;
GO: GO:0005529; F:sugar binding; IEA.
                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                         Created)
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01-OCT-2002 (TrEMBLrel. 22, Last seq
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Eukaryota, Entamoebidae, Entamoeba.
NCBI_TaxID=5759;
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NCBI_TaxID=5759;
EMBL; U33444; AAA75552.1; -.
                                                                                                                                        Match 34.5%;
Local Similarity 40.0%;
es 12; Conservative
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194 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 88:3248-3251(1991).
--!- FUNCTION: Lectin that binds galactose.
-!- SUBINIT: Heterodimer of a heavy (170 kDa) and a light subunit (35 kDa) linked by disulfide bonds.
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=91195330; PubMed=2014248;
Mann B.J., Torian B.E., Vedvick T.S., Petri W.A. Jr.;
"Sequence of a cysteine-rich galactose-specific lectin of Entamoeba
                                                                                                                                                                                                                                                                       Э;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Potential)
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                                                                                                                                                                                                                 Score 55.5; DB 2; Length 372;
Pred. No. 56;
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                                                                                                                                                                    41961 MW; 1FF00CE22FBF5100 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, M59850; -; NOT ANNOTATED CDS.
Direct protein sequencing; Glycoprotein; Lectin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 55.5; DB 1;
Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Galactose-inhibitable lectin 170 kDa subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GlcNAc.
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                                                                                                                                                                                                                                                                  4; Mismatches
                                                                                                                                                                                                                                                                                                          1 CRIXNOKCFOHLDDCCSRK--CNRFN-KCV 27
from clinical isolates.",
Exp. Parasitol. 101:157-163(2002).
EMBL; AF501277; AAM22198.1; -
GO; GO:0005529; F:sugar binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-linked
N-linked
N-linked
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Entamoeba histolytica.
Eukaryota, Entamoebidae; Entamoeba.
NCBI_TaxID=5759;
                                                                                                                                                                                                                   34.5%;
                                                                                                                                                                                                                                          40.0%;
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                                                                                                                                                                                                  Query Match
Best Local Similarity 40.09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  kDa) linked by alban-
                                                                                                                                             372
                                                                                                                                                                    372 AA;
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                                                                                                                     372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GIL1 ENTHI P32022;
                                                                                            Lectin.
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                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 39
    RT KW DR SO FT SO 
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OSJNBa0038P21.2 protein.
Name=OSJNBa0038P21.2;
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                                     Xenopodinae; Xenopus
                                                                        SEQUENCE FROM N.A.
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                                               NCBI_TaxID=8355;
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MEDLINE=20231140; PubMed=10861934;

MEDLINE=20231140; PubMed=10861934;

MOSBAH A., Kharrat R., Fajloun Z., Renisio J.-G., Blanc E.,

Sabatier J.-M., El Ayeb M., Darbon H.;

A new fold in the scorpion toxin family, associated with an activity
on a ryanodine-sensitive calcium channel.";

Proteins 40:436-442(2000)

-I- FUNCTION: Pocently and reversibly modifies channel gating behavior
of the type I ryanodine receptor (RYR1) by inducing prominent
subconductance behavior. Binds a different site as ryanodine.
                                                                                                                                                                                                                                         SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
PubMed=10713267; DOI=10.1016/S0014-5793(00)01239-4;
Fajloun Z., Kharrat R., Chen L., Lecomte C., Di Luccio E., Bichet D.,
El Ayeb M., Rochat H., Allen P.D., Pessah I.N., De Waard M.,
Sabatier J.M.;
                                                                                                                                                                                                                                                                                                     "Chemical synthesis and characterization of maurocalcine, a scorpion toxin that activates Ca(2+) release channel/ryanodine receptors."; FBBS Lett. 469:179-185(2000).
   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                         Scorpio maurus palmatus (Chactoid scorpion).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Iurida; Scorpionoidea; Scorpionidae; Scorpioninae; Scorpio.
NCBI_TaxID=53957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PDB; 1C6W; NWR; -. 3D-structure; Calcium channel inhibitor; Direct protein sequencing; Ionic channel inhibitor; Neurotoxin; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- TOXIC DOSE: LD(50) is 20 ug/mice by intracerebroventricular injection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the venom gland.
-!- MASS SPECTROMETRY: WW=3858.2; METHOD=MALDI; RANGE=1-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 55; DB 1; Length 33; Pred. No. 7.6; 4; Indels 1; Mismatches 4; Indels
  11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: Belongs to the scorpion calcine family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 32
33 AA; 3865 MW; ASFE70F945FEC8E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2003 (TrEMBLrel. 23, Last annotation update)
Homeobox protein Lim-1 (Fragment).
Name=Xlim-1;
                                                                                                                                29-MAR-2004 (Rel. 43, Created)
29-MAR-2004 (Rel. 43, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
                                                                                                          33 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 AA
                                      4; Mismatches
                         1 CRIXNQKCFQHLDDCCSRK--CNRFN-KCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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Best Local Similarity 47.6%;
12; Conservative
                                                                                                          STANDARD;
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                                                                                                                                                                    Maurocalcine (MCa).
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                                                                                                          SCOMA
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                                                                                                                      P60254;
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                                                                                  RESULT 40
SCXC_SCOMA
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09PSU2
1D 09PSU
AC 09PSU
DT 01-MA
DT 01-MA
DT 01-MA
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 Matches
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GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0000156; F:two-component response regulator activity; IEA.
GO; GO:0000160; P:sensory perception; IEA.
GO; GO:000160; P:two-component signal transduction system (p. . .; IEA.
InterPro; IPR011006; Chey like.
InterPro; IPR009057; Homeodomain_like.
InterPro; IPR006447; Myb_SHAQKYF.
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Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AL731588; CAE05509-1; --
                                                                                                                                                                                                                               MEDLINE=97420748; PubMed=9275190; DOI=10.1073/pnas.94.18.9717; Rebbert M.L., Dawid I.B.; PubMed=9275190; DOI=10.1073/pnas.94.18.9717; Rebbert M.L., Dawid I.B.; PubMed I.B.; Pubmed I.B.; Pubmed I.B.; Proc. Natl Acad Sci. U.S.A. 94:9717-9722(1997).

-i - STMILARITY: Contains 2 LiM zinc-binding domains. EMBL; AF012342; AAB70190.1; -... EMBL; AF012342; AAB70190.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Epermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112 AA; 12975 MW; F491D6CCF80D882F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO: 0005634; C:nucleus; IEA.
InterPro; IPR001781; LIM.
Pfam; PF00412; LIM; 2.
ProDom; PD000094; LIM; 2.
PROSITE; PS00478; LIM DOMAIN 1; 2.
PROSITE; PS00478; LIM DOMAIN 2; 2.
LIM domain; Metal-binding; Nuclear protein; Zinc.
NON TER 112
SEQÜENCE 112 AA; 12975 MW; F491D6CCF80D882F CRC6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-077-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34.2%; Score 55; 44.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 RIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 RAWHVKCVQ----CCECKCNLTEKC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001789; Response_reg.
Pfam; PF00072; Response_reg; 1.
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Best Local Similarity 44.04
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-1994 (Rel. 30, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
05-0UJ-2004 (Rel. 44, Last annotation update)
LIM/homeobox protein Linx5 (Homeobox protein Linx-5) (XLIM-2A).
Name-Linx5, Synonyms-Lin-2A, Lin2A, Linx5,
Kenopus laevis (African Clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=95377545; PubMed=7649385; DOI=10.1006/dbio.1995.1238;
Toyama R., Curtiss P.E., Otani H., Kimura M., Dawid I.B., Taira M.;
"The LIM class homeobox gene lim5: implied role in CNS patterning in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5,
                                                                                                                                                                                                        DB 2; Length 380;
66;
                                                                                                                                                                                                                                                               10; Indels
                             SMART; SM00448; REC; 1. Tright SHORY SHORY SHOWN SHORY SHOWN SHORY SHOWS TICREAMS; TICREAMS; TICREAMS; TICREAMS; PROSITE; PSS0110; RESPONSE REGULATORY; 1. Phosphory Hallon; Sensory transduction; SEQUENCE 380 AA; 42765 MW; 69DBD43F0CD200E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diencephalon.
SUBCELLULAR LOCATION: Nuclear (Probable).
SIMILARITY: Contains 1 homeobox domain.
SIMILARITY: Contains 2 LIM zinc-binding domains.
                                                                                                                                                                                                     Query Match
34.2%; Score 55; DB
Best Local Similarity 44.0%; Pred. No. 66;
Matches 11; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                402 AA
                                                                                                                                                                                                                                                                                                             3 IXNOKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                  17 IDEDKC--HADSTCSMICTOLNFCV 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001356; Homeobox.
InterPro; IPR009057; Homeodomain_like.
InterPro; IPR001781; LiM.
InterPro; IPR007107; LiM_homeo.
Pfan; PF00046; Homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
ProDom; PD000039; Response_reg; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS, PRO0024; HOMEGBOX.
ProDom; PD000010; Homeobox; 1.
ProDom; PD000094; LIM; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopus and zebrafish.";
Dev. Biol. 170:583-593(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L42546; AAA99464.1; -.
EMBL; Z11587; CAA77672.1; -.
HSSP; P06601; 1FJL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00389; HOX; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T04209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LHX5 XENLA
P37137;
                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRANSFAC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LHKS XENLA

JUNE XENLA

JUNE XENLA

OT 01-0CT-1

DT 01-0CT-1

OS Name=LIM/hor

ON Name=LIM/hor

ON NCBI_T:

RP SEQUEN

RA TOYAMA

RA TOYAMA

RA TAIRA I

CC --- SU

CC --- S
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Ry PubMed=1247932; DOI=10.1073/pnas.242603899;

Ry Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Ry Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Ry Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Ry Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Ry Diatchenko L., Warusina K., Farmer A.A., Rubin G.M., Hong L.,

Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Rapleton M., Soares M.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano M.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Raha S., Wallayon D.K., Muzny D.M., Sodergren E.D., Lu X., Gibbs R.A.,

Raha S., Marra M.A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Ry Vallalon M.A., Wallaka U., Smailus D.E., Schnerch A., Schein J.E.,

Ry Jones S.J., Marra M.A.;

Ry Generation and initial analysis of more than 15,000 full-length human man mouse conna sequences.
                                                                                                                                                                                                                                                                                                                    Gaps
           PROSITE; PS00027; HOMEDBOX 1; 1.
PROSITE; PS50071; HOMEDBOX 2; 1.
PROSITE; PS00478; LIM DOMAĪN 1; 2.
PROSITE; PS50023; LIM DOMAĪN 1; 2.
Developmental protein; DNA-bīnding; Homeobox; LIM domain;
Metal-binding; Nuclear protein; Repeat; Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Embryo;
MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                    4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost.
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                 ch 34.2%; Score 55; DB 1; Length 402; l Similarity 44.0%; Pred. No. 69; ll; Conservative 2; Mismatches 8; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Embryo;
Klein S., Gerhard D.S.;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                            3 61 LIM 1.
62 125 LIM 2.
180 239 Homeobox.
402 AA; 44959 MW; AS852B94747E09F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                   2 RIXNOKCFOHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                           23 RAWHVKCVQ----CCECKCNLTEKC 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-0CT-2004 (TrEMBLrel. 28,
25-0CT-2004 (TrEMBLrel. 28,
25-0CT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dev. Dyn. 225:384-391(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
LIM; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopus.
                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            initiative.
                                                                                                                                                                                                      DNA BIND
SEQÜENCE
                                                                                                                                                            DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q63ZR3
                                                                                                                                                                                                                                                                                          Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 44
Q632R3
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44934 MW; 4147EB3A2774C110 CRC64;

403 AA;

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DNA BIND
SEQUENCE
        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProDom;
                                                                                                                                                                                                                                                                                                                                                                               P48742;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                   RESULT 46
LHX1 HUMAN
                                                                                                                 Matches
                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-92122449; PubMed=1347750;
MEDLINE-92122449; PubMed=1347750;
MEDLINE-92122449; PubMed=1347750;
MEDLINE-92122449; PubMed=1347750;
MT Taira M., Jamrich M., Good P.J., Dawid I.B.;
Genes Dev. 6.136-136(1992)
Genes Dev. 6.136(1992)
Gene
                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=LHX1; Synonyms=LIM-1, LIM1;
Senopus laevis (African clawed frog).
Eukaryota: Metazoa; Chordar, Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobarrachia; Pipoidea; Pipidae;
                                                                                                                                                                      4
                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
LIM/homeobox protein Lhxl (Homeobox protein LIM-1) (XLIM-1).
                                                                                                           34.2%; Score 55; DB 2; Length 402; 44.0%; Pred. No. 69; Live 2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; BC082847; AAH82847.1; -.
Hypothetical protein.
SEQUENCE 402 AA; 44898 MW; 1928D588311BDA5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                 403 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSPAC, T01962; -.
InterPro; IPR001356; Homeobox.
InterPro; IPR001356; Homeodomain_like.
InterPro; IPR001761; LIM.
InterPro; IPR001701; LIM.
Pfam; PF001046; Homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ношеорох.
                                                                                                                                                                                                                      2 RIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                   EMBL; X63889; CAA45353.1; -.
                                                                                       Query Match
Best Local Similarity 44.09
Watches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S23802; S23802.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P06601; 1FJL.
                                                                                                                                                                                                                                                                                                                                                                                                            LHX1 XENLA
P29674;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA BIND
                                                                                                                                                                                                                                                                                                                                                         RESULT 45
LHX1_XEBLA
LHX1_XEBLA
AC P29674;
DT 01-APR-
D
  SXS
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                                                   Ή,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genew: HGNC:6593; LHXI.
MIM; 601999; -- GO; GO:0003702; F:RNA polymerase II transcription factor acti. . .; TAS.
GO; GO:0007399; P:neurogenesis; TAS.
                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50071; HOMBOBOX-2; 1.
PROSITE; PS500471; LIM DOWAIN 1; 2.
PROSITE; PS500473; LIM DOWAIN 1; 2; 2.
DNA-Dinding; Homeobox; LIM domain; Metal-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                   4,
  Length 403;
                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAF2847A340B393F CRC64;
                                                                                                                                                                                                                                                                                                           01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
LIM/homeobox protein Lhx1 (Homeobox protein Lim-1).
Name=LHX1; Synonyms=LIM1;
    DB 1;
69;
                                                                                                                                                                                                                                                                   404 AA
  34.2%; Score 55; DB 44.0%; Pred. No. 69; tive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001356; Homeobox.
InterPro; IPR001956; Homeodomain_like.
InterPro; IPR001781; LIM.
InterPro; IPR007107; LIM.homeo.
Pfam; PF00046; Homeobox; 1.
Pfam; PF00412; LIM; 2.
PRINTS; PR00121; LIM; 2.
PRINTS; PR00012; HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIM 1.
LIM 2.
Homeobox.
                                                                                              2 RIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                             22 RAWHVKCVQ----CCECKCNLTEKC 42
                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00027; HOMEOBOX 1; 1
PROSITE; PS50071; HOMEOBOX 2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44482 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, U14755, AAA21644.1; -. PIR, G01507, G01507.
HSSP, P06601; 1FJL.
                                                 11; Conservative
                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRANSFAC; T01960; -
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               404 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Repeat; Zinc.
                                                                                                                                                                                                                                                                      LHX1 HUMAN
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                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
05-0JU-2004 (Rel. 44, Last annotation update)
15-0JU-2004 (Rel. 44, Last annotation update)
Name=LHX1; Synoryms=LiM-1, LiM1;
Gallus gallus (Chicken).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Gallus.
Gallus.
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA-binding; Homeobox; LIM domain; Metal-binding; Nuclear protein;
                                            4,
 Score 55; DB 1; Length 404;
Pred. No. 70;
2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIM 1.
LIM 2.
Homeobox.
; DF1B7BF1F32B9056 CRC64;
                                                                                                                                                                                              406 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, L35569; AAA62173.1; --
PIR; 150375; 150375.
HSSP; P06601; 1FUL.
INTERPRO; 1PR001356; Homeobox.
INTERPRO; 1PR001356; Homeodomain_like.
INTERPRO; 1PR001781; LIM.
INTERPRO; 1PR007107; LIM.
Pfam; PF00412; Homeobox; 1.
                                                                  2 RIXNOKCFOHLDDCCSRKCNRFNKC 26
                                                                                        22 RAWHVKCVQ----CCECKCNLTEKC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIM DOMAIN 1; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HOMEOBOX 1; 1.
HOMEOBOX 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProDom; PD000010; Homeobox; 1.
ProDom; PD000094; LIM; 2.
PROSITE; PS00027; HOMEOBOX 1; 1
   34.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44845 MW;
                Best Local Similarity 44.0
                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00024; HOMEOBOX
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           406 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS00478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS50023;
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                                                                                                                                                                                         CHICK
Query Match
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PROSITE;
PROSITE;
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SEQUENCE
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                                                            Gaps
                                                                                                                                                                                                                                                            Gaps
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SMART; SM001389; HOX; 1.

SMART; SM001329; HOX; 1.

PROSITE; PS50071; HOMEOBOX 1; 1.

PROSITE; PS00478; LIM DOWALD. 1; 1.

PROSITE; PS00478; LIM DOWALD. 1; 2.

PROSITE; PS00403; LIM DOWALD. 1; 2.

PROSITE; PS00043; LIM domain; Metal-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=95083670; PubMed=7991607;
Rudnick A., Ling T.Y., Odagiri H., Rutter W.J., German M.S.;
Pancreatic beta cells express a diverse set of homeobox genes.";
Proc. Natl. Acad. Sci. U.S.A. 91:12203-12207(1994).
-!- SUBCELLULAR LOCATION: Nuclear (Probable).
-!- SIMILARITY: Contains 1 homeobox domain.
-!- SIMILARITY: Contains 2 LIM zinc-binding domains.
                                                                                                                                                                                                                                                                                                                                                                                                                          Name-Lhx1; Synonyms-Lim-1, Lim1, Lmx2;
Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                              4,
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       Score 55, DB 1; Length 406; Pred. No. 70; 2; Mismatches 8; Indels
                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.2%; Score 55; DB 1; Length 406; 44.0%; Pred. No. 70;
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TRANSPAC, T04264; -
InterPro; IPR001356; Homeobox.
InterPro; IPR001356; Homeodomain_like.
InterPro; IPR001781; LIM.
InterPro; IPR001707; LIM.homeo.
Pfam; PF00046; Homeobox; 1.
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                                                                                                                                            22 RAWHVKCVQ----CCECKCNLTEKC 42
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     34.2%;
ilarity 44.0%;
Conservative
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PIR; I48186; I48186.
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TISSUE=Pancreatic islets;
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63
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                                                  11;
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Matches
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2 RIXNQKCFQHLDDCCSRKCNRFNKC 26

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=BALB/C; TISSUE=Brain; MEDLINE=94220754; PubMed=7909459; Pujii T., Pichel J.G., Taira M., Toyama R., Dawid I.B., Westphal H.; Fujii T., Pichel J.G., Taira M., Toyama R., Dawid I.B., Westphal H.; Expression patterns of the murine LIM class homeobox gene liml in the developing brain and excretory system."; Dev. Dyn. 199:73-83(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=94123850; PubMed=7904966; DOI=10.1006/dbio.1994.1018; Barnes J.D., Crosby J.L., Jones C.M., Wright C.V., Hogan B.L.; "Embryonic expression of Lim-1, the mouse homolog of Xenopus Xlim-1, suggests a role in lateral mesoderm differentiation and
                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Homeobox protein LIM-1)
                                                                                                                                                                                    LHX1_MOUSE STANDARD; PRT; 406 AA. P6306; P36199; 01-JUN-1994 (Rel. 29, Created) 01-JUN-1994 (Rel. 29, Last sequence update) 25-OCT-2004 (Rel. 45, Last annotation update) LIM/homeobox protein LhX1 (Homeobox protein LIM) mame=Lim1; Synonyms=Lim-1, Lim1; Muls musculus (Mouse).
| 3: || | | | || || || RAWHVKCVQ----CCECKCNLTEKC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:99783; Lhx1.
InterPro; IPR001356; Homeobox.
InterPro; IPR001356; Homeodomain_like.
InterPro; IPR001781; LIM.
InterPro; IPR001701; LIM. homeo.
Pfam; PF00046; Homeobox; 1.
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SMART; SM00139; HOX; 1.
PR0SITE; PS00027; HOMEGBOX 1; 1.
PROSITE; PS00011; HOMEGBOX 2; 1.
PROSITE; PS00478; LIM DOMAĪN 1; 2.
PROSITE; PS50023; LIM DOMAĪN 1; 2.
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EMBL; AF039706; AAD02169.1; --
EMBL; AF039705; AAD02169.1; JOINED.
PIR; 148637; 148637.
HSSP; P06601; IFJL.
TRANSFAC; T01961; --
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                                                                                                                                                   LHX1 MOUSE

ID LHX1 MOUSE

OC 01-010N

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                                                                                                                                                                                  Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94336075; PubMed=7914684; DOI=10.1016/0304-3940(94)90334-4; Purvyama T., Inagaki S., Iwahashi Y., Takagi H.; Purvyama T., Inagaki S., Iwahashi Y., Takagi H.; Pubitribution of Rlim, an LIM homeodomain gene, in the rat brain."; Neurosci. Lett. 170:266-268(1994).
-!- SUBCELLUIAR LOCATION: Nuclear (Probable).
-!- SIMILARITY: Contains 1 homeobox domain.
-!- SIMILARITY: Contains 2 LIM zinc-binding domains.
DNA-binding; Homeobox; LIM domain; Metal-binding; Nuclear protein;
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                                                                                                                                                                                                                                                                                                                   P63007; P36199;
01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
LIM/homeobox protein Lhx1 (Homeobox protein LIM-1) (Rlim).
Name=Lhx1; Synonyms=Lim-1, Lim1;
                        LIM 1.
LIM 2.
LIM 2.
LAGUSTON (in Ref. 2).
Missing (in Ref. 2).
R - A (in Ref. 2).
R - H (in Ref. 2).
W, CC6637984998ADAF CRC64;
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                                                                                                                                                                                                                                                                                                           406 AA.
                                                                                                                                                                  Pred. No. 70;
2; Mismatches
                                                                                                                                                     Score 55;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interpro; IPR001356; Homeobox.
InterPro; IPR009057; Homeodomain_like.
InterPro; IPR001701; LIM.
InterPro; IPR007107; LIM.
Pfam; PF0046; Homeobox; 1.
Pfam; PF00412; LIM; 2.
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LIM 2.
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PROSITE; PS00071; HOMEOBOX_2; 1.
PROSITE; PS00478; LIM DOMAIN_1; 2.
PROSITE; PSS0023; LIM DOMAIN_2; 2.
DNA-binding; Homeobox; LIM domain;
                                                                                                                         44780 MW;
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44.0%;
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HSSP; P06601; 1FJL.
                                                                                                                                     PRINTS; PR00024; HOMEOBOX.
SMART; SM00389; HOX; 1.
SMART; SM00132; LIM; 2.
                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
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117
239
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335
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180 2
12 24 24 335 3
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180 2
406 AA;
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              Repeat; Zinc.
DOMAIN
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SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
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STRAIN=C57BL/6; TISSUE=Brain;
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SM00181; EGF; 6.
                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
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nes 11; Conserv
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Best Local S:
Matches 11,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Plasmodium reichenowi: deduced amino acid sequence of sexual stage-specific surface antigen Prs48/45 and comparison with its homologue in Plasmodium falciparum.";
                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22925870; PubMed=14563886;

MEDLINE=22925870; PubMed=14563886;

DOI=10.1128/JB.126.21.6481-6485.2003;

Mmolawa P.T., Schmieger H., Heuzenroeder M.W.;

"Bacteriophage ST648, a genetic mosaic of genes from diverse sources isolated from Salmonella enterica serovar typhimurium DT 64.";

J. Bacteriol. 18:5481-6485(2003).

BMBL, AV055382; AAL28811; -

InterPro; IPR005021; Phage Lermin.

Pfam; PF03354; Terminase 1; 1.

SEQUENCE 577 AA; 65361 MW; 8088047EC2D6F024 CRC64;
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Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae.
NCBI_TaxID=175950;
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MEDLINE=97467681; PubMed=9326890; DOI=10.1006/expr.1997.4204;
Milek R.L., Kocken C.H., Kaan A.M., Jansen J., Meijers H.,
Konings R.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium reichenowi.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5854;
                       DB.1; Length 406; 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34.2%; Score 55; DB 2; Length 448; 40.9%; Pred. No. 76; Live 5; Mismatches 8; Indels
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Pred. No. 95;
5; Mismatches 9; Indels
                                                                                8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D2ED630F439D3757 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
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Last annotation update)
34.2%; Scor.
44.0%; Pred. No. /v,
2; Mismatches
                                                                                                                                2 RIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                         22 RAWHVKCVQ----CCECKCNLTEKC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     227 CELINKKCFQETNDKALYKSNK 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CRIXNOKCFQHLDDCCSRKCNR 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXP. Parasitol. 87:150-152(1997).
EMBL, 133802, AAA91881.1; -
INTERPRO; IPRO10884; 548-45.
Pfam; PF07422; 948-45; 1.
SEQUENCE 448 AA; 51563 MW; D23
                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 34.2%;
Best Local Similarity 39.1%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2004 (TrEMBLrel. 26,
                                                                          11; Conservative
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                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Surface antigen.
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                 Query Match
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Q26107
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Q8HAD6
ID Q8HAD
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DT 01-MP
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Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: Contains 6 EGF-like domains.
EMBL; BCO52002; AAHS2002.1;
-- HSSP; P00740; 1EDM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  585 AA; 61125 MW; EB276F608998D4E9 CRC64;
                                                                                                                                                                            01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Delta-like 3, isoform 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0016021; C:integral to membrane; TAS.
GO; GO:0007386; P:compartment specification; IMP.
                                                                                                                                             585 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000742; EGF 2.
InterPro; IPR001438; EGF II.
InterPro; IPR006210; EGF II.
InterPro; IPR006210; IEGF.
InterPro; IPR001005; Myb_DNA_binding.
Pfam; PF00008; EGF; 5.
                       27 CQYVIQACQRHIDDMAAEKSKRF 49
1 CRIXNOKCFQHLDDCCSRKCNRF 23
                                                                                                                                          PRT;
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PROSITE; PS00186; EGF_2; 6.
PROSITE; PS0026; EGF 3; 5.
PROSITE; PS00334; MYB_2; UNKNOWN_1.
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formation of somite boundaries during segmentation of the
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457
589 AA;
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Matches 11; Conserv
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  Boulter J., Greenfield A., Weinmaster G., Reatus norvegicus mRNA for Delta 3: a putative ligand for Notch."; Submitted (AuG-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Inhibits primary neurogenesis. May be required to divert neurons along a specific differentiation pathway. Play a role in
                                                                                                                                                                                                                                                                                                                                                                                                                                     Geogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T., Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K., Yamamato J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K., Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N., Hattori A., Okumura K., Iwayanagi T., Ninomiya K.; Submitted (MAR-2002) to the EMBJ/GenBank/DDBJ databases.

-: SIMILARITY: Contains 6 EGF-like domains.

HSSP; P00740; IEDM.
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Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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16-OCT-2001 (Rel. 40, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Della: protein 3 precursor (Drosophila Delta homolog 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34.2%; Score 55; DB 2; Length 587; 37.9%; Pred. No. 97; tive 2; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    587 AA; 61144 MW; 2FF5E3EA66789B1B CRC64;
                                                                                                                                                                                                                01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                             377 CRAGFAGPRCEHDLDDCAGRACANGGTCV 405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INCEPPO: 1 PRO0143; EGF 2.
INCEPPO: 1 PR00143; EGF 2.
INCEPPO: 1 PR00143; EGF 11.
INCEPPO: 1 PR006209; EGF 11.
INCEPPO: 1 PR006209; EGF 11.
INCEPPO: 1 PR00105; Myb_DNA_binding.
PERMITS: PR00010; EGF 5.
PRANT: SM0181; EGF 6.
PROSITE; PS01186; EGF 2; 6.
PROSITE; PS01186; EGF 3; 6.
                    CR--IXNOKCFOHLDDCCSRKCNRFNKCV
                                                                                                                                                                                                                                                                                Hypothetical protein FLJ90821.
Homo sapiens (Human).
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                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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088671;
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                                                                                                                                RESULT 54
Q8NBS4
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
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paraxial mesoderm (By similarity).
SUBUNIT: Can bind and activate Notch-1 or another Notch receptor
                                    (By similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
-!- DOMAIN: The DSL domain is required for binding to the Notch
                                                                                                                                                                                                                                                                                                                                                                                                  5
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                                                                                                                   -!- SIMILARITY: Contains 1 DSL domain.
-!- SIMILARITY: Contains 6 EGF-like domains.
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By similarity.
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EGF-like 2.
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EGF-like 6.
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EGF-like 4
EGF-like 4
EGF-like 5
EGF-like 5
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Pred. No.
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                                                EMBL, AF068865; AAC40170.1; -.
EMBL, AF068865; AAC40169.1; -.
EMBL, Y11895; CAA72637.1; -.
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401
592 AA;
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                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=129/SvJ;
MEDLINE=98324780; PubMed=9662403; DOI=10.1038/961;
Kusumi K., Sun E.S., Kerrebrock A.W., Bronson R.T., Chi D.-C.,
Bulotsky M.S., Spencer J.B., Birren B.W., Frankel W.N., Lander E.S.;
"The mouse pudgy mutation disrupts Delta homologue Dl13 and initiation of early somite boundaries.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DLL3_MOUSE STANDARD; PRT; 592 AA.
088516; 031675; 090WL9; 090WZ7;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Delta-like protein 3 precursor (Drogophila Delta homolog 3) (M-Delta-
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 1).
STRAIN=CS7BL/6 x DBA; TISSUE=Embryo;
MEDLINE=97417575; PubMed=9272946;
Dunwoodie S.L., Henrique D.M.P., Harrison S.M., Beddington R.S.P.;
"Mouse D113: a novel divergent Delta gene which may complement the function of other Delta homologues during early pattern formation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISEASE: A truncating mutation in D113 is the cause of the pudgy (pu) phenotype. Pudgy mice exhibit patterning defects at the earliest stages of somitogenesis. Adult pudgy mice present severe vertebral and rib deformities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  paraxial mesoderm.
SUBUNIT: Can bind and activate Notch-1 or another Notch receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isold=088516-2; Sequence=VSP 001376; TISSUE SPECIFICITY: Predominantly expressed in the neuroectoderm
                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and paraxial mesoderm during embryogenesis.
DOMAIN: The DSL domain is required for binding to the Notch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Type I membrane protein (Probable). ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Contains 1 DSL domain.
SIMILARITY: Contains 6 EGF-like domains.
                              381 CRAGPAGPRCEHDLDDCAGRACANGGTCV 409
       CR--IXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=O88516-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                Development 124:3065-3076(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE-FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genet. 19:274-278(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Neural tube;
                                                                                                                                                                                                                                                                                                                                    the mouse embryo."
                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Probable)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptor.
                                                                                                                                                                      3).
Name=D113;
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(See http://www.isb-sib.ch/announce/
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                                                                                                                                                  R EMBL; AB013440; BA33716.1;
R HSSP; P00740; 1EDM.
R MGD; MGI:1096877; D113.
R GO; GO:0005102; F:Notch binding; NAS.
R GO; GO:0007109; P:cell fate determination; NAS.
R GO; GO:0007389; P:cempartment specification; IMP.
R GO; GO:0001701; P:embryonic development (sensu Mammalia); NAS.
R GO; GO:0007101; P:embryonic development (sensu Mammalia); NAS.
R GO; GO:0007101; P:Notch signaling pathway; NAS.
R GO; GO:0001501; P:skeletal development; IMP.
R InterPro; IPR001418; EGF 2.
R InterPro; IPR001418; EGF 1.
R InterPro; IPR0016209; EGF 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein; Differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PERNIS, PRO0008; EGF, 5.
PRINTS, PRO0010; EGFBLOOD.
PROSITE; PS00022; EGF 1; 6.
PROSITE; PS01026; EGF 3; 6.
PROSITE; PS01026; EGF 3; 6.
Alternative splicing; Developmental protein; Differentiati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DWLIQVLF -> A (in isoform 1).
/FTId=VSP 001376.
E -> K (in Ref. 3).
G -> A (in Ref. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Length 592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Potential.
Delta-like protein 3.
Extracellular (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1A84F8022E7E7DCC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytoplasmic (Potential).
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AF241371; AAF62542.1;
AF241372; AAF62542.1;
BC000218; AAH00218.1;
                                                    HSSP; P00740; IEDM.
Genew; HGNC:2909; DLL3.
H-InvDB; HIX0015121; -.
MIM; 602768; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              618 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 385
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TRANSMEM
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                                          EMBL;
                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loca
Matches
                                                                                                  MIM;
MEDLINE=22388257; PubMed=12477912; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Ridanfar R.D., Colling F.S., Wagner L., Shemmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A stapleton M., Soares M.B., Bonaldo M.F., Carvinci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunstane P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Multing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,
T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swies Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse CDNA sequences.",
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: Inhibits primary neurogenesis. May be required to divert neurons along a specific differentiation pathway. Play a role in the formation of somite boundaries during segmentation of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISEASE: Defects in DLL3 are the cause of autosomal recessive spondylocostal dysostosis type 1 (SCDO1) [MIM:277300]. SCDO1 is characterized by multiple hemivertebrae, rib fusions and deletions
                                                                                                                                                                                                SEQUENCE FROM N.A., AND VARIANT SCDOI ASP-385.
MEDLINE-20206573; PubMed=10742114; DOI=10.1038/74307;
Bulman M.P., Kusumi K., Frayling T.M., McKeown C., Garrett C.,
Lander E.S., Krumlauf R., Hattersley A.T., Ellard S., Turnpenny P.D.;
"Muteations in the human delta homologue, DLi3, cause axial skeletal
defects in spondylocostal dysostosis.";
Nat. Genet. 24:438-441(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    paraxial mesoderm (By similarity).
SUBUNIT: Can bind and activate Notch-1 or another Notch receptor
                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (By similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
-!- DOMAIN: The DSL domain is required for binding to the Notch
                                                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Delta-like protein 3 precursor (Drosophila Delta homolog 3)
Name=DLL3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  with a non-progressive kyphosocilosis.
SIMILARITY: Contains 1 DSL domain.
SIMILARITY: Contains 6 EGF-like domains.
                           618 AA.
                           PRT;
                           STANDARD;
                                                                                                                             Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                  TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor.
                           DLL3 HUMAN
          DLL3_HUMAN
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1,
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R GO; GO:0016021; C:integral to membrane; NAS.
R GO; GO:0016021; F:Notch binding; NAS.
R GO; GO:000710; P:cell fate determination; ISS.
R GO; GO:0001701; P:cell fate determination; ISS.
R GO; GO:0001701; P:cell fate determination; ISS.
R GO; GO:0001701; P:motrogenesis; ISS.
R GO; GO:0007219; P:Notch signaling pathway; ISS.
R GO; GO:0001201; P:Notch signaling pathway; ISS.
R InterPro; IPR000742; EGF_1:
R InterPro; IPR0006209; EGF_1:
R InterPro; IPR0006209; EGF_1:
R PRINTS; PR00006; EGF_2:
R PROSITE; PS00025; EGF_1:
R PROSITE; PS00025; EGF_2: 6.
R PROSITE; PS0026; EGF_2: 6.
                                                                                                                                                                                                                                                                                                                                                                                                        Developmental protein; Differentiation; Disease mutation;
EGF-like domain; Notch signaling pathway; Polymorphism; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         By similarity.
FridevAR_009952.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Delta-like protein 3.
Extracellular (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58A9BC0A7DEAD1A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytoplasmic (Potential).
DSL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     379 CRAGFAGPRCEHDLDDCAGRACANGGTCV 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CR--IXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGF-like 3.
EGF-like 4.
EGF-like 5.
EGF-like 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Potential
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Signal; Transmembrane.
SIGNAL 1 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
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58 RESULT

EMBL, AF241373; AAF62542.1; -EMBL, AF241367; AAF62542.1; JOINED.
EMBL, AF241368; AAF62542.1; JOINED.
EMBL, AF241369; AAF62542.1; JOINED.

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SEOUENCE
                                                                                                                                                                                                                                                                                                                                       Query Match
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P05484;
                                                                                                                                                                                                                                                                                                                                                        Best Loc
Matches
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                                                                                                                                                                                                                                MEDINE=2225708; PubMed=12368867; DCI=10.1038/nature01095; AM MEDINE=22255708; PubMed=12368867; DCI=10.1038/nature01095; AM Hall N., Pain A., Betriman M., Churcher C., Harris B., Harris D., Burnows C., Cherevach I., Chillingworth C., Cherevach I., Chillingworth C., Cherevach I., Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C., Croin A., Davis B., Dear P., Dearden F., Doggett J., Feltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z., Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P., Angels K., James K.D., Johnson D., Kerhornou A., Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N., Line A., Maddison M., Mclean J., Mooney P., Moule S., Murphy L., Angels K., Smith R., Squares S., Stevens K., Samonds M., Stewens K., Sharp S., Smith R., Squares S., Stevens K., Sulston J.E., Craig A., Unwin L., Whitehead S., Woodward J., Squarce S., Stevens K., Squence of Plasmodium falciparum chromosomes I, 3-9 and 13."; Dennary M. Dennary M. Dennary M. Dennary M., Dennary M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carlton J.M., Angluoli S.V., Suh B.B., Kooij T.W., Pertea M., Sluvad J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L., Sheterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L., Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V., Cho J.K., Cuackenbush J., Sedegah M., Shoaibi A., Cummings L.M., Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmodium yoelii yoelii.
Eukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=73239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 55; DB 2; Length 162
Pred. No. 2.4e+02;
5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     191996 MW; 31A7292B814ACE0F CRC64;
                                                                     01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein PFA0170c.
Name-PFA0170c; Synonyms-MALIP1.74b;
Plasmodium falciparum (isolate 3D7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0004182; F:carboxypeptidase A activity; IEA. GO; GO:0006508; P:proteolysis and peptidolysis; IEA. InterPro; IPR000834; Peptidase M14. InterPro; IPR0246; Peptidase_M14; I. Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 5309 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   161 YTNKCNQYNDDDYTNKCNQYNDDDYTNKC 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 XNOKCFQHLDDCCSRKCNRF----NKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=12368865; DOI=10.1038/nature01099;
                      PRT;
                                                        (TrEMBLrel. 23, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AL031745; CAD48994.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34.2%;
                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                  NCBI_TaxID=36329;
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parasite Plasmodium yoelli yoeli.";

"Nature 419:512-519 (2002).

"I- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

EMBL; AABLO1000171; ENAI7439.1; -.

GO, GO:0003677; F:DNA binding; IEA.

GO; GO:000160; P:two-component signal transduction system (p. .; IEA.
Genome sequence and comparative analysis of the model rodent malaria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chung D., Gaur S., Bell J.R., Ramachandran J., Nadasdi L.; "Determination of disulfide bridge pattern in omega-conopeptides."; Int. J. Pept. Protein Res. 46:320-325(1995).
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Zeikus R.D., McIntosh J.M., Galyean R., Varga J., Gray W.R.,
Rivier J.E.,
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Apogastropoda; Caenogastropoda; Sorbecconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
NCBI_TaxID=6492;
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MEDLINE=86070213; PubMed=4071055;
Olivera B.M., Gray W.R., Zeakus R.D., McIntosh J.M., Varga J.,
Rivier J.E., de Santos V., Cruz L.J.;
"Peptide neurotoxins from fish-hunting cone snails.";
Science 230:1338-1343(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Venom duct;
MEDLINE=20519630; PubMed=10938268; DOI=10.1074/jbc.M002255200;
MEDLINE=20519630; PubMed=10938268; DOI=10.1074/jbc.Mddms D.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34.2%; Score 55; DB 2; Length 5309; 32.4%; Pred. No. 6.8e+02;
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tive 5; Mismatches 10; Indels
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28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Omega-conotain WVIIa precursor (SNX-111) (Ziconotide).
Conus magus (Magus cone)
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InterPro; IPR002078; Sig54 interact.
PROSITE; PS00012; PHOSPHOPĀNTETHEINE; UN
PROSITE; PS00675; SIGMAS4_INTERACT_1; 1.
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J. Biol. Chem. 275:35335-35344(2000)
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MEDLINE=87299637; PubMed=2441741;
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Q646V4
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-!- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind and block voltage-sensitive calcium channels (VSCC). This toxin blocks N-type calcium channels.
-!- SUBCELLULAR LOCATION: Secreted.
-!- FUNCTION: SPECIFICITY: Expressed by the venom duct.
-!- PHARMACEUTICAL: Is under clinical trial by Neurex. It blocks acute pain in patients who no longer obtain relief from opiate drugs. It is 100 to 1000 times more potent than morphine. By blocking calcium channels it disable nerves that transmit pain signals.
-!- SIMILARITY: Belongs to the conotoxin O-superfamily. Omega-type
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                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-95385787; PubMed=7656969; DOI=10.1016/0014-5793(95)00819-U; Basus V.J., Nadasdi L., Ramachandran J., Miljanich G.P.; "Solution structure of omega-conotoxin MVIIA using 2D NMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Structure-activity relationships of omega-conotoxins MVIIA, MVIIC 14 loop splice hybrids at N and P/Q-type calcium channels."; J. Mol. Biol. 289:1405-1421(1999).
                                                Kim J.I., Takahashi M., Ohtake A., Wakamiya A., Sato K.; Tayril she essential for the activity of omega-conotoxin MVIIA and GVIA, specific N-type calcium channel blockers."; Biochem. Biophys. Res. Commun. 206:449-454(1995).
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                                                                                                                                                                                                                MEDLINE=95367555; PubMed=7640281; Kodera Y., Maeda T., Sato K.; Kohno T., Kim J.-I., Kobayashi K., Kodera Y., Maeda T., Sato K.; "Three-dimensional structure in solution of the calcium channel blocker omega-conotoxin MVIIA."; Blochemistry 34:10256-10265(1995).
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Goldenberg D.P., Koehn R.E., Gilbert D.E., Wagner G.;
"Solution structure and backbone dynamics of an omega-conotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR004214; Conotoxin.
Pfam; PF02350; Conotoxin; 1.
3D-structure; Amidation; Calcium channel inhibitor;
Direct protein sequencing; Ionic channel inhibitor; Neurotoxin;
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MEDLINES-97070382; PubMed=8913308; DOI=10.1006/jmbi.1996.0576;

MEDLINES-97070382; PubMed=8913308; DOI=10.1006/jmbi.1996.0576;

Nielsen K.J., Thomas L., Lewis R.J., Alewcod P.F., Craik D.J.;

"A consensus structure for omega-conotoxins with different
selectivities for voltege-sensitive calcium channel subtypes:
comparison of MVIIA, SVIB and SNX-202.";

J. Mol. Biol. 263:297-310(1996).
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MEDLINE=99303703; PubMed=10373375; DOI=10.1006/jmbi.1999.2817;
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MEDLINE=20213238; PubMed=10747778; DOI=10.1021/bi992651h;
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SYNTHESIS, ÅND MUTAGENESIS OF LYS-47 AND TYR-58
MEDLINE=95126938; PubMed=7826361;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   spectroscopy.";
FEBS Lett. 370:163-169(1995)
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1 DW5; NWR; A=1-25.
1 FFO; NMR; A=1-25.
1 MVI; NWR; @=1-25.
1 OMG; NMR; @=1-25.
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"Patterns of Diversifying Selection in the Phytotoxin-like scr74 Gene Family of Phytophthora infestans."; Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases. EMBL, AY723713; AAU21454.1.
                                                                                                                                                                                                                                             Gaps
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                                                                                                              Cysteine amide (G-71 provides amide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Liu Z., Bos J.I.B., Armstrong M., Whisson S.C., da Cunha b.,
Torto-Alalibo T., Win J., Avrova A.O., Wright F., Birch P.R.J.,
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Liu Z., Bos J.I.B., Armstrong M., Whisson S.C., da Cunha L.,
Torto-Alalibo T., Win J., Avrova A.O., Wright F., Birch P.R.J.,
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                                                                                                                                         S--F. Little decrease in activity. Y->A: Strong decrease in activity. E2A32725C81AF31D CRC64;
                                                                                                                                                                                                        Score 54.5; DB 1; Length 71;
Pred, No. 17;
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Phytophthora infestans (Potato late blight fungus).
Eukaryota, stramenopiles, Oomycetes, Pythiales, Pythiaceae,
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Eukaryota, stramenopiles, Oomycetes, Pythiales, Pythiaceae;
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 Presynaptic neurotoxin; Signal; Toxin.
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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Last annotation update)
                                               Omega-conotoxin MVIIa
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                Potential
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25-OCT-2004 (TrEMBLrel. 28,
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es 10; Conservative
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Pharmaceutical;
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"Patterns of Diversifying Selection in the Phytotoxin-like scr74 Gene Family of Phytophroxa infestans.";
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY723705; AAU21446.1;
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Liu Z., Bos J.I.B., Armstrong M., Whisson S.C., da Cunha L.,
Torto-Alalibo T., Win J., Avrova A.O., Wright F., Birch P.R.J.,
                                                                                          7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
                                                               74;
                                                                                                                                                                                                                                                                               Phytoxin-like SCR74.

Phytophthora infestans (Potato late blight fungus).

Eukaryota, stramenopiles; Oomycetes; Pythiales; Pythiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'Genome sequence of the nematode C.elegans: A platform for
                                                                                          Indels
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
                                                               DB 2; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kershaw J.K.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; Z81587; CAB04705.2; -.
WormBase; WBGene00011548; T06G6.6.
                     -.
537318AAFF612545 CRC64;
                                                                                                                                                                                                                                    25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                         . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                          Score 54.5; DE Fred. No. 18; 4; Mismatches
                                                                                                                                                                                                                 74 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
33.9%; Score 54.5; I
Best Local Similarity 37.0%; Pred. No. 18;
Matches 10; Conservative 4; Mismatches
                                                                                                                               45 KCCQAINADPIAFHDCCSKSCNTGSPC 71
                                                                                                               7 KCFQHLD-----DCCSRKCNRFNKC 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45 KCCQAINPDPIAFHDCCSKSCNTGSPC 71
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01-JAN-1998 (TrEMBLrel. 05, Last seqn
01-JUN-2003 (TrEMBLrel. 24, Last ann
Hypothetical protein T06G6.6.
                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                          33.9%;
              EMBL; AY723711; AAU21452.1;
SEQUENCE 74 AA; 7825 MW;
                                                    Query Match
Best Local Similarity 37.0°
Matches 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 investigating biology.";
Science 282:2012-2018(1998)
                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4787;
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                                                                                                                                                                                                                             Q646W1;
                                                                                                                                                                                                             0646W1
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Q646W1
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018052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21359325; PubMed=11466286; DoI=10.1128/JB.183.16.4823-4838.2001; DoI=10.1128/JB.183.16.4823-4838.2001; Medling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q., Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I., Tatusov R.L., Sabathe F., Doucette-Stamm L.A., Soucaille P., Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.; Genome sequence and comparative analysis of the solvent-producing J. Bacterium Clostridium acetobutylicum."; J. Bacteriol. 183:4823-4838(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clostridium acetobutylicum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                          7;
                                                                                                                                                                                    DB 2; Length 247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 252;
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                               Hypothetical protein.
SEQUENCE 247 AA; 27954 MW; 26FAB589C121FBEB CRC64;
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InterPro; IPR001173; Glyco trans 2.
Complete proteome; Transferase.
SEQUENCE 252 AA; 29892 MW; C7A45BA39F534DE9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Glycosyltransferase.
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01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JANR-2004 (TrEMBLrel. 26, Last annotation update)
Gal/GalNAc-inhibitable adherence lectin.
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                                                                                                                                                                           Score 54.5; DE
Pred. No. 52;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        252 AA
                                                                                                                                                                                                                                                                                                                                                                                                         3 IXNOKCFQHLD-----DCCSRKCNRFNK 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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NCBI_TaxID=46681;
                                                                                                                                                              33.9%;
Local Similarity 33.3%;
hes 10; Conservative ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OrderedLocusNames=CAC2351;
T06G6.6; CE13343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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Entamoeba dispar.
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WormPep;
                                                                                                                                                                           Query Match
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Matches
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018720
AC 01872
AC 01872
AC 01872
DT 01-JA
DT 0
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247 AA.

RL DR DR DR SQ SW XW

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STRAIN-ADDNOOL;
MEDLINE=22963401; PubMed=14599801; DOI=10.1016/j.virol.2003.08.002;
MEDLINE=22963401; PubMed=14599801; DOI=10.1016/j.virol.2003.08.002;
Nakai M., Goto C., Kang W., Shikata M., Luque T., Kunimi Y.;
"Genome sequence and organization of a nucleopolyhedrovirus isolated from the smaller tea tortrix, Adoxophyes honmai.";
Virology 316:171-1832(2003).
                                                                            01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein.
Adoxophyes hommal nucleopolyhedrovirus.
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AP006270; BAC67260.1; -. Hypothetical protein.
                                         PRELIMINARY;
                                                                                                                                                                                                     Nucleopolyhedrovirus
                                                                                                                                                                                                                        NCBI_TaxID=224399;
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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Q90476;
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                                         Q80LT7
RESULT 68
Q80LT7
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J. Biol. Chem. 275:35335-35344(2000).
-!- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bin and block voltage-sensitive calcium channels (VSCC) (By similarity). This toxin blocks N-type calcium channels.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the venom duct.
-!- SIMILARITY: Belongs to the conotoxin O-superfamily. Omega-type
                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Amidation; Calcium channel inhibitor; Direct protein sequencing;
Ionic channel inhibitor; Neurotoxin; Presynaptic neurotoxin; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., SEQUENCE OF 46-72, SYNTHESIS, AND STRUCTURE BY
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Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                         Length 1282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 54; DB 1; Length 73; Pred. No. 20;
                                                                                                                                                                                                   11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                      1282 AA; 143481 MW; 48BD2FA64140C33E CRC64;
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C4CEBD30C77DAEC3 CRC64;
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                                                                                                                                                           Score 54.5; DB 2;
Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Omega-conotoxin CVID precursor.
                                                                                                                                                                                                                                                                                                                                                                                 73 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          By similarity.
                                                                                                                                                                                                   4; Mismatches
Mol. Biochem. Parasitol. 87:101-105(1997).
EMBL; U73710; AAC47580.1; -.
                                                                                                                                                                                                                                                                              708 CSMGTDNVISYCEDCASRKSQCGNFNGKC 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         By similarity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Potential.
                    EMBL; U73710; AAC47580.1; -.
GO; GO:0005529; F:sugar binding; IEA.
InterPro; IPR006209; EGF_like.
                                                            InterPro, IPR006209; EGF_like.
PROSITE; PS00022; EGF_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CRIXNOKCFOHLDDCCSRKCN 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR004214; Conotoxin.
                                                                                                                                                           33.9%;
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                                                                                                                                                                                                   11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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445
72
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72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conus catus (Cat cone)
                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=101291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P05484; 1DW4
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wes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 AA;
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46
46
53
72
                                                                                                                                                                                                                                                                                                                                                                             CXOD CONCT P58920;
                                                                                                                    SEQUENCE
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MOD RES
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SIGNAL
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         There are no restrictions on
                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
LIM/homeobox protein Lhx1 (Homeobox protein LIM-1).
Name=lhx1a; Synonyms=lhx1, lim1;
Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Gastrula, and Neurula;
MEDLINE=95285760; PubMed=7768180;
TOyama R., O'Connell M.L., Wright C.V.E., Kuehn M.R., Dawid I.B.;
"Nodal induces ectopic goosecoid and liml expression and axis
duplication in zebrafish.";
Development 121:383-391(1995).
                                       DB 2; Length 247;
                                                                   Indels
.1 protein.
247 AA; 28773 MW; 9E53E54D3E022C25 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between the Swiss Institute of Bioinformatics
                                                                                                                                                                                             405 AA.
                                     33.5%; Score 54; DB 40.7%; Pred. No. 60; Live 3; Mismatches
                                                                                                                       168 CEKKCFTAPRLHLDGLVCDKCNGYNFC 194
                                                                                              4 XNQKCFQ----HLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute.
                                                                                                                                                                                             PRT;
                                                    Local Similarity 40.7 tes 11; Conservative
                                                                                                                                                                                             STANDARD;
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RtnoidX_receptor.

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InterPro; IPR000003;
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nogili M.O., Henrich V.C., Imhof M.O., Lezzi M.;

Nologili M.O., Henrich V.C., Imhof M.O., Lezzi M.;

Nologili M.O., M.O., M.C., M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=99457719; PubMed=10528412; DOI=10.1016/S0965-1748(99)00068-5;
Vogtli M., Imhof M.O., Brown N.E., Rauch P., Spindler-Barth M.,
Lezzi M., Henrich V.C.;
"Functional characterization of two Ultraspiracle forms (CtUSP-1 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4;
                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Chironomoidea;
Chironomidae; Chironominae; Chironomus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33.5%; Score 54; DB 1; Length 405; 44.0%; Pred. No. 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 238 Homeobox.
405 AA; 45153 MW; 186EEBEB59C88123 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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Insect Biochem. Mol. Biol. 29:931-942(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  552 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 RAWHIKCVQ----CCECKCNLTEKC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 RIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chironomus tentans (Midge).
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es 11; Conserv
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SEQUENCE
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1045117
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R InterPro; IPR001723; Stdhrmn.__creptor.

R InterPro; IPR001846; Str_ncl_receptor.

R InterPro; IPR001628; Znf_C4steroid.

R InterPro; IPR001628; Znf_C4steroid.

R Ffam; PP00104; Hormone_recep; 1.

R PRINTS; PR00394; STRDHORNONER.

R PRINTS; PR00394; STRDHORNONER.

R PRINTS; PR00399; ZnF C4; 1.

SMART; SM00430; HOLI; 1.

SMART; SM00399; ZnF C4; 1.
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Thomas J.T., Weih K.A., Prakash D., Moos M. Jr.;
"Vgl and CDMP-1/GDF5 Have Specific Processing Requirements That
Restrict their Sites of Action to Body Axis and Joint Patterning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
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Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AX685229; AX79305.1;
R GO; GO:0008233; F:peptidase activity; IEA.
R InterPro; IPR006212; Furin repeat.
R InterPro; IPR006210; Grow Fac recept.
R InterPro; IPR006210; IEGF.
R InterPro; IPR006210; Prot inh propept.
R InterPro; IPR009209; Prot inh propept.
R EAM; PR00082; Peptidase S8; 1.
R Fam; PR00181; Peptidase S8; 1.
R FRINTS; PR00723; SUBTILIASE, 1.
R SMART; SM00261; FU; 5.
R SMART; SM00261; FU; 5.
R RRSITE; PS00137; SUBTILIASE ASP; 1.
R PROSITE; PS00138; SUBTILIASE ASP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33.5%; Score 54; DB 2; Length 552
40.0%; Pred. No. 1.2e+02;
ive 6; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     911 AA; 101427 MW; E75C63CB60D3B82F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Subtilisin-like protease SPC6A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               911 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               345 CAMVNKQVFQHMDFC--RRLPHFTK 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CRIXNOKCFQHLDDCCSRKCNRFNK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopus laevis (African clawed frog).
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 40.0%;
...rhes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopodinae; Xenopus.
NCBI_TaxID=8355;
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Q68KF8
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Matches
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Matches
                                                                                              RESULT 73
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                                                                                                                  Hypothetical protein W02C12.1.
Name=W02C12.1; ORFNames=W02C12.1;
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                      investigating biology. The C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.5%; Score 54; DB 2; Length 1372; 29.2%; Pred. No. 2.7e+02;
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                                                                                                                                                                                                                                                                                                                                                         STRAIN-Bristol N2;
Murray J., Wohldmann P.;
"The sequence of C. elegans cosmid W02C12.";
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; VB0815; AAB37995.1; -.
PIR; T25933; T25933.
HSSP, Q12780; 1HAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Waterston R.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wormbase; WaGene0020928; W02C12.1.
Wormpep; W02C12.1; CE14412.
GG; GO:0005509; F:calcdium ion binding; IEA.
InterPro; IPR00152; Asx hydroxyl S.
InterPro; IPR001985; Cona like_lec_gl.
InterPro; IPR001891; EGF_Ca.
InterPro; IPR001438; EGF_II.
InterPro; IPR001438; EGF_II.
InterPro; IPR001439; EGF_II.
InterPro; IPR001439; EGF_II.
InterPro; IPR001438; EGF_II.
InterPro; IPR001438; EGF_II.
InterPro; IPR001438; Submiscreept.
InterPro; IPR001438; Submiscreept.
InterPro; IPR001438; Submiscreept.
InterPro; IPR001458; Submiscreept.
InterPro; IPR001458; Submiscreept.
InterPro; IPR001458; Submiscreept.
InterPro; IPR001488; II.
                                                      PRT; 1372 AA
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                                                                                   Created)
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                                                                                                                                                                                                                                          STRAIN-Bristol N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRODOIO; EGFBLOOD.
ProDom; PD002153; Pentaxin; 1.
SMART; SM0032; CCP; 1.
SMART; SM00179; EGF_CA; 4.
                                                                                             (TrEMBLrel. 03, (TrEMBLrel. 26,
                                                                                 01-MAY-1997 (TrEMBLrel. 03,
                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PS50923; SUSHI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Bristol N2;
WormBase Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1372 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                             01-MAR-2004
                                                                                              01-MAY-1997
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                                                     P91526
P91526;
                         RESULT 72
                                         P91526
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Best Local Similarity

Query Match

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Gaps
                                                                                                                                                                                                               Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                           MEDLINE=21098742; PubMed=11161558; DOI=10.1006/dbio.2000.0105; Yeo S.Y., Little M.H., Yamada T., Miyashita T., Halloran M.C., Kuwada J.Y., thuh T.L., Okamoto H.; Malloran M.C., T., Woverexpression of a slit homologue impairs convergent extension of the mesoderm and causes cyclopia in embryonic zebrafish.";
ö
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1515 AA; 166871 MW; 12FD111277D18D5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZFIN; ZDB-GENE-010306-4; slit3.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
                                                                                                                                                     01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
10;
                                                                                                                            PRT; 1515 AA.
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000152; Asx hydroxyl 5.
InterPro; IPR000152; Asx hydroxyl 5.
InterPro; IPR000805; Conā like lec_gl.
InterPro; IPR0008057; Cys knot c.
InterPro; IPR00080181; EGF_Ca.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001881; EGF_like.
InterPro; IPR00181; Laminin_G.
InterPro; IPR001791; Laminin_G.
InterPro; IPR001611; LRR.
InterPro; IPR000483; LRR_Cterm.
InterPro; IPR0003931; LRR_Nterm.
InterPro; IPR0013129; TSP_N.
                                           : : | |::|:| : | |: | 95 TGENCDQNIDECAASPCQNDAKCI 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30; GO:0007155; P:cell adhesion; IEA.
                            4 XNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS01187; EGF_CA; 2.
PS50025; LAM_G_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCK 1; UNKNOWN CTCK 2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00008; EGF; 7.
Pfam; PF02210; Laminin G 2; 1.
Pfam; PF01463; LRRCT; 4.
Pfam; PF01462; LRRNT; 4.
Pfam; PF00560; LRR 1; 19.
PRINTS; PR00019; LEURICHRPT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PRO116; ASX HYDROXYL;
                                                                                                                                                                                                                                                                                                                                                                                                                  Dev. Biol. 230:1-17(2001).
EMBL; AF210320; AAG36772.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00041; CT; 1.
SMART; SM00179; EGF CA; 1.
SMART; SM00274; FOLN; 3.
7; Conservative
                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LRRNT; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P01132; IGK5
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=Michigan;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00282;
SMART; SM00082;
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SMART; SM00369;
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EGF-like
SEQUENCE
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A Gimenez-Bonafe P., Ribes E., Sautiere P., Gonzalez A., Kasinsky H.E.,
A Kouach M., Sautiere P.-E., Ausio J., Chiva M.;
Thromatin condensation, cysteine-rich protamine, and establishment of
Tirhomatin condensation, cysteine-rich protamine, and establishment of
Tirhosa (Cephalopoda).";
Eur. J. Cell Biol. 81:341-349 (2002).
L Eur. J. Cell Biol. 81:341-349 (2002).
C-I- FUNCTION: Protamines substitute for histones in the chromatin of
Sperm during the haploid phase of spermatogenesis. They compact
Sperm DNA into a highly condensed, stable and inactive complex.
This protamine condenses spermiogenic chromatin in a pattern which
Comprises fibres with a progressively larger diameter and lamellae
C-I- Subgunit: Cross-linked by interchain disulfide bonds around the
DNA-helix (By similarity).
C-I- SUBGLELIOLAR LOCATION: Nuclear.
-I- TIGGELELIOLAR LOCATION: Nuclear.
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                                               Gaps
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                                                                                                                                                                                                                                                                                  Elegone cirrhosa (Curled octopus) (Ozaena cirrosa).
Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
Octopodiformes; Octopoda; Incirrata; Octopodidae; Eledone.
NCBI_TaxID=102876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001212; Somatomedin B. Chromosomal protein; Direct protein sequencing; DNA condensation; DNA-binding; Nuclear protein; Nucleosome core; Spermatogenesis. DISULFID 12 12 Interchain (with C-31) (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (By similarity) (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY
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Query Match 33.5%; Score 54; DB 2; Length 1515; Best Local Similarity 37.5%; Pred. No. 38+02; Matches 9; Conservative 4; Mismatches 11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
3-hydroxy-3-methylglutaryl-CoA synthase (EC 2.3.3.10).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70932DAC3C71837E CRC64;
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Interchain (with C-63)
                                                                                                                                                                                                                            (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 44, Last annotation update)
                                                                                                                                                                                                84 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CRIXNQKCFQHLDDCCSRK---CNRFNKC 26
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                                                                                         1059 VGQCCEQDYNDCLENKCQHGAECV 1062
                                                                     4 XNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22108191; PubMed=12113475;
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31.0%;
                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                             Cysteine-rich protamine.
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                                                                                                                                                       LT 74
ELECI
HSPC ELECI
P83183;
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DISULFID
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1069308
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OC EURAL
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Taxaceae; Taxus.
NCBL_TaxID=85957;
[1]

Taxus x media.

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             A Kai G., Miao Z., Tang K.;

A Kai G., Miao Z., Tang K.;

T. "Cloning and expression analyses of a new gene encoding 3-hydroxy-3-
T. "Cloning and expression analyses of a new gene encoding 3-hydroxy-3-
T. "Cloning and expression analyses of a new gene encoding 3-hydroxy-3-
T. Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.

R GG GO.0008415; F.acvItransferase activity; IEA.

R GG GO.000441; F.hydroxymeth/lglutaryl-CoA synthase activity; IEA.

R GG GO.0016740; F.transferase activity; IEA.

R InterPro; IPR008260; HMG CoA synth.

DR InterPro; IPR010122; HMG CoA synth.

DR Pfam; PP01154; HMG COA synth.

R Pfam; PP01154; HMG COA synt.

R TGRFAMS; TIGRRAMS; TIGRRAMS; HMG-CoA-S_euk; 1.
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ftz-fl, is required
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-!- FUNCTION: Orphan nuclear receptor. Seems to be required during development. Disruption of nhr-25 function leads to embryonic arrest due to failure of the epidermally mediated process of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISOId=019345-2; Sequence=VSP 003723;
-!- TISSUB SPECIFICITY: Expressed in the epidermis, the developing somatic gonad, and a subset of other epithelial cells.
-!- SIMILARITY: Belongs to the nuclear hormone receptor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20237592; PubMed=10772806; DOI=10.1006/dbio.2000.9679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52863 MW; 973883623142EE0D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 33.2%; Score 53.5; DB 2; Local Similarity 43.5%; Pred. No. 1.2e+02; les 10; Conservative 5; Mismatches 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gissendanner C.R., Sluder A.E., "nhr-25, the Caenorhabditis elegans ortholog of for epidermal and somatic gonad development."; Dev. Biol. 221:259-272(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NH25_CAEEL STANDARD; PRT; 5/2 AA. 019345; O9NJ95; O9NJ97; O9NJ95; O9NJ97; OPNJ97; OPNJ97; OPNJ97; OPNJ97; OPNJ97; OPNJ97; OPNJ98; OPNJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=Q19345-1; Sequence=Displayed;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 XNOKCF-OHLDDCCSRKCNRFNK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Acyltransferase; Transferase.
SEQUENCE 476 AA; 52863 MW.
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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NCBI_TaxID=6239;
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Matches
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CAEEL
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release channel of skeletal and cardiac muscle.";
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Best Local Similarity 37.5
Matches 12, Conservative
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                                                                                                                                                                                                                                                   Garcia J.;
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE-9751909; PubMed-9108323; DOI=10.1016/S0014-5793(97)00227-5;
Zamudio F.Z., Gurrola G.B., Arevalo C., Sreekumar R., Walker J.W.,
Valdivia H.H., Possani L.D.;
"Primary structure and synthesis of Imperatoxin A (IpTx(a)), a peptide
activator of Ca2+ release channels/ryanodine receptors.";
PEBS Lett. 405:385-389(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=93101692; Pubmed=1334561;
Valdivia H.H., Kirby M.S., Lederer W.J., Coronado R.;
"Scorpion toxins targeted against the sarcoplasmic reticulum Ca(2+)-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pandinus imperator (Emperor scorpion).
Eukaryota, Metazoa, Archropoda, Chelicerata, Arachnida, Scorpiones,
Lurida, Scorpionoidea, Scorpionidae, Pandinus.
NCBI_TaxID=55084;
                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0398; STRDHOKMONER.
PRINTS; PRO0309; STROIDFINGER.
PRINTS; PRO0301; STROIDFINGER.
ProDom; PD000035; Znf C4steroid; 1.
SMART; SM00309; ZnF C4; 1.
SMART; SM00399; ZnF C4; 1.
SMART; SM00399; ZnF C4; 1.
Alternative splicing; Developmental protein; DNA-binding;
Nuclear protein; Receptor; Transcription regulation; Zinc-finger.
DNA_BIND
18
83
Nuclear receptor-type.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33.2%; Score 53.5; DB 1; Length 572; 32.4%; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C4-type.
Missing (in isoform Beta).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
25-0CT-2004 (Rel. 45, Last annotation update)
Imperatoxin A (IpTxa) (Imperatoxin activator)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33 AA
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                                                                                       C4-type.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       572 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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P59868;
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ZN FING
ZN FING
VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                             containing ryanddine receptor, type 3.";
Biophys. J. 82:1319-1328(2002).
-!-FUNCTION: Strong agonist of ryanddine receptors (calcium release channels). Induces voltage- and concentration-dependent subconductance states in both skeletal (RYR1 and RYR3) and cardiac (RYR2) ryanodine receptors by binding to a single, cytosolically accessible site different from the ryanodine binding site.
-:-SUBCELLULAR LOCATION: Secreted.
-:-SUBCELLULAR LOCATION: Secreted.
-:-TISSUE SPECIFICITY: Expressed by the venom gland.
                                                                        MEDIINE=98232223; PubMed=9565405; Tripathy A., Resch W., Xu L., Valdivia H.H., Meissner G.; Ingeratoxin A induces subconductance states in Ca2+ release channels (ryanodine receptors) of cardiac and skeletal muscle."; J. Gen. Physiol. 111:679-690(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                           "Imperatoxin A enhances Ca(2+) release in developing skeletal muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=13;
MEDLINE=21664373; PubMed=11792842; DOI=10.1073/pnas.022493799;
Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
"Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clostridium perfringens.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . 9
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                                                                                                                                                                                                                                                         FUNCTION ON RYR3.
MEDLINE=21855993; PubMed=11867448;
Nabhani T., Zhu X., Simeoni I., Sorrentino V., Valdivia H.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 53; DB 1; Length 33;
Pred. No. 13;
2; Mismatches 4; Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 53; DB 2; Length 85;
Pred. No. 31;
5; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- SIMILARITY: Belongs to the scorpion calcine family. Calcium channel inhibitor; Direct protein sequencing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  By similarity.
By similarity.
By similarity.
DODF8EFFFE294537 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 flesh-eater.";
Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
EMBL; AP001319; BAB81092.1; -..
PRINTS; PRO0003; 4DISULPHCORE.
Complete Protecome; Hypothetical protein.
SEQUENCE 85 AA; 9440 MW; 90EA03381BBDB681 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
11-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein CPE1386.
OrderedLocusNames=CPE1386;
Proc. Natl. Acad. Sci. U.S.A. 89:12185-12189(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       channel inhibitor; Neurotoxin; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 CFQHL-----DDCCSRKCNR 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 CLPHLKRCKADNDCCGKKCKR 23
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37.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION ON RYR1 AND RYR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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us-10-627-685a-26.rup

CRIXNO-KCFQHLDDCCSRK-----CNRFNKC 26

RESULT 79

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Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P., Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A., "Sequence and analysis of chromosome 2 of Dictyostellum discoideum."; Nature 418:79-85(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bevan M., Stiekema W., Murphy G., Wambutt R., Pohl T., Terryn N., Kreis M., Kavanagh T., Entian K.D., Rieger M., James R., Puigdomenech P., Hatzopoulos P., Obermaier B., Duesterhoft A., Jones J., Palme K., Ansorge W., Delseny M., Bancroft I., Mewes H.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress)

Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein d13245w (Hypothetical protein AT4g14110)
(Putative bHLH transcription factor).
Name=d13245w; Synonyms=AT4g14410;
                                                                                                                                                                                                                                                                                                  MEDLINE-22092622; PubMed=12097910; DOI=10.1038/nature00847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32.9%; Score 53; DB 2; Length 234; 40.0%; Pred. No. 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAR.2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AC116305; AA052288.1; -.
Hypothetical protein.
SEQUENCE 234 AA; 27944 MW; BB426ECDAF9B3032 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EU Arabidopsis sequencing project;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schueller C., Chalwatzis N.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                            Dictyostelium discoideum (Slime mold).
Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
NCBI_TaxID=44689;
                                                                                                                        01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Hypothetical protein.
                                                                         234 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | :|: | :|: | :|| 36 ITNENIFNKNYLNKCCNCKINNYNK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 IXNOKCF--OHLDDCCSRKCNRFNK 25
                                                                                                          (TrEMBLrel. 24, Created)
                                                                       PRT;
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                                                                     PRELIMINARY;
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                                                                                                          -JUN-2003
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                                                                                                                                                                                                                                                                                  STRAIN=AX4;
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                            RESULT 81
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Matches
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                                                                                                                                                                                                                                                                                                                                                                              STRAIN=52 / LL;
Hendrickson E.L., Kaul R., Zhou Y., Bovee D., Chapman P., Chung J.,
Conway de Macario E., Dodsworth J., Gillett W., Graham D.E.,
Haydock A.K., Kang A., Land M.L., Levy R., Lie T.J., Major T.,
Moore B., Porat I., Overbeek R., Palmeiri A., Rouse G.,
Saenphimmachak C., Soll D., Whitman W.B., Larimer F.W., Olson M.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Notch-like protein la (Fragment).
Griffithsia japonica (Red alga).
Eukarycta; Rhodophyta; Florideophyceae; Ceramiales; Ceramiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete genome sequence of the mesophilic hydrogenotrophic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 53; DB 2; Length 191;
Pred. No. 63;
6; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        methanogen Methanococus maripaludis.";
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
BMBL; BMS57220; CAF30170.1;
InterPro; IRNO5025; FMN red.
Pfam; PF03358; FMN red.
Complete proteome.
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                                                                                                                                                                                                                                                                                      Archaea; Euryarchaeota; Methanococci; Methanococcales; Methanococcaceae; Methanococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu C.L., Lee Y.K., Lee H.K.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY123122; AAM93994.1;
NON_TER 225 225
                                                                                                                                                                            05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Related to iron-sulfur flavoprotein of Methanosarcina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191 AA; 21019 MW; BCF6A6F18BDF7163 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              225 AA; 25897 MW; 1D93A3AA1531D058 CRC64;
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191 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     225 AA
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05-JUL-2004 (TrEMBLrel. 27, Last seg
05-JUL-2004 (TrEMBLrel. 27, Last ann
                                                                                                                  PRT;
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                                                                                                                                                                                                                                                   OrderedLocusNames=MMP0614;
                                                                                                                                                                                                                                                                      Methanococcus maripaludis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 38.13
Best Local 8; Conservative
                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=39152;
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                                                                                                            Q6LZL1
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RESULT 80 Q7XZ30

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Query Match
Best Local Similarity 58.8
Matches 10; Conservative
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                                                                                                                                                                                                                                                      Pfam; PF00010; HLH; 1.
SMART; SM00353; HLH; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Waterston R.;
Submitted (NOV-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wilson R.;
Submitted (AUG-2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-Bristol N2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-Bristol N2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                               Hypothetical
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     044635;
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                     MEDLINE=22598051; PubMed=12679534; DOI=10.1093/molbev/msg088; Heim M.A., Jakoby M., Werber M., Martin C., Weisshaar B., Bailey P.C.; "The basic helix-loop-helix transcription factor family in plants: a genome-wide study of protein structure and functional diversity."; Mol. Biol. Evol. 20:735-747(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
05-UL-2004 (TrEMBLrel. 27, Last annotation update)
A74g14410/d13245w (Hypotherical protein).
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Shinn P., Chenk R., Kim C.J., Meyers M.C., Banh J.,
Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou P.
Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shinn P., Chen H., Cheuk R., Kim C.J., Banh J., Bowser L.,
Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
                                                                                                                                                                                     TISSUE=Whole plant;
Jakoby M.J., Heim M.A., Bailey P., Martin C., Weisshaar B.;
Jakoby M.J., Heim M.A., Bailey P., Martin C., Weisshaar B.;
Submitred (FEB-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Conteains 1 basic helix-loop-helix (bHLH) domain.
EMBL; 297336; CAB10220.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32.9%; Score 53; DB 2; Length 277; 58.8%; Pred. No. 88; ive 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brower V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell Feldmann K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00010; HLH; 1. SMART; SM00353; HLH; 1. SMART; SM00353; HLH; 1. HPROSITE; PSS0088; HLH; 1. Hypothetical protein. SEQUENCE 277 AA; 31190 MW; 17D79957B8B77B48 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   annotation.";
Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                       EMBL; AL161538; CAB78483.1; -. EMBL; AF4886238; AAM10963.1; -. PIR; B71406; B71406. InterPro; IPR001092; HLH_basic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106 EHLDDDCSRKRARTGSC 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10; Conservative
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TISSUE=Whole plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Q8L467;
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Gaps
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Rhabditidae, Peloderinae, Caenorhabditis.
Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Jin J., Miranda M., Narusaka M., Nguyen M., Ondodera C.S., Palm C.J., Quach H.L., Sakurai T., Sarou M., Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S. Shinozaki K., Davis R.W., Theologis A., Ecker J.R., Submitted (JUL-2002) to the BMBL/GenBank/DDBJ databases.
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STRANTE-Briscol N2;
MEDLINE-99069613; PubMed-9851916;
WormBase Consortium;
"Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 53; DB 2; Length 283;
Pred. No. 89;
1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wilson R.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Davidson S., Wohldmann P., Bauer C., O'Neal D.;
"The sequence of C. elegans cosmid F16B4.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
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Wilson R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                             AB758D25A07E12BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 421 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1998 (TrEMBLrel. 06, Created)
01-OCT-2003 (TrEMBLrel. 25, Last seq
01-MR-2004 (TrEMBLrel. 26, Last ann
Hypothetical protein F1684.9.
Name-F1684.9; ORFNames=F1684.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                               EMBL; AY133565; AAM91395.1; -. InterPro; IPR01092; HLH_basic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AY102106; AAM26676.1; -. EMBL; AY088053; AAM65599.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                  l protein.
283 AA; 31995 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32.9%;
58.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 QHLDDCCSRKCNRFNKC
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InterPro; IPR001211; PhospholipaseA2
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NCBI_TaxID=7654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         016004;
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Matches
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016004
                           DR DR DR DR KW KW KW SQ
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RC STRAINBAILSTOOLN.A.

RC WormBase Consortium,

Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.

CC -1 SUBCELLULAR LOCATION: Nuclear (By similarity).

-1 SINGLARITY: Belongs to the nuclear hormone receptor family.

BRBL, AF039048; AAB94240.2; -..

BR GO; GO:0003700; FISBA.9.

BR GO; GO:0003700; FISBA.9.

BR GO; GO:0003700; F: transcription factor activity; IEA.

BR InterPro; IPR009346; Str ncl. receptor.

BR InterPro; IPR00946; Str ncl. receptor.

BR InterPro; IPR00935; Str C4steroid.

BR PRINTS; PR00043; STROIDFINGER.

BR PRINTS; PR000435; AR C4steroid, 1.

BR PRART; SM00439; ADR C4steroid; 1.

BR SWART; SM00439; ABP C44:

BR PRODER: 421 AA; 48753 MW; 04720B0S20F4FS9C CRC64;
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anopheles Genome Sequencing Consortium, Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shortgun (WGS) entry which is preliminary data.
EMBL; AAABO1008859; EAA07783.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32.9%; Score 53; DB 2; Length 421; 40.7%; Pred. No. 1.3e+02; Live 4; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07QCT2;
01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP, P00740; IEDM.

GO: GO: 0005509; F: calcium ion binding; IEA.
InterPro; IPR00152; Asx hydroxyl S.
InterPro; IPR001525; Con like lec_gl.
InterPro; IPR000742; EGF 2.
InterPro; IPR001491; EGF 2.
InterPro; IPR001491; EGF 1.
InterPro; IPR001491; EGF 1.
InterPro; IPR001491; EGF 1.
InterPro; IPR001491; EGF 1.
InterPro; IPR001791; Laminin G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AgCP1804 (Fragment).
Name=agCG51928; ORFNames=ENSANGG0000014325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1286 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CRIXNOKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 CRGGMNKCIVNTNDRYQCRLCRFNKCV 98
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LRR_Nterm.
LRR_typ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 40.7
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000372;
InterPro; IPR003591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR000483;
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Q7QCT2
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Lytechinus variegatus (Sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Temnopleuroida; Toxopneustidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=97454256; PubMed=9310331;
Sherwood D.R., McClay D.R.;
"Identification and localization of a sea urchin Notch homologue:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      insights into vegetal plate regionalization and Notch receptor regulation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match
Local Similarity 33.3%; Score 53; DB 2; Length 128
Local Similarity 33.3%; Pred. No. 3.4e+02;
es 8; Conservative 4; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE 1286 AA; 144156 MW; EE919D876B21BB3E CRC64;
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| RembL, AF000634; AAB82088.1; -... |
| PIR, T31070; T31070.
| R HSCP; POL132; 18GF.
| GO; GO:0016020; C:membrane; IEA.
| GO; GO:0016020; C:membrane; IEA.
| GO; GO:0005039; P:cell differentiation; IEA.
| GO; GO:0005039; P:cell differentiation; IEA.
| GO; GO:0050793; P:regulation of development; IEA.
| R GO; GO:0050793; P:regulation of development; IEA.
| InterPro; IPR00115; ASE.
| InterPro; IPR00115; ASE.
| InterPro; IPR001891; EGF. I... |
| InterPro; IPR001891; EGF. II... |
| InterPro; IPR001801; IAC. |
| Inter
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 2531 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00022; EGF 1; 7.
PROSITE; PS00186; EGF 2; 4.
PROSITE; PS5026; EGF 3; 7.
PROSITE; PS01187; EGF 3; 7.
PROSITE; PS01187; EGF 26; 2.
PROSITE; PS01187; EGF 26; 2.
PROSITE; PS0119; PA2_ASP; UNKNOWN 1.
EGF-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            801 TGSRCEVNIDDCVGHKCQNNGTCV 824
PÉGN, PP00008; EGF; 7.

PÉGN; PF01463; LRRCT; 3.

PÉGN; PF01462; LRRNT; 3.

PEGN; PR00560; LRR 1; 14.

PRINTS; PR00010; EĞPBLOOD.

PROSITE; PS00010; ASX HYDRY.

PROSITE; PS01186; CTCK 1; 1.

PROSITE; PS0125; CTCK 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 XNOKCFQHLDDCCSRKCNRFNKCV 27
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MEDLINE-98250176; PubMed-9590294;

MEDLINE-98250176; PubMed-9590294;

MEDLINE-98250176; PubMed-9590294;

Ordentlich P., Kadesch T., Attavanis-Tsakonas S.;

Ordentlich P., Kadesch T., Attavanis-Tsakonas S.;

"Human deltex is a conserved regulator of Notch signalling.";

I. Nat. Genet. 19:74-78(1998).

- I- FUNCTION: Functions as a receptor for membrane-bound ligands
Jaggedl, Jagged2 and Deltal to regulate cell-fate determination.

C Jupon ligand activation through the released notch intracellular domain (NICD) it forms a transcriptional activator complex with RBP-J kappa and activates genes of the enhancer of split locus.

Affects the implementation of differentiation, proliferation and apportic programs May be important for normal lymphocyte current for normal lymphocyte complex with apportic programs. May be important for normal lymphocyte contribute to transformation or progression in some T-cell neoplasms. Involved in the maturation
                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SECUENCE OF 1-2444 FROM N.A. MRDIALLINE-91347367; PubMed=1831692; DOI=10.1016/0092-8674(91)90111-B; Blisen L.W., Bird J., West D.C., Soreng A.L., Reynolds T.C., Smith S.D., Sklar J.; West D.C., Soreng A.L., Reynolds T.C., "TMAN J., the human homolog of the Drosophila notch gene, is broken by cellomosomal translocations in T lymphoblastic neoplasms."; cell 66:649-661(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gray G.E., Mann R.S., Mitgiadis E., Henrique D., Carcangiu M.-L., Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Teakonas S. "Human ligands of the Notch receptor."; Am. J. Pathol. 154:785-7867999).
                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (Rel. 32, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FCB-2005 (Rel. 46, Last annotation update)
Neurogenic locus notch homolog protein 1 precursor (Notch 1) (hN1)
(Translocation-associated notch protein TAN-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                              ö
                                                                                                                                                                                  32.9%; Score 53; DB 2; Length 2531; 45.0%; Pred. No. 6.2e+02;
                                                                                                                                                       2531 AA; 273982 MW; 5BF42BEC627CA303 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mann R.S., Blaumueller C.M., Zagouras P.;
"Complete human notch 1 (hN1) cDNA sequence.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                             3; Mismatches
                                           PROSITE; PS50089; ANK REPEAT; 5.
PROSITE; PS50297; ANK REP REGION; 1.
PROSITE; PS00100; ASX_HYDROXYL; 21.
PROSITE; PS00102; EGF 1; 33.
PROSITE; PS01186; EGF 2; 25.
PROSITE; PS01186; EGF 2; 35.
PROSITE; PS01187; EGF CA; 20.
ANK repeat; EGF-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99180765; PubMed=10079256;
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                                                                                                                                                                                                                                        8 CFQHLDDCCSRKCNRFNKCV 27
SMART; SMO0248; ANK; 6.
SMART; SMO0179; EGF_CA; 23.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=NOTCH1; Synonyms=TAN1;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDENTIFICATION OF LIGANDS.
                                                                                                                                                                                             Local Similarity 45.0 tes 9; Conservative
                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                     NTC1_HUMAN
                                                                                                                                                        SEQUENCE
                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                   P46531;
                                                                                                                                                                                                                                                                                                         RESULT 87
NTC1 HUMAN
                                                                                                                                                                                                              Matches
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brain stem and lung. Also present in most adult tissues where it is found mainly in lymphoid tissues.

-!- PTM: Synthesized in the endoplasmic reticulum as an inactive form which is proteolytically cleaved by a furin-like convertase in the trans-Golgi network before it reaches the plasma membrane to yield an active, ligand-accessible form. Cleavage results in a C-terminal fragment N(TM) and a N-terminal fragment N(EC). Following ligand binding, it is cleaved by TNF-alpha converting enzyme (TACE) to yield a membrane-associated intermediate fragment called notch-derived peptide containing the intracellular domain (NICD) from the membrane (By similarity).

First the membrane (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                           SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-terminal fragment N(EC) which are probably linked by disulfide bonds (By similarity). Interacts with DTX1 and DTX2.
SUBCELLULAR LOCATION: Type I membrane protein. Following proteolytical processing NICD is translocated to the nucleus (By
                                                                                                                                                                                                                                                        TISSUE SPECIFICITY: In fetal tissues most abundant in spleen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIM: Phosphorylated (By similarity).
DISEASE: NOTCH1 truncation is associated with T-cell acute
both CD4+ and CD8+ cells in the thymus (By similarity)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0016021; C:integral to membrane; NAS.
GO; GO:0016955; P:immune response; NAS.
InterPro; IPR00110; ANK.
InterPro; IPR000122; Ask. hydroxyl_S.
InterPro; IPR00143; EGF_2.
InterPro; IPR00143; EGF_I.
InterPro; IPR001438; EGF_II.
InterPro; IPR001438; EGF_II.
InterPro; IPR001609; NOD.
InterPro; IPR010609; NOD.
InterPro; IPR010609; NOT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- SIMILARITY: Belongs to the NOTCH family.
-1- SIMILARITY: Contains 5 ANK repeats.
-1- SIMILARITY: Contains 35 EGF-like domains.
-1- SIMILARITY: Contains 3 Lin/Notch repeats.
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PROSITE; PS50297; ANK_REP_REGION; 1.
PROSITE; PS00010; ASX_HYDROXYL; 20.
PROSITE; PS00022; EGF_1; 34.
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PIRSF; PIRSF002279; Notch; 1.
PRINTS; PR01415; ANKYRIN.
PRINTS; PR00010; EGFBLOOD.
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2; 26.
3; 36.
CA; 18.
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SMART; SM00179; EGF_CA; 23.
SMART; SM00004; NL; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genew; HGNC:7881; NOTCH1.
MIM; 190198; -.
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Pfam; PF00008; EGF; 35.
Pfam; PF06816; NOD; 1.
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GGF-like 11, calcium-binding (Potential).

EGF-like 12, calcium-binding (Potential).

EGF-like 13, calcium-binding (Potential).

EGF-like 14, calcium-binding (Potential).

EGF-like 15, calcium-binding (Potential).

EGF-like 16, calcium-binding (Potential).

EGF-like 19, calcium-binding (Potential).

EGF-like 20.

EGF-like 21, calcium-binding (Potential).

EGF-like 21, calcium-binding (Potential).

EGF-like 22.

EGF-like 23, calcium-binding (Potential).

EGF-like 23, calcium-binding (Potential).

EGF-like 24.

EGF-like 25, calcium-binding (Potential).

EGF-like 26.
                                                                                                                                                                                                                                                                                                     EGF-11ke 28.

EGF-11ke 29.

EGF-11ke 31.

EGF-11ke 31.

EGF-11ke 32.

EGF-11ke 33.

EGF-11ke 34.

EGF-11ke 35.

EGF-11ke 36.

Lin/Notch 1.

Lin/Notch 2.

Lin/Notch 2.

Lin/Notch 3.

ANK 2.

ANK 3.

ANK 4.

ANK 5.
                                                                                                                                               (Potential). (Potential). (Potential).
                                            protein
                                                                                                                                   (Potential)
Notch signaling pathway; Phosphorylation; Receptor; Repeat; Signal; Signal, SignAL 18 Potenfish CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cleavage (by furin-like protease)
                                 Potential.
Neurogenic locus notch homolog
Notch extracellular truncation
                                                              Notch intracellular domain (By
                                                                                                                                              calcium-binding (calcium-binding (calcium-binding )
                                                                                                                                calcium-binding
                                                                      similarity).
Extracellular (Potential).
                                                                                             Cytoplasmic (Potential)
EGF-like 1.
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                                                                                                                EGF-like 3.
EGF-like 4.
EGF-like 5, c
EGF-like 7, c
EGF-like 8, c
EGF-like 9, c
EGF-like 10.
                                                        similarity)
                                                                                      Potential.
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Poly-Gly.
Poly-Gln.
Poly-Pro.
Poly-Ser.
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y-Glu.
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Poly-Arg.
Poly-Pro.
Poly-Ala.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Phylogenet. Evol. 22:333-341(2002).
FUNCTION: Protamines substitute for histones in the chromatin of sperm during the haploid phase of spermatogenesis. They compact sperm bNA into a highly condensed, stable and inactive complex (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1] -
SEQUENCE FROM N.A.
MEDLINE=21881971; PubMed=11884158; DOI=10.1006/mpev.2001.1051;
Wan Den Bussche R.A., Hoofer S.R., Hansen E.W.;
"Characterization and phylogenetic utility of the mammalian protamine
                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF435940; AAL35574.1; -
EMBL; AF435940; AAL35574.1; -
Plan; PF00260; Protamine P1.
PROSITE; PS00048; PROTAMINE P1.1.
Chromosomal protein; DNA condensation; DNA-binding; Nuclear protein; Nucleosome core; Spermatogenesis; Testis.
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                                                                                                                                                                                                                                                                                                                                                                           Plecotus townsendii (Townsend's big-eared bat).
Bukaryota; Metazoa; Chordata; Craniata; Vortebrata; Euteleostomi;
Mammalia; Butheria; Chiroptera; Microchiroptera; Vespertilionidae;
Corynorhinus.
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                                                                                             Score 53; DB 1; Length 2556;
Pred. No. 6.3e+02;
4; Mismatches 12; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity).
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
-!- TISSUE SPECIFICITY: Testis.
-!- SIMILARITY: Belongs to the protamine P1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B4670EB886CEDB19 CRC64;
                                                                                                                                                                                                                                                                                            25-OCT-2004 (Rel. 45, Created)
25-OCT-2004 (Rel. 45, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
   / similarity.
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32.6%; Score 52.5; I
Best Local Similarity 26.7%; Pred. No. 21;
Matches 8; Conservative 8; Mismatches
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250 TGQNCEENIDDCPGNNCKNGGACV 273
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ilarity 33.3%;
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8; Conserva
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Q8WNZ0;
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Schistosomatoidea; Schistosomatidae; Schistosoma
NCBI_TaxID=6182;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochim. Biophys. Acta 1350:247-252(1997).
                                                                                                                                                                                                                                      1 CRIXNOKCFQHLDDCCSRKCNRFN 24
                                                                                                                                                                                                                                                           66 CLPDKQQCRRN-KDCCSKSCYRGN 88
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                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 03, Created)
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Name=P0016F11.13;
                                                                     Yu_C., Zhang F., Mihoko K., M. Submitted (MAR-2004) to the E. EMBL, AYS70752; AAS68257.1; - SEQUENCE 92 AA, 10345 MW,
                                                                                                                                                              32.6%;
                                                                                                                                                                             Local Similarity 41.7 tes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 10; Conserv
                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=3349;
                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1997
                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QEKSW7;
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                                                                                                                                                                                                                                                                                                                                                                P93773
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 SOREARISO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ä
                                                                                                                                                                                                                                Kamoun S.;
Patterns of Diversifying Selection in the Phytotoxin-like scr74 Gene Family of Phytophthora infestans.";
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY723722; AAU21463.1;
EMBL; AY723721; AAU21462.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kamoun S.;
"Patterns of Diversifying Selection in the Phytotoxin-like scr74 Gene Family of Phytophthora infestans.";
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY723720; AAU21461.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Egg protein CP422.
Name=CP422;
Schistosoma japonicum (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                Liu Z., Bos J.I.B., Armstrong M., Whisson S.C., da Cunha L.,
Torto-Alalibo T., Win.J., Avrova A.O., Wright F., Birch P.R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Liu Z., Bos J.I.B., Armstrong M., Whisson S.C., da Cunha L.,
Torto-Alalibo T., Win J., Avrova A.O., Wright F., Birch P.R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ä
                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phytophthora infestans (Potato late blight fungus).
Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32.6%; Score 52.5; DB 2; Length 74; 34.6%; Pred. No. 32;
                                                                                                         Bukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                       10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57A8231D29AB5F8F CRC64;
                25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Phytoxin-like SCR74.
Phytophthora infestans (Potato late blight fungus).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                              32.6%; Score 52.5; C
34.6%; Pred. No. 32;
tive 6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |::| ::| ::| CKAINAEPVA-FNDCCSKSCNTGSPC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | : : | : : | | : | | : | CKAINAEPVA-FNDCCSKSCNTGSPC 71
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                                                                                                                                                                                                                                                                                                                                                                                                  ilarity 34.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7802 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 34.6
nes 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phytoxin-like SCR74.
                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 9; Conserv
                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 AA;
                                                                                                                                             NCBI_TaxID=4787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phytophthora.
NCBI_TaxID=4787;
                                                                                                                        Phytophthora
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05-JUL-2004
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                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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Q646U7
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Matches
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Q6PYV0
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CORPORATION

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TISSUB=Needles;
MEDLINE=972146737; PubMed=9061017; DOI=10.1016/S0005-2760(96)00161-0;
MEDLINE=972146737; PubMed=9061017; DOI=10.1016/S0005-2760(96)00161-0;
Wegener A., Gimbel W., Werner T., Hani J., Ernst D., Sandermann H.;
"Molecular cloning of ozone-inducible protein from Pinus sylvertris L.
with high sequence similarity to vertbrate 3-hydroxy-3-methylglutaryl-
                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BINGLY 1805. 1863. CARSESSO. 1; -...
PIR; T09688; T09688. CO; GO:000421; F:hydroxymethylglutaryl-CoA synthase activity; IEA. GO; GO:0006421; F:hydroxymethylglutaryl-CoA synthase activity; IEA. InterPro; IPR000886; ER target S. InterPro; IPR000886; ER target S. InterPro; IPR008860; HWG CoA synth. InterPro; IPR010122; HWG CoA synth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Coniferopsida, Coniferales, Pinaceae, Pinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza sativa (japonica cultivar-group).
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzees, Oryza.
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                                                                                                                                                              92;
Masahiro I., Zhu Y., Hirayama
EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                          DB 2; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFam; PF01154; HMG COA Synt; 1.
TIGRPAMS; TIGR01833; HMG-COA-S euk; 1.
PROSITE; PS00014; ER TARGET; UNKNOWN 1.
SEQUENCE 474 AA; 52998 MW; 3ECB48ESF23D37BA CRC64;
                                                                                            052F01B53D379F5F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
3-hydroxy-3-methylglutaryl-CoA-synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL-2004. (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                               8,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                474 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
Hypothetical protein F46B3.9.
ORFNames=46B3.9.
Caenorhabditis elegans.
Bukaryota, Metazoa; Nematoda, Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                         Direct protein sequencing; Glycoprotein; Lectin; Phosphorylation; Repeat; Signal; Transmembrane. SIGNAL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Potential).
(Potential).
(Potential).
(Potential).
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(Potential).
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                                                                                                                                                                                                                                                                                                                                                                          X approximate tandem repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of the nematode C.elegans: A platform for investigating biology.";
Science 282:2012-2018(1998).
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              > G (in Ref. 3).
64BB2DFD2AD8ECBA CRC64;
                                                                                                                                                                                                                                                                                                         Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                         Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                     170 kDa surface lectin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 52.5; DB 1;
Pred. No. 3.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlcNAc.
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                                                                                                                                                                                                                                                                                                                        Potential
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N-linked
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N-linked
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G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144410 MW;
                                                                                                                                                                                           EMBL; M60498; AAA29106.1; -. EMBL; X61003; CAA43321.1; -.
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12; Conservative
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                      transduction.
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                                                                                                                                                                                                                                                                                   CHAIN
DOMAIN
TRANSMEM
DOMAIN
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
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REPEAT
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Q9XV21;
                                                                                                                                                                                                                                                                                                                                                                                                                         REPEAT
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REPEAT
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                                              Lasaki T., Matsumoto T., Katayose Y.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

E. Submitted (MAY-2002) F. Pare Inding; IEA.

E. GO; GO:0005524; F. Pare Inding; IEA.

E. GO; GO:00064664; F. Piprotein serine/threonine kinase activity; IEA.

E. GO; GO:0006464; F. Piprotein amino acid phosphorylation; IEA.

E. GO; GO:0006464; F. Piprotein amino acid phosphorylation; IEA.

E. R. InterPro; IPR001291; For Kinase interPro; IPR001291; For the pkinase.

E. InterPro; IPR001291; For the pkinase.

E. Endom; PD000001; Frot kinase; 1.

E. SMART; SM00129; FYRC; 1.

E. SMART; SM0019; ERCP CA; 1.

E. SMART; SM0010; ERCP CA; 1.

E. SMART; ERCP CA; 1.

E. 
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J. Balol. Chem. 264:3007-3012(1989).
-!- FUNCTION: Mediates adherence of E.histolytica to colonic mucins, an essential step for pathogenic tissue invasion.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- PIM: Phosphorylated regions may have a role in signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 16-30.
MEDLINE=89123408; PubMed=2536731;
Petri M.A. Jr., Chapman M.D., Snodgrass T., Mann B.J., Broman J.
Ravdin J.I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15;
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MEDLINE=91156704; PubMed=2000392;
Tannich E., Ebert F., Horstmann R.D.;
"Primary structure of the 170-kDa surface lectin of pathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.6%; Score 52.5; DB 2; Length 7
26.2%; Pred. No. 2.5e+02;
Live 6; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        280 CRSTNSECFDTIDGGGYRCNCCQGYEGNPYLDGGCTDINECL 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REVISIONS TO N-TERMINUS.
Tannich E., Nickel R., Ebert F.; Horstmann R.D.;
Submitted (AUG-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               764 AA; 85266 MW; SECABSIB666C88C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CRIXNQKCFQHLD-----DCC-----SRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Entamoeba histolytica.";
Proc. Natl. Acad. Sci. U.S.A. 88:1849-1853(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1991 (Rel. 20, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1285 AA
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Name=CEL-170/4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 26.28
Matches 11, Conservative
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                                   SEQUENCE FROM N.A.
   NCBI_TaxID=39947;
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Gaps

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Pfam; PF00008; EGF; 8
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Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.

FlyBase; FBgn00000368; czb.
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Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.3%; Score 52; DB 2; Length 354; 35.7%; Pred. No. 1.4e+02; ive 5; Mismatches 11; Indels
                                                                                                                       Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                         354 AA; 37229 MW; 5769BF095E8E03F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                158 CKLVNGSPKCVPELDQCSHIKCSIGSHC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CRIXN--QKCFQHLDDCCSRKCNRFNKC 26
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                                                                                                                                                      EMBL, Z81540, CAB04398.1, -.
PIR, T22274, T22274
Wormbase, WBGene00009762, F46B3.9.
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                                                                                                                                                                                                                                                               Mormbep; F46B3.9; CE18691.
InterPro; IPR003645; F01 N.
SMART; SM00274; F0LN; 8.
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                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein. SEQUENCE 354 AA; 3
                                                  STRAIN=Bristol N2;
FROM N.A.
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                                                                                     Ainscough R.;
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08MSXS
AC 08MSXS
AC 08MSXX
AC 08MSXX
AC 01-0CC
DT 01-0CC
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           SKA D D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C D D R L A C 
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MEDLINE=21966109; PubMed=11970894; DOI=10.1016/S1534-5807(02)00142-9;
Cohen E.D., Mariol M.-C., Wallace R.M.H., Weyers J., Kamberov Y.G.,
Pradel J., Wilder E.L.;
"DWnr4 regulares cell movement and focal adhesion kinase during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2005 (Rel. 46, Last annotation update)
Whit-4 procesh precursor (dWnt. 4).
Name=Whit; Synonyms=Whit-4; ORFNames=CG4698;
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Bukaryota; Ephydroidea; Brosophila;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        32.3%; Score 52; DB 2; Length 487; 30.4%; Pred. No. 1.9e+02; ive 6; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                  487 AA; 52498 MW; C69E5B14E36B3D22 CRC64;
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Pfam, PF00054; Laminin G 1; 1.

PRINTS; PR00010; EGFBLÖOD.

SMART; SMO0179; EGF CA; 3.

PROSITE; PS00022; EGF 1; 7.

PROSITE; PS01186; EGF 2; 6.

PROSITE; PS01186; EGF 2; 6.

PROSITE; PS01025; EGF 3; 4.

PROSITE; PS00025; LAM G DOMAIN; 1.
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Dev. Cell 2:437-448(2002).
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                               EGF-like domain.
SEQUENCE 487 A
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Referring N.L., Berrys D.A., Benner T.J., Bernandez J.R., Houck J., R. Mostin D. F., Goldisa C.D., Kreft C.K., Kradicz S., Kill D. M., Kallen F., Kaper C.H., Kez K. R., Kallen D., Linzary Y. Lin X., March B. W., Malton E., Kodisa C.D., Kreft C.K., Kradicz S., Kill D. M., Malson D., R. M. Marcel B., Martine B., Martine B., Kodisa C.D., Kreft C.K., Kardicz S., Kill D. M., Malson D., R. M. Marcel B., Martine B., Martine B., Will D. M., Malson D., R. M. Marcel B., Martine B., Walthon R.V., Welden W.P., Melber D. D. M., Malson D. M.,
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MEDLINE=20245325; PubMed=10781962; DOI=10.1016/S0925-4773(00)00280-X;
Kuriyama S., Miyatani S., Kinoshita T.;
"Xerl; a novel secretory protein expressed in eye and brain of Xenopus
PRINTS; PR01349; WNTPROTEIN.
SMART; SM00097; WNT1; 1.
PROSITE; PS00246; WNT1; 1.
Whe signaling pathway; Glycoprotein; Lipoprotein; Palmitate; Signal; Signal.
                                                                                                                                                                                                                                                                            Gaps
                                                                                            Wnt-4 protein.

N-linked (GlcNAc. ..) (Potential).
N-linked (GlcNAc. ..) (Potential).
N-linked (GlcNAc. ..) (Potential).
S-palmitoyl cysteine (By similarity).
F -> L (in Ref. 1).
G -> R (in Ref. 1).
F -> A (in Ref. 5).
R -> A (in Ref. 5).
R -> A (in Ref. 5).
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                                                                                                                                                                                                                                            32.3%; Score 52; DB 1; Length 539; 39.1%; Pred. No. 2.1e+02; ive 5; Mismatches 9; Indels
                                                                                                                                                                                                                       6682C8B3D729D067 CRC64;
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GO; GO:0005199; F:calcium ion binding; IEA.
GO; GO:0007155; P:cell adhesion; IEA.
InterPro; IPR000152; Asx hydroxyl S.
InterPro; IPR000742; EGF Z.
InterPro; IPR000742; EGF Z.
InterPro; IPR001881; EGF Z.
InterPro; IPR001881; EGF Z.
InterPro; IPR001881; EGF Z.
InterPro; IPR001881; EGF Z.
InterPro; IPR001919; EGF Z.
InterPro; IPR001919; EGF Z.
InterPro; IPR001919; Laminin G.
InterPro; IPR001919; Laminin G.
Pfam; PF00200; EGF; 12.
Pfam; PF00200; EGF; 12.
Pfam; PR00109; EGF; CA; G.
SMART; SM0019; EGF CA; G.
                                                                                                                                                                                                                                                                                                             514 CRFNNGRCCQLICDYCQRLENKY 536
                                                                                                                                                                                                                                                                                             1 CRIXNOKCFOHLDDCCSRKCNRF 23
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01-OCT-2000 (TrEMBLrel. 15, Last sec
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                                                                                                                                                                                                                      58685 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mech. Dev. 93:233-237(2000).
EMBL; AB027453; BAA95001.1; -.
HSSP; Q12780; 1HAE.
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                                                                                                                                                                                                                                                        Local Similarity 39.1 tes 9; Conservative
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                                                                                                                                                                                                         532 :
539 AA;
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                                                                                            CHAIN
                                                                                                                   CARBOHYD
CARBOHYD
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                                                                                                                        Gaps
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Murphy L., Quail M., Harris D., Hall N., Wakefield A., Smulian A.G.,
Cushion M.T., Stringer J.R., Keely S.E., Barrell B.G.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Crumbs encodes an EGF-like protein expressed on apical membranes of Drosophila epithelial cells and required for organization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-GREGOR-R; TISSUE-Embryo;
MEDLINE-SP2023104; Pubmed-2344615; DOI=10.1016/0092-8674(90)90189-L;
Tepass U., Theres C., Knust E.;
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1069;
                                                                          Score 52, DB 2; Length 778;
Pred. No. 2.9e+02;
6; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 52; DB 2; Length 100:
Pred. No. 3.86+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha
Ephydroidea, Drosophilidae, Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120586 MW; 791A8C514D3BFB0B CRC64;
                                         462D2C84AE435CF6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     318 CKKALEKCDASKHLDDDLKKLCDDKTNRDAKC 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAX-1989 (Rel. 10, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CRIXNQKC--FQHLDD----CCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                      PRT; 1069 AA.
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                        Potential
                                                                                                                                                                                                  285 DGELCQODIDECQSQPCQNGGRCV 308
                                                                                                                                                             4 XNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                        Probable major surface glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Embryo;
MEDLINE=87218537; PubMed=3107986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, ALS9282; CAC43459.1; -.
InterPro; IPR003330; MSG.
Pfam; PF02349; MSG; 7.
SEQUENCE 1069 AA; 120586 MW:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1663-1955 FROM N.A.
                                       SEQUENCE 778 AA; 85516 MW;
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                                                                              Query Match
Best Local Similarity 33.3%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-OCT-2002 (TrEMBLrel. 22,
EGF-like domain; Signal.
SIGNAL 1 27
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                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell 61:787-799(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                               Pneumocystis carinii.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4754;
                                                                                                                                                                                                                                                                                                                                                                                                                        Name=PCCW03G5.13
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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"Interaction of Par-6 and Crumbs complexes is essential for
"Interaction of Par-6 and Crumbs complexes is essential for
photocreceptor morphogenesis in Drosophila.";
Development 130:4369-4372(2003).
-!- FUNCTION: Plays a central role in cell polarity establishment.
Participates in the assembly, positioning and maintenance of
adherens junctions via its interaction with the SAC complex.
Controls the coalescence of the spots of zonula adherens (ZA) into
a adhesive ring around the cells. It may act as a signal. Involved
in morphogenesis of the photoreceptor rhabdomere, for positioning
and growth of rhabdomere and AJ during the crucial period of
photoreceptor extension along the proximodistal axis of the
                                                                                                                                                                                                                                                                                                   MEDLINE=99200394; PubMed=10102271; DOI=10.1016/S0092-8674(00)80593-0; Bhat M.A., Izaddoost S., Lu Y., Cho K.-O., Choi K.-W., Bellen H.J.; "Discs Lost, a novel multi-PDZ domain protein, establishes and maintains epithelial polarity."; Cell 96:833-845(1999).
Knust E., Dietrich U., Tepass U., Bremer K.A., Weigel D., Vaessin H., Campos-Ortega J.A.;
"EGF homologous sequences encoded in the genome of Drosophila melanogater, and their relation to neurogenic genes.";
EMBO J. 6:761-766(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bhat M.A., Izaddoost S., Lu Y., Cho K.-O., Choi K.-W., Bellen H.J.;
Cell 115:765-766(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=11076972; DOI=10.1083/jcb.151.4.891;
Tanentzapf G., Smith C., McGlade J., Tapens U.;
"Apical, lateral, and basal polarization cues contribute to the development of the follicular epithelium during Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytoplasmic tail.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDENTIFICATION IN A SAC COMPLEX WITH PATJ AND SDT.
MEDLINE=21603015; PubMed=11740560; DOI=10.1038/414638a;
Bachmann A., Schneider M., Theilenberg E., Grawe F., Knust E.;
"Drogophila Stardust is a partner of Crumbs in the control of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION, AND INTERACTION WITH PATJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A35672; A35672.
PIR; B26637; B36637.
HSSP; P00740; 1EDM.
F) PBase; FBgn0000368; crb.
GO; GO:0016324; C:apical plasma membrane; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERACTION WITH THE PAR-6 COMPLEX.
PubMed=12900452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M33753; AAA28428.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell Biol. 151:891-904 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       epithelial cell polarity.";
Nature 414:638-643(2001).
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                                                                                                                                                                                                                                                                        INTERACTION WITH PATJ.
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Search completed: April 18, 2005, 20:37:49
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Extracellular (Potential).

Potential.

Cytoplasmic (Potential).

EGF-like 1.

EGF-like 2.

EGF-like 3.

EGF-like 4.

EGF-like 6.

EGF-like 10.

EGF-like 10.

EGF-like 10.

EGF-like 10.

EGF-like 11.

EGF-like 11.

EGF-like 12.

EGF-like 13.

EGF-like 13.

EGF-like 14.

Calcium-binding (Potential).

EGF-like 13.

EGF-like 14.

EGF-like 15.

EGF-like 16.

EGF-like 17.

EGF-like 17.

EGF-like 18.

EGF-like 19.

EGF-like 20.

Laminin G-like 2.

EGF-like 21.

EGF-like 21.

EGF-like 22.

EGF-like 23.

EGF-like 24.

EGF-like 25.

EGF-like 26.

EGF-like 27.

EGF-like 27.

EGF-like 28.

EGF-like 29.

EGF-like 20.

E
DR GO; GO:0016327; C:apicolateral plasma membrane; IDA.

GO; GO:0016332; P:establishment and/or maintenance of cell po. .;

GO; GO:0016332; P:establishment and/or maintenance of polarit. .;

GO; GO:0016332; P:establishment and/or maintenance of polarit. .;

DR GO; GO:002009; P:morphogenesis of an epithelium; NAS.

DR GO; GO:0042084; P:photoreceptor maintenance; IMP.

GO; GO:0042084; P:photoreceptor maintenance; IMP.

DR GO; GO:0042084; P:photoreceptor maintenance; IMP.

GO; GO:0042084; P:ponula adherens assembly; IMP.

DR InterPro; IPR000152; Aax hydroxyls

InterPro; IPR000142; EGF Z.

DR InterPro; IPR000143; EGF Z.

DR InterPro; IPR00189; EGF Z.

DR InterPro; IPR00189; EGF Z.

DR InterPro; IPR00199; EGF Z.

DR InterPro; IPR00199; EGF Z.

DR Fam; PF00006; EGF Z.

DR Pfam; PF00009; EGF Z.

DR Pfam; PF00009; EGF Z.

DR RANT; SM00179; EGF Z.

DR PROSITE; PS00100; ASX LYDROXYL; 15.

DR RNAT; ENGOLOS; EGF Z.; 17.

DR RNAT
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Pred. No. 7.1e+02;
i; Mismatches 10; Indels
By similarity. By similarity.
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32.3%;
Best Local Similarity 30.4%;
Matches 7; Conservative
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